GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 16:01:58 ; Search time 27 Seconds
(without alignments)
3.571 Million cell updates/sec

Title: US-10-619-253-3
Perfect score: 4324
Sequence: 1 gtactacaaacctggcttgc.....aataaaagtgaagtgaatct 4324

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 644 seqs, 11150 residues

Total number of hits satisfying chosen parameters: 1288

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1012 summaries

Database : rge.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	39	0.9	39	1	AR003340	ACCESSION:AR003340
	2	23.8	0.6	27	1	AX662645	ACCESSION:AX662645
	3	23.8	0.6	27	1	AX662648	ACCESSION:AX662648
c	4	20.8	0.5	26	1	AR228739	ACCESSION:AR228739
	5	20.2	0.5	25	1	AX043066	ACCESSION:AX043066
c	6	20	0.5	20	1	AR373540	ACCESSION:AR373540
c	7	19.4	0.4	21	1	AR299686	ACCESSION:AR299686
c	8	18.8	0.4	23	1	S61964	ACCESSION:S61964
c	9	18.8	0.4	23	1	S61969	ACCESSION:S61969
	10	18	0.4	18	1	E32451	ACCESSION:E32451
	11	18	0.4	21	1	AX825124	ACCESSION:AX825124
	12	17.8	0.4	22	1	AX104716	ACCESSION:AX104716
	13	17.8	0.4	22	1	AX547769	ACCESSION:AX547769
c	14	17.4	0.4	19	1	CQ759632	ACCESSION:CQ759632
	15	17.4	0.4	20	1	I19906	ACCESSION:I19906
	16	17.4	0.4	20	1	BD089857	ACCESSION:BD089857
	17	17.4	0.4	20	1	AB068200	ACCESSION:AB068200
	18	17.4	0.4	21	1	A23592	ACCESSION:A23592
	19	17.4	0.4	21	1	AR074334	ACCESSION:AR074334
	20	17.4	0.4	21	1	I21708	ACCESSION:I21708
	21	17.4	0.4	21	1	AX032696	ACCESSION:AX032696
	22	17.4	0.4	21	1	AX825126	ACCESSION:AX825126
	23	17	0.4	17	1	BD142810	ACCESSION:BD142810
	24	17	0.4	17	1	BD143836	ACCESSION:BD143836
	25	17	0.4	17	1	BD167837	ACCESSION:BD167837
	26	17	0.4	17	1	BD167909	ACCESSION:BD167909
	27	17	0.4	17	1	BD168113	ACCESSION:BD168113
	28	17	0.4	17	1	BD171179	ACCESSION:BD171179
	29	17	0.4	17	1	E34260	ACCESSION:E34260
	30	17	0.4	17	1	E59657	ACCESSION:E59657
	31	17	0.4	17	1	AR256849	ACCESSION:AR256849
	32	17	0.4	17	1	AR266626	ACCESSION:AR266626
	33	17	0.4	17	1	AX671929	ACCESSION:AX671929
	34	17	0.4	17	1	AX673524	ACCESSION:AX673524
	35	17	0.4	17	1	AX737809	ACCESSION:AX737809
c	36	17	0.4	17	1	AX759616	ACCESSION:AX759616
	37	17	0.4	17	1	AX761072	ACCESSION:AX761072
	38	17	0.4	17	1	BD011732	ACCESSION:BD011732
	39	17	0.4	17	1	BD091744	ACCESSION:BD091744
	40	17	0.4	17	1	BD091752	ACCESSION:BD091752
	41	17	0.4	17	1	BD091775	ACCESSION:BD091775
	42	17	0.4	17	1	BD097336	ACCESSION:BD097336
	43	17	0.4	18	1	E32454	ACCESSION:E32454
	44	17	0.4	18	1	E32457	ACCESSION:E32457
	45	17	0.4	18	1	E32460	ACCESSION:E32460
	46	17	0.4	20	1	AR139960	ACCESSION:AR139960
	47	17	0.4	20	1	AR140279	ACCESSION:AR140279
	48	17	0.4	20	1	AR140557	ACCESSION:AR140557
c	49	17	0.4	20	1	AR142677	ACCESSION:AR142677
	50	17	0.4	20	1	E15159	ACCESSION:E15159
c	51	17	0.4	20	1	E22402	ACCESSION:E22402
c	52	17	0.4	20	1	E28096	ACCESSION:E28096
	53	17	0.4	20	1	AR562156	ACCESSION:AR562156
c	54	17	0.4	20	1	AX498246	ACCESSION:AX498246
c	55	17	0.4	21	1	AX498247	ACCESSION:AX498247
	56	17	0.4	21	1	AX825123	ACCESSION:AX825123
	57	17	0.4	21	1	AX825125	ACCESSION:AX825125
	58	17	0.4	21	1	AX825156	ACCESSION:AX825156
	59	16.8	0.4	20	1	DOGP18802	ACCESSION:L24215
c	60	16.8	0.4	20	1	AR084583	ACCESSION:AR084583
	61	16.8	0.4	20	1	AR084604	ACCESSION:AR084604
c	62	16.8	0.4	20	1	BD145051	ACCESSION:BD145051
	63	16.8	0.4	20	1	BD145062	ACCESSION:BD145062
c	64	16.8	0.4	20	1	BD166051	ACCESSION:BD166051
	65	16.8	0.4	20	1	BD166062	ACCESSION:BD166062
	66	16.8	0.4	20	1	BD228445	ACCESSION:BD228445
	67	16.8	0.4	20	1	BD230765	ACCESSION:BD230765
	68	16.8	0.4	20	1	I16926	ACCESSION:I16926
c	69	16.8	0.4	20	1	AR264947	ACCESSION:AR264947
c	70	16.8	0.4	20	1	AR350279	ACCESSION:AR350279
	71	16.8	0.4	20	1	AR359670	ACCESSION:AR359670
	72	16.8	0.4	20	1	AR437004	ACCESSION:AR437004
c	73	16.8	0.4	20	1	AR478228	ACCESSION:AR478228
c	74	16.8	0.4	20	1	BD072892	ACCESSION:BD072892
	75	16.8	0.4	20	1	BD072903	ACCESSION:BD072903
	76	16.8	0.4	20	1	BD084130	ACCESSION:BD084130
c	77	16.8	0.4	20	1	BD084130	ACCESSION:BD084130
c	78	16.8	0.4	20	1	BD107519	ACCESSION:BD107519
	79	16.8	0.4	20	1	BD107530	ACCESSION:BD107530
	80	16.8	0.4	21	1	A64735	ACCESSION:A64735
	81	16.8	0.4	21	1	A64736	ACCESSION:A64736
	82	16.8	0.4	21	1	A64738	ACCESSION:A64738
	83	16.8	0.4	21	1	A64739	ACCESSION:A64739
	84	16.8	0.4	21	1	AR540710	ACCESSION:AR540710
	85	16.8	0.4	21	1	AX825134	ACCESSION:AX825134
	86	16.8	0.4	21	1	AX825150	ACCESSION:AX825150
	87	16.8	0.4	21	1	BD056566	ACCESSION:BD056566
	88	16.4	0.4	18	1	BD145036	ACCESSION:BD145036
	89	16.4	0.4	18	1	BD166036	ACCESSION:BD166036
	90	16.4	0.4	18	1	E32450	ACCESSION:E32450
	91	16.4	0.4	18	1	E32452	ACCESSION:E32452
c	92	16.4	0.4	18	1	AR241816	ACCESSION:AR241816
	93	16.4	0.4	18	1	AR264932	ACCESSION:AR264932
	94	16.4	0.4	18	1	AR478213	ACCESSION:AR478213
	95	16.4	0.4	18	1	BD072877	ACCESSION:BD072877
	96	16.4	0.4	18	1	BD107504	ACCESSION:BD107504
	97	16.4	0.4	18	1	AB175211	ACCESSION:AB175211
	98	16.4	0.4	19	1	AX129706	ACCESSION:AX129706
	99	16.4	0.4	20	1	BD143136	ACCESSION:BD143136
	100	16.4	0.4	20	1	BD161924	ACCESSION:BD161924
	101	16.4	0.4	20	1	AR309844	ACCESSION:AR309844
c	102	16.4	0.4	20	1	AX296109	ACCESSION:AX296109
	103	16.4	0.4	20	1	AX404077	ACCESSION:AX404077
	104	16	0.4	17	1	BD142808	ACCESSION:BD142808
	105	16	0.4	17	1	BD142809	ACCESSION:BD142809
	106	16	0.4	17	1	BD143834	ACCESSION:BD143834

	107	16	0.4	17	1	BD143835
	108	16	0.4	17	1	BD167835
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	110	16	0.4	17	1	BD167907
	111	16	0.4	17	1	BD167908
	112	16	0.4	17	1	BD168111
	113	16	0.4	17	1	BD168112
	114	16	0.4	17	1	BD171177
	115	16	0.4	17	1	BD171178
	116	16	0.4	17	1	E34258
	117	16	0.4	17	1	E34259
	118	16	0.4	17	1	AX673525
	119	16	0.4	17	1	AX692526
	120	16	0.4	17	1	AX692527
	121	16	0.4	17	1	AX735811
	122	16	0.4	17	1	AX758271
	123	16	0.4	17	1	AX762966
	124	16	0.4	17	1	BD011730
	125	16	0.4	17	1	BD011731
	126	16	0.4	17	1	BD091742
	127	16	0.4	17	1	BD091743
	128	16	0.4	17	1	BD091750
	129	16	0.4	17	1	BD091751
	130	16	0.4	17	1	BD091773
	131	16	0.4	17	1	BD091774
	132	16	0.4	17	1	BD097334
	133	16	0.4	17	1	BD097335
c	134	16	0.4	18	1	A14689
	135	16	0.4	18	1	E32453
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	140	16	0.4	18	1	E32461
	141	16	0.4	18	1	AR208425
	142	16	0.4	18	1	AR208426
	143	16	0.4	18	1	AX028845
	144	16	0.4	18	1	AX085251
	145	16	0.4	18	1	AX085252
	146	16	0.4	18	1	AX224044
c	147	16	0.4	19	1	AX643396
	148	16	0.4	19	1	AX643399
	149	16	0.4	20	1	AR162375
c	150	16	0.4	20	1	BD196130
c	151	16	0.4	20	1	BD234126
c	152	16	0.4	20	1	AR382921
	153	16	0.4	20	1	AX067205
c	154	15.8	0.4	19	1	AR072539
c	155	15.8	0.4	19	1	AR121569
c	156	15.8	0.4	19	1	BD251066
	157	15.8	0.4	19	1	CQ798891
c	158	15.8	0.4	19	1	AR214207
	159	15.8	0.4	19	1	AR360576
c	160	15.8	0.4	19	1	AR363387
c	161	15.8	0.4	19	1	AX080722
	162	15.8	0.4	19	1	AX132689
c	163	15.8	0.4	19	1	BD064203
	164	15.6	0.4	17	1	BD217905
c	165	15.6	0.4	19	1	AX643397
	166	15.6	0.4	19	1	AX643400
c	167	15.4	0.4	17	1	AR047358
c	168	15.4	0.4	17	1	AR047360
c	169	15.4	0.4	17	1	I54410
c	170	15.4	0.4	17	1	I54412
	171	15.4	0.4	17	1	AR187061
	172	15.4	0.4	17	1	AR323671
c	173	15.4	0.4	17	1	AX672990
	174	15.4	0.4	17	1	AX692528
c	175	15.4	0.4	17	1	AX729110
	176	15.4	0.4	17	1	HSDNA2128
	177	15.4	0.4	18	1	BD145037
	178	15.4	0.4	18	1	BD145040
	179	15.4	0.4	18	1	BD166037

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	182	15.4	0.4	18	1	E28534
c	183	15.4	0.4	18	1	E28534
	184	15.4	0.4	18	1	AR264933
	185	15.4	0.4	18	1	AR264936
	186	15.4	0.4	18	1	AR478214
	187	15.4	0.4	18	1	AR478217
	188	15.4	0.4	18	1	AX355057
c	189	15.4	0.4	18	1	AX355057
	190	15.4	0.4	18	1	AX361600
	191	15.4	0.4	18	1	AX814932
c	192	15.4	0.4	18	1	AX837956
	193	15.4	0.4	18	1	BD072878
	194	15.4	0.4	18	1	BD072881
	195	15.4	0.4	18	1	BD096968
c	196	15.4	0.4	18	1	BD104774
	197	15.4	0.4	18	1	BD107505
	198	15.4	0.4	18	1	BD107508
	199	15.4	0.4	18	1	AB069500
	200	15.4	0.4	19	1	AX129035
	201	15.4	0.4	19	1	AX129036
	202	15.4	0.4	19	1	AX129707
c	203	15.4	0.4	19	1	AX188729
	204	15.2	0.4	17	1	AR183909
	205	15.2	0.4	17	1	AR429726
c	206	15.2	0.4	19	1	AR163080
	207	15.2	0.4	19	1	E08331
c	208	15.2	0.4	19	1	AR491869
	209	15.2	0.4	19	1	AR528447
c	210	15.2	0.4	20	1	BD161924
	211	15	0.3	15	1	AR029402
c	212	15	0.3	15	1	AR029403
	213	15	0.3	15	1	AR034895
c	214	15	0.3	15	1	AR034898
c	215	15	0.3	15	1	AR048768
	216	15	0.3	15	1	AR049970
c	217	15	0.3	15	1	AR049971
	218	15	0.3	15	1	AR056157
	219	15	0.3	15	1	AR056158
	220	15	0.3	15	1	AR080676
c	221	15	0.3	15	1	AR084516
	222	15	0.3	15	1	AR084520
	223	15	0.3	15	1	AR105981
	224	15	0.3	15	1	AR113915
	225	15	0.3	15	1	AR113916
c	226	15	0.3	15	1	AR132213
c	227	15	0.3	15	1	AR170375
	228	15	0.3	15	1	BD184668
	229	15	0.3	15	1	BD206432
	230	15	0.3	15	1	BD209488
	231	15	0.3	15	1	CQ832330
	232	15	0.3	15	1	CQ840762
	233	15	0.3	15	1	CQ840854
	234	15	0.3	15	1	E08522
	235	15	0.3	15	1	E12591
c	236	15	0.3	15	1	I29068
	237	15	0.3	15	1	I38641
	238	15	0.3	15	1	AR200476
c	239	15	0.3	15	1	AR200477
c	240	15	0.3	15	1	AR222461
	241	15	0.3	15	1	AR266630
	242	15	0.3	15	1	AR371280
c	243	15	0.3	15	1	AR371281
	244	15	0.3	15	1	AR410213
	245	15	0.3	15	1	AR438809
	246	15	0.3	15	1	AR439678
	247	15	0.3	15	1	AR452072
	248	15	0.3	15	1	AR489501
c	249	15	0.3	15	1	AR489502
	250	15	0.3	15	1	AR491112
c	251	15	0.3	15	1	AR491113
	252	15	0.3	15	1	AX004877

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	254	15	0.3	15	1	AX048407	ACCESSION:AX048407
c	255	15	0.3	15	1	AX106973	ACCESSION:AX106973
	256	15	0.3	15	1	AX127272	ACCESSION:AX127272
	257	15	0.3	15	1	AX127273	ACCESSION:AX127273
	258	15	0.3	15	1	AX180140	ACCESSION:AX180140
	259	15	0.3	15	1	AX180141	ACCESSION:AX180141
	260	15	0.3	15	1	AX429224	ACCESSION:AX429224
c	261	15	0.3	15	1	AX525141	ACCESSION:AX525141
c	262	15	0.3	15	1	AX525143	ACCESSION:AX525143
	263	15	0.3	15	1	AX633197	ACCESSION:AX633197
	264	15	0.3	15	1	AX633199	ACCESSION:AX633199
	265	15	0.3	15	1	AX696087	ACCESSION:AX696087
c	266	15	0.3	15	1	AX711176	ACCESSION:AX711176
	267	15	0.3	15	1	BD074424	ACCESSION:BD074424
	268	15	0.3	15	1	BD084687	ACCESSION:BD084687
	269	15	0.3	16	1	AR027678	ACCESSION:AR027678
	270	15	0.3	16	1	AR037355	ACCESSION:AR037355
c	271	15	0.3	16	1	AR104584	ACCESSION:AR104584
c	272	15	0.3	16	1	AR175845	ACCESSION:AR175845
c	273	15	0.3	16	1	BD167413	ACCESSION:BD167413
c	274	15	0.3	16	1	BD167414	ACCESSION:BD167414
	275	15	0.3	16	1	CQ800970	ACCESSION:CQ800970
c	276	15	0.3	16	1	CQ827693	ACCESSION:CQ827693
	277	15	0.3	16	1	I38676	ACCESSION:I38676
	278	15	0.3	16	1	I38682	ACCESSION:I38682
	279	15	0.3	16	1	I38700	ACCESSION:I38700
	280	15	0.3	16	1	AR221692	ACCESSION:AR221692
	281	15	0.3	16	1	AR221693	ACCESSION:AR221693
	282	15	0.3	16	1	AR221694	ACCESSION:AR221694
	283	15	0.3	16	1	AR221695	ACCESSION:AR221695
	284	15	0.3	16	1	AR221696	ACCESSION:AR221696
	285	15	0.3	16	1	AR221697	ACCESSION:AR221697
	286	15	0.3	16	1	AR221698	ACCESSION:AR221698
c	287	15	0.3	16	1	AR222462	ACCESSION:AR222462
	288	15	0.3	16	1	AR257437	ACCESSION:AR257437
	289	15	0.3	16	1	AR257438	ACCESSION:AR257438
	290	15	0.3	16	1	AR257439	ACCESSION:AR257439
	291	15	0.3	16	1	AR257440	ACCESSION:AR257440
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	294	15	0.3	16	1	AR257443	ACCESSION:AR257443
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	296	15	0.3	16	1	AR561693	ACCESSION:AR561693
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	298	15	0.3	16	1	AX235176	ACCESSION:AX235176
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	306	15	0.3	17	1	AR187062	ACCESSION:AR187062
	307	15	0.3	17	1	AR187063	ACCESSION:AR187063
	308	15	0.3	17	1	AR187064	ACCESSION:AR187064
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	311	15	0.3	17	1	AR236087	ACCESSION:AR236087
	312	15	0.3	17	1	AR241830	ACCESSION:AR241830
	313	15	0.3	17	1	AR266625	ACCESSION:AR266625
	314	15	0.3	17	1	AR323672	ACCESSION:AR323672
	315	15	0.3	17	1	AR323673	ACCESSION:AR323673
	316	15	0.3	17	1	AR323674	ACCESSION:AR323674
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	318	15	0.3	17	1	AX361606	ACCESSION:AX361606
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	323	15	0.3	18	1	AR034896	ACCESSION:AR034896
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c	325	15	0.3	18	1	AR058305	ACCESSION:AR058305
	326	15	0.3	18	1	AR097579	ACCESSION:AR097579
c	327	15	0.3	18	1	AR106506	ACCESSION:AR106506
c	328	15	0.3	18	1	BD190553	ACCESSION:BD190553
	329	15	0.3	18	1	BD222596	ACCESSION:BD222596
c	330	15	0.3	18	1	E28535	ACCESSION:E28535
	331	15	0.3	18	1	E28536	ACCESSION:E28536
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	333	15	0.3	18	1	AR208427	ACCESSION:AR208427
	334	15	0.3	18	1	AR215435	ACCESSION:AR215435
c	335	15	0.3	18	1	AR222464	ACCESSION:AR222464
	336	15	0.3	18	1	AR412363	ACCESSION:AR412363
	337	15	0.3	18	1	AR473365	ACCESSION:AR473365
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	340	15	0.3	18	1	AX004875	ACCESSION:AX004875
	341	15	0.3	18	1	AX004879	ACCESSION:AX004879
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	344	15	0.3	18	1	AX008122	ACCESSION:AX008122
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	346	15	0.3	18	1	AX028843	ACCESSION:AX028843
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	351	15	0.3	18	1	AX104721	ACCESSION:AX104721
	352	15	0.3	18	1	AX104747	ACCESSION:AX104747
	353	15	0.3	18	1	AX105651	ACCESSION:AX105651
	354	15	0.3	18	1	AX108642	ACCESSION:AX108642
	355	15	0.3	18	1	AX268883	ACCESSION:AX268883
	356	15	0.3	18	1	AX355809	ACCESSION:AX355809
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	362	15	0.3	18	1	AX814725	ACCESSION:AX814725
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	364	15	0.3	18	1	BD085545	ACCESSION:BD085545
	365	14.8	0.3	18	1	AR063243	ACCESSION:AR063243
	366	14.8	0.3	18	1	AR152179	ACCESSION:AR152179
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	368	14.8	0.3	18	1	AR178168	ACCESSION:AR178168
	369	14.8	0.3	18	1	CQ807858	ACCESSION:CQ807858
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	371	14.8	0.3	18	1	AX599310	ACCESSION:AX599310
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	377	14.8	0.3	18	1	AX796164	ACCESSION:AX796164
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	379	14.8	0.3	18	1	AX823056	ACCESSION:AX823056
	380	14.8	0.3	18	1	AX826696	ACCESSION:AX826696
	381	14.6	0.3	23	1	S61969	ACCESSION:S61969
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c	383	14.4	0.3	16	1	A88821	ACCESSION:A88821
	384	14.4	0.3	16	1	AR002257	ACCESSION:AR002257
	385	14.4	0.3	16	1	AR045207	ACCESSION:AR045207
	386	14.4	0.3	16	1	AR051238	ACCESSION:AR051238
	387	14.4	0.3	16	1	I16032	ACCESSION:I16032
	388	14.4	0.3	16	1	I28367	ACCESSION:I28367
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c	392	14.4	0.3	16	1	AX359760	ACCESSION:AX359760
c	393	14.4	0.3	16	1	BD066334	ACCESSION:BD066334
c	394	14.4	0.3	16	1	BD089822	ACCESSION:BD089822
	395	14.4	0.3	16	1	HSDNA2129	ACCESSION:AJ002129
c	396	14.4	0.3	16	1	AB068105	ACCESSION:AB068105
	397	14.4	0.3	17	1	AR046267	ACCESSION:AR046267
c	398	14.4	0.3	17	1	AR047356	ACCESSION:AR047356

c 399	14.4	0.3	17	1	AR047362
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401	14.4	0.3	17	1	BD199224
402	14.4	0.3	17	1	BD199225
403	14.4	0.3	17	1	BD199226
404	14.4	0.3	17	1	BD199227
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406	14.4	0.3	17	1	BD202794
407	14.4	0.3	17	1	BD202802
408	14.4	0.3	17	1	BD202803
409	14.4	0.3	17	1	I53319
c 410	14.4	0.3	17	1	I54408
c 411	14.4	0.3	17	1	I54414
412	14.4	0.3	17	1	AR187060
c 413	14.4	0.3	17	1	AR187065
c 414	14.4	0.3	17	1	AR187066
c 415	14.4	0.3	17	1	AR190427
416	14.4	0.3	17	1	AR323670
c 417	14.4	0.3	17	1	AR323675
c 418	14.4	0.3	17	1	AR323676
c 419	14.4	0.3	17	1	AR325352
c 420	14.4	0.3	17	1	AR327337
421	14.4	0.3	17	1	AR434321
422	14.4	0.3	17	1	AR434322
c 423	14.4	0.3	17	1	AX217422
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c 425	14.4	0.3	17	1	AX578222
c 426	14.4	0.3	17	1	AX673808
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c 428	14.4	0.3	17	1	AX724631
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430	14.4	0.3	18	1	AR241816
c 431	14.4	0.3	18	1	AR098809
c 432	14.4	0.3	18	1	AR130254
c 433	14.4	0.3	18	1	BD139558
434	14.4	0.3	18	1	BD145035
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c 445	14.4	0.3	18	1	AR302718
446	14.4	0.3	18	1	AR302719
c 447	14.4	0.3	18	1	AR324046
c 448	14.4	0.3	18	1	AR430883
c 449	14.4	0.3	18	1	AR442120
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452	14.4	0.3	18	1	AX329281
c 453	14.4	0.3	18	1	AX472780
454	14.4	0.3	18	1	AX472781
c 455	14.4	0.3	18	1	AX937388
456	14.4	0.3	18	1	BD072876
457	14.4	0.3	18	1	BD072880
458	14.4	0.3	18	1	BD107503
459	14.4	0.3	18	1	BD107507
460	14.2	0.3	16	1	E52143
461	14.2	0.3	16	1	E53842
462	14.2	0.3	20	1	BD145051
c 463	14.2	0.3	20	1	BD145062
464	14.2	0.3	20	1	BD166051
c 465	14.2	0.3	20	1	BD166062
466	14.2	0.3	20	1	AR264947
467	14.2	0.3	20	1	AR478228
468	14.2	0.3	20	1	BD072892
c 469	14.2	0.3	20	1	BD072903
470	14.2	0.3	20	1	BD107519
c 471	14.2	0.3	20	1	BD107530

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c 472	14.2	0.3	21	1	AX825150
c 473	14	0.3	14	1	AR029886
474	14	0.3	14	1	AR029887
475	14	0.3	14	1	AR174022
476	14	0.3	14	1	BD132850
c 477	14	0.3	14	1	BD176795
c 478	14	0.3	14	1	BD176796
479	14	0.3	14	1	BD176803
480	14	0.3	14	1	BD176804
c 481	14	0.3	14	1	BD237464
c 482	14	0.3	14	1	CQ827692
c 483	14	0.3	14	1	AR222460
484	14	0.3	14	1	AR364948
c 485	14	0.3	14	1	AR364949
486	14	0.3	14	1	AR491866
487	14	0.3	14	1	AX016298
488	14	0.3	14	1	AX048406
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c 492	14	0.3	14	1	AX839906
493	14	0.3	14	1	BD073884
c 494	14	0.3	14	1	BD084127
495	14	0.3	14	1	BD096963
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497	14	0.3	15	1	AR056156
498	14	0.3	15	1	AR056159
c 499	14	0.3	15	1	AR084518
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c 502	14	0.3	15	1	AR132214
c 503	14	0.3	15	1	AR132215
c 504	14	0.3	15	1	I29065
c 505	14	0.3	15	1	I29066
506	14	0.3	15	1	AR241870
507	14	0.3	15	1	AR560062
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509	14	0.3	15	1	AX190915
c 510	14	0.3	15	1	AX190916
511	14	0.3	15	1	AX633195
512	14	0.3	15	1	AX633201
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514	14	0.3	17	1	AR187065
515	14	0.3	17	1	AR323675
516	14	0.3	17	1	BD197546
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518	14	0.3	17	1	BD255102
c 519	14	0.3	17	1	AX421959
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525	14	0.3	17	1	AX692523
526	14	0.3	17	1	AX726054
c 527	14	0.3	17	1	AX727280
c 528	14	0.3	17	1	AX729364
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c 530	14	0.3	17	1	AX739654
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c 532	13.8	0.3	17	1	AR187064
c 533	13.8	0.3	17	1	AR241830
c 534	13.8	0.3	17	1	AR323674
c 535	13.8	0.3	17	1	AX692524
c 536	13.8	0.3	17	1	AX692523
537	13.8	0.3	17	1	A88312
538	13.8	0.3	17	1	A90279
539	13.8	0.3	17	1	AR029813
540	13.8	0.3	17	1	AR039423
541	13.8	0.3	17	1	AR040167
c 542	13.8	0.3	17	1	AR045379
c 543	13.8	0.3	17	1	AR045381
c 544	13.8	0.3	17	1	AR046269

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c 546	13.8	0.3	17	1	AR074707	ACCESSION:AR074707
547	13.8	0.3	17	1	AR074708	ACCESSION:AR074708
548	13.8	0.3	17	1	AR074709	ACCESSION:AR074709
c 549	13.8	0.3	17	1	BD197617	ACCESSION:BD197617
c 550	13.8	0.3	17	1	BD197742	ACCESSION:BD197742
551	13.8	0.3	17	1	BD202801	ACCESSION:BD202801
c 552	13.8	0.3	17	1	BD202896	ACCESSION:BD202896
c 553	13.8	0.3	17	1	BD203005	ACCESSION:BD203005
554	13.8	0.3	17	1	BD203051	ACCESSION:BD203051
555	13.8	0.3	17	1	BD241222	ACCESSION:BD241222
c 556	13.8	0.3	17	1	BD254535	ACCESSION:BD254535
c 557	13.8	0.3	17	1	BD256600	ACCESSION:BD256600
558	13.8	0.3	17	1	BD256796	ACCESSION:BD256796
c 559	13.8	0.3	17	1	BD257048	ACCESSION:BD257048
560	13.8	0.3	17	1	BD257747	ACCESSION:BD257747
561	13.8	0.3	17	1	BD258509	ACCESSION:BD258509
c 562	13.8	0.3	17	1	BD258513	ACCESSION:BD258513
c 563	13.8	0.3	17	1	CQ615333	ACCESSION:CQ615333
564	13.8	0.3	17	1	CQ616034	ACCESSION:CQ616034
c 565	13.8	0.3	17	1	CQ616269	ACCESSION:CQ616269
c 566	13.8	0.3	17	1	CQ623194	ACCESSION:CQ623194
567	13.8	0.3	17	1	E03610	ACCESSION:E03610
568	13.8	0.3	17	1	E12897	ACCESSION:E12897
c 569	13.8	0.3	17	1	I28581	ACCESSION:I28581
c 570	13.8	0.3	17	1	I32318	ACCESSION:I32318
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c 573	13.8	0.3	17	1	I52431	ACCESSION:I52431
c 574	13.8	0.3	17	1	I52433	ACCESSION:I52433
c 575	13.8	0.3	17	1	I53321	ACCESSION:I53321
c 576	13.8	0.3	17	1	I58743	ACCESSION:I58743
577	13.8	0.3	17	1	I94333	ACCESSION:I94333
578	13.8	0.3	17	1	AR186534	ACCESSION:AR186534
c 579	13.8	0.3	17	1	AR187067	ACCESSION:AR187067
580	13.8	0.3	17	1	AR188493	ACCESSION:AR188493
581	13.8	0.3	17	1	AR190587	ACCESSION:AR190587
c 582	13.8	0.3	17	1	AR196417	ACCESSION:AR196417
583	13.8	0.3	17	1	AR286352	ACCESSION:AR286352
584	13.8	0.3	17	1	AR323165	ACCESSION:AR323165
c 585	13.8	0.3	17	1	AR323677	ACCESSION:AR323677
586	13.8	0.3	17	1	AR324346	ACCESSION:AR324346
587	13.8	0.3	17	1	AR325510	ACCESSION:AR325510
588	13.8	0.3	17	1	AR398342	ACCESSION:AR398342
589	13.8	0.3	17	1	AR402473	ACCESSION:AR402473
c 590	13.8	0.3	17	1	AR433770	ACCESSION:AR433770
c 591	13.8	0.3	17	1	AR433771	ACCESSION:AR433771
c 592	13.8	0.3	17	1	AR433773	ACCESSION:AR433773
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594	13.8	0.3	17	1	AR434323	ACCESSION:AR434323
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c 600	13.8	0.3	17	1	AR457332	ACCESSION:AR457332
c 601	13.8	0.3	17	1	AR464257	ACCESSION:AR464257
602	13.8	0.3	17	1	AR482723	ACCESSION:AR482723
603	13.8	0.3	17	1	AX060746	ACCESSION:AX060746
604	13.8	0.3	17	1	AX060925	ACCESSION:AX060925
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c 607	13.8	0.3	17	1	AX214795	ACCESSION:AX214795
c 608	13.8	0.3	17	1	AX215330	ACCESSION:AX215330
c 609	13.8	0.3	17	1	AX217114	ACCESSION:AX217114
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c 612	13.8	0.3	17	1	AX217981	ACCESSION:AX217981
c 613	13.8	0.3	17	1	AX218200	ACCESSION:AX218200
c 614	13.8	0.3	17	1	AX226806	ACCESSION:AX226806
615	13.8	0.3	17	1	AX227120	ACCESSION:AX227120
c 616	13.8	0.3	17	1	AX262940	ACCESSION:AX262940
617	13.8	0.3	17	1	AX262941	ACCESSION:AX262941
618	13.8	0.3	17	1	AX272510	ACCESSION:AX272510
619	13.8	0.3	17	1	AX422191	ACCESSION:AX422191
c 620	13.8	0.3	17	1	AX422333	ACCESSION:AX422333
621	13.8	0.3	17	1	AX423696	ACCESSION:AX423696
c 622	13.8	0.3	17	1	AX475032	ACCESSION:AX475032
623	13.8	0.3	17	1	AX499406	ACCESSION:AX499406
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c 625	13.8	0.3	17	1	AX500501	ACCESSION:AX500501
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c 627	13.8	0.3	17	1	AX531623	ACCESSION:AX531623
c 628	13.8	0.3	17	1	AX531624	ACCESSION:AX531624
629	13.8	0.3	17	1	AX531875	ACCESSION:AX531875
c 630	13.8	0.3	17	1	AX615502	ACCESSION:AX615502
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633	13.8	0.3	17	1	AX674470	ACCESSION:AX674470
c 634	13.8	0.3	17	1	AX687430	ACCESSION:AX687430
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642	13.8	0.3	17	1	AX691269	ACCESSION:AX691269
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c 652	13.8	0.3	17	1	AX729740	ACCESSION:AX729740
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655	13.8	0.3	17	1	AX734075	ACCESSION:AX734075
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c 657	13.8	0.3	17	1	AX735055	ACCESSION:AX735055
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659	13.8	0.3	17	1	AX735164	ACCESSION:AX735164
660	13.8	0.3	17	1	AX737844	ACCESSION:AX737844
661	13.8	0.3	17	1	AX738005	ACCESSION:AX738005
c 662	13.8	0.3	17	1	AX757155	ACCESSION:AX757155
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664	13.8	0.3	17	1	AX757248	ACCESSION:AX757248
c 665	13.8	0.3	17	1	AX758931	ACCESSION:AX758931
666	13.8	0.3	17	1	AX760266	ACCESSION:AX760266
c 667	13.8	0.3	17	1	AX760827	ACCESSION:AX760827
668	13.8	0.3	17	1	AX760846	ACCESSION:AX760846
669	13.8	0.3	17	1	AX761467	ACCESSION:AX761467
670	13.8	0.3	17	1	BD065825	ACCESSION:BD065825
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c 674	13.8	0.3	18	1	BD166037	ACCESSION:BD166037
c 675	13.8	0.3	18	1	AR264933	ACCESSION:AR264933
c 676	13.8	0.3	18	1	AR478214	ACCESSION:AR478214
c 677	13.8	0.3	18	1	BD072878	ACCESSION:BD072878
c 678	13.8	0.3	18	1	BD107505	ACCESSION:BD107505
c 679	13.8	0.3	20	1	BD143136	ACCESSION:BD143136
c 680	13.8	0.3	20	1	AR309844	ACCESSION:AR309844
c 681	13.8	0.3	20	1	AX404077	ACCESSION:AX404077
682	13.6	0.3	20	1	AR373540	ACCESSION:AR373540
683	13.6	0.3	20	1	AR142677	ACCESSION:AR142677
684	13.6	0.3	20	1	E28096	ACCESSION:E28096
c 685	13.6	0.3	20	1	AX067205	ACCESSION:AX067205
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c 688	13.4	0.3	18	1	I73187	ACCESSION:I73187
c 689	13.4	0.3	19	1	AR528447	ACCESSION:AR528447
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c 692	13.2	0.3	18	1	AR034896
693	13.2	0.3	18	1	AR034899
694	13.2	0.3	18	1	AR058305
c 695	13.2	0.3	18	1	AR097579
696	13.2	0.3	18	1	AR106506
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c 698	13.2	0.3	18	1	BD222596
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c 700	13.2	0.3	18	1	E28536
c 701	13.2	0.3	18	1	I79509
c 702	13.2	0.3	18	1	AR208427
c 703	13.2	0.3	18	1	AR215435
704	13.2	0.3	18	1	AR222464
c 705	13.2	0.3	18	1	AR412363
c 706	13.2	0.3	18	1	AR473365
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c 708	13.2	0.3	18	1	AR487020
c 709	13.2	0.3	18	1	AX004875
c 710	13.2	0.3	18	1	AX004879
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c 712	13.2	0.3	18	1	AX008118
c 713	13.2	0.3	18	1	AX008122
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731	13.2	0.3	18	1	AX814736
c 732	13.2	0.3	18	1	BD085545
733	13.2	0.3	19	1	AX643396
c 734	13.2	0.3	19	1	AX643399
c 735	13.2	0.3	20	1	AR139960
c 736	13.2	0.3	20	1	AR140279
c 737	13.2	0.3	20	1	AR140557
c 738	13.2	0.3	20	1	AR562156
739	13.2	0.3	20	1	BD234126
c 740	13.2	0.3	21	1	AX825124
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c 760	12.8	0.3	17	1	AR187061
c 761	12.8	0.3	17	1	AR323671
c 762	12.8	0.3	17	1	AR187062
c 763	12.8	0.3	17	1	AR187063

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c 777	12.8	0.3	18	1	AR478213
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c 787	12.8	0.3	18	1	AX814932
c 788	12.8	0.3	18	1	BD072881
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c 795	12.4	0.3	15	1	AR056159
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c	843	12.2	0.3	17	1	AR141074	ACCESSION:AR141074
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c	847	12.2	0.3	17	1	AR187060	ACCESSION:AR187060
c	848	12.2	0.3	17	1	AR323670	ACCESSION:AR323670
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c	850	12.2	0.3	17	1	AX692529	ACCESSION:AX692529
	851	12.2	0.3	17	1	I32318	ACCESSION:I32318
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	854	12.2	0.3	18	1	A14689	ACCESSION:A14689
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c	860	12.2	0.3	18	1	BD145039	ACCESSION:BD145039
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c	862	12.2	0.3	18	1	BD166039	ACCESSION:BD166039
c	863	12.2	0.3	18	1	AR264931	ACCESSION:AR264931
c	864	12.2	0.3	18	1	AR264935	ACCESSION:AR264935
c	865	12.2	0.3	18	1	AR478212	ACCESSION:AR478212
c	866	12.2	0.3	18	1	AR478216	ACCESSION:AR478216
c	867	12.2	0.3	18	1	BD072876	ACCESSION:BD072876
c	868	12.2	0.3	18	1	BD072880	ACCESSION:BD072880
c	869	12.2	0.3	18	1	BD107503	ACCESSION:BD107503
c	870	12.2	0.3	18	1	BD107507	ACCESSION:BD107507
c	871	12	0.3	16	1	E52143	ACCESSION:E52143
c	872	12	0.3	16	1	E53842	ACCESSION:E53842
c	873	12	0.3	17	1	AR183909	ACCESSION:AR183909
c	874	12	0.3	17	1	AR429726	ACCESSION:AR429726
	875	12	0.3	17	1	AR187067	ACCESSION:AR187067
	876	12	0.3	17	1	AR323677	ACCESSION:AR323677
	877	12	0.3	19	1	AR491869	ACCESSION:AR491869
c	878	12	0.3	20	1	E15159	ACCESSION:E15159
	879	12	0.3	20	1	E22402	ACCESSION:E22402
c	880	11.8	0.3	15	1	AR029402	ACCESSION:AR029402
	881	11.8	0.3	15	1	AR029403	ACCESSION:AR029403
c	882	11.8	0.3	15	1	AR034895	ACCESSION:AR034895
	883	11.8	0.3	15	1	AR034898	ACCESSION:AR034898
	884	11.8	0.3	15	1	AR048768	ACCESSION:AR048768
c	885	11.8	0.3	15	1	AR049970	ACCESSION:AR049970
	886	11.8	0.3	15	1	AR049971	ACCESSION:AR049971
c	887	11.8	0.3	15	1	AR056157	ACCESSION:AR056157
c	888	11.8	0.3	15	1	AR056158	ACCESSION:AR056158
c	889	11.8	0.3	15	1	AR080676	ACCESSION:AR080676
	890	11.8	0.3	15	1	AR084516	ACCESSION:AR084516
c	891	11.8	0.3	15	1	AR084520	ACCESSION:AR084520
c	892	11.8	0.3	15	1	AR105981	ACCESSION:AR105981
c	893	11.8	0.3	15	1	AR113915	ACCESSION:AR113915
c	894	11.8	0.3	15	1	AR113916	ACCESSION:AR113916
	895	11.8	0.3	15	1	AR170375	ACCESSION:AR170375
c	896	11.8	0.3	15	1	BD184668	ACCESSION:BD184668
c	897	11.8	0.3	15	1	BD206432	ACCESSION:BD206432
c	898	11.8	0.3	15	1	BD209488	ACCESSION:BD209488
c	899	11.8	0.3	15	1	CQ832330	ACCESSION:CQ832330
c	900	11.8	0.3	15	1	CQ840762	ACCESSION:CQ840762
c	901	11.8	0.3	15	1	CQ840854	ACCESSION:CQ840854
c	902	11.8	0.3	15	1	E08522	ACCESSION:E08522
c	903	11.8	0.3	15	1	E12591	ACCESSION:E12591
	904	11.8	0.3	15	1	I29068	ACCESSION:I29068
c	905	11.8	0.3	15	1	I38641	ACCESSION:I38641
c	906	11.8	0.3	15	1	AR200476	ACCESSION:AR200476
	907	11.8	0.3	15	1	AR200477	ACCESSION:AR200477
	908	11.8	0.3	15	1	AR222461	ACCESSION:AR222461
c	909	11.8	0.3	15	1	AR266630	ACCESSION:AR266630
c	910	11.8	0.3	15	1	AR371280	ACCESSION:AR371280
	911	11.8	0.3	15	1	AR371281	ACCESSION:AR371281
c	912	11.8	0.3	15	1	AR410213	ACCESSION:AR410213
c	913	11.8	0.3	15	1	AR438809	ACCESSION:AR438809
c	914	11.8	0.3	15	1	AR439678	ACCESSION:AR439678
c	915	11.8	0.3	15	1	AR452072	ACCESSION:AR452072
c	916	11.8	0.3	15	1	AR489501	ACCESSION:AR489501
	917	11.8	0.3	15	1	AR489502	ACCESSION:AR489502
c	918	11.8	0.3	15	1	AR491112	ACCESSION:AR491112
	919	11.8	0.3	15	1	AR491113	ACCESSION:AR491113
c	920	11.8	0.3	15	1	AX004877	ACCESSION:AX004877
c	921	11.8	0.3	15	1	AX026066	ACCESSION:AX026066
c	922	11.8	0.3	15	1	AX048407	ACCESSION:AX048407
	923	11.8	0.3	15	1	AX106973	ACCESSION:AX106973
c	924	11.8	0.3	15	1	AX127272	ACCESSION:AX127272
c	925	11.8	0.3	15	1	AX127273	ACCESSION:AX127273
c	926	11.8	0.3	15	1	AX180140	ACCESSION:AX180140
c	927	11.8	0.3	15	1	AX180141	ACCESSION:AX180141
c	928	11.8	0.3	15	1	AX429224	ACCESSION:AX429224
	929	11.8	0.3	15	1	AX525141	ACCESSION:AX525141
	930	11.8	0.3	15	1	AX525143	ACCESSION:AX525143
c	931	11.8	0.3	15	1	AX633197	ACCESSION:AX633197
c	932	11.8	0.3	15	1	AX633199	ACCESSION:AX633199
c	933	11.8	0.3	15	1	AX696087	ACCESSION:AX696087
	934	11.8	0.3	15	1	AX711176	ACCESSION:AX711176
c	935	11.8	0.3	15	1	BD074424	ACCESSION:BD074424
c	936	11.8	0.3	15	1	BD084687	ACCESSION:BD084687
c	937	11.8	0.3	16	1	AR027678	ACCESSION:AR027678
c	938	11.8	0.3	16	1	AR037355	ACCESSION:AR037355
	939	11.8	0.3	16	1	AR104584	ACCESSION:AR104584
	940	11.8	0.3	16	1	AR175845	ACCESSION:AR175845
	941	11.8	0.3	16	1	BD167413	ACCESSION:BD167413
	942	11.8	0.3	16	1	BD167414	ACCESSION:BD167414
c	943	11.8	0.3	16	1	CQ800970	ACCESSION:CQ800970
	944	11.8	0.3	16	1	CQ827693	ACCESSION:CQ827693
c	945	11.8	0.3	16	1	I38676	ACCESSION:I38676
c	946	11.8	0.3	16	1	I38682	ACCESSION:I38682
c	947	11.8	0.3	16	1	I38700	ACCESSION:I38700
c	948	11.8	0.3	16	1	AR221692	ACCESSION:AR221692
c	949	11.8	0.3	16	1	AR221693	ACCESSION:AR221693
c	950	11.8	0.3	16	1	AR221694	ACCESSION:AR221694
c	951	11.8	0.3	16	1	AR221695	ACCESSION:AR221695
c	952	11.8	0.3	16	1	AR221696	ACCESSION:AR221696
c	953	11.8	0.3	16	1	AR221697	ACCESSION:AR221697
c	954	11.8	0.3	16	1	AR221698	ACCESSION:AR221698
	955	11.8	0.3	16	1	AR222462	ACCESSION:AR222462
c	956	11.8	0.3	16	1	AR257437	ACCESSION:AR257437
c	957	11.8	0.3	16	1	AR257438	ACCESSION:AR257438
c	958	11.8	0.3	16	1	AR257439	ACCESSION:AR257439
c	959	11.8	0.3	16	1	AR257440	ACCESSION:AR257440
c	960	11.8	0.3	16	1	AR257441	ACCESSION:AR257441
c	961	11.8	0.3	16	1	AR257442	ACCESSION:AR257442
c	962	11.8	0.3	16	1	AR257443	ACCESSION:AR257443
	963	11.8	0.3	16	1	AR561628	ACCESSION:AR561628
c	964	11.8	0.3	16	1	AR561693	ACCESSION:AR561693
	965	11.8	0.3	16	1	AX039049	ACCESSION:AX039049
c	966	11.8	0.3	16	1	AX235176	ACCESSION:AX235176
c	967	11.8	0.3	16	1	AR002257	ACCESSION:AR002257
c	968	11.8	0.3	16	1	AR045207	ACCESSION:AR045207
c	969	11.8	0.3	16	1	AR051238	ACCESSION:AR051238
c	970	11.8	0.3	16	1	I16032	ACCESSION:I16032
c	971	11.8	0.3	16	1	I28367	ACCESSION:I28367
	972	11.8	0.3	16	1	AX359760	ACCESSION:AX359760
c	973	11.8	0.3	17	1	AX692526	ACCESSION:AX692526
c	974	11.8	0.3	17	1	AX692527	ACCESSION:AX692527
c	975	11.8	0.3	17	1	AR172076	ACCESSION:AR172076
c	976	11.8	0.3	17	1	AR173367	ACCESSION:AR173367
c	977	11.8	0.3	17	1	AR266625	ACCESSION:AR266625
	978	11.8	0.3	17	1	AR047356	ACCESSION:AR047356
	979	11.8	0.3	17	1	I54408	ACCESSION:I54408
	980	11.8	0.3	17	1	BD203005	ACCESSION:BD203005
c	981	11.8	0.3	18	1	AR208426	ACCESSION:AR208426
c	982	11.8	0.3	18	1	AX085252	ACCESSION:AX085252

c 983	11.8	0.3	18	1	AX599310	ACCESSION:AX599310
c 984	11.8	0.3	18	1	AX599902	ACCESSION:AX599902
c 985	11.8	0.3	18	1	AX767726	ACCESSION:AX767726
c 986	11.8	0.3	18	1	AX796164	ACCESSION:AX796164
987	11.6	0.3	18	1	AR098809	ACCESSION:AR098809
988	11.6	0.3	19	1	AR072539	ACCESSION:AR072539
989	11.6	0.3	19	1	AR121569	ACCESSION:AR121569
990	11.6	0.3	19	1	BD251066	ACCESSION:BD251066
991	11.6	0.3	19	1	AR214207	ACCESSION:AR214207
c 992	11.6	0.3	19	1	AR360576	ACCESSION:AR360576
993	11.6	0.3	19	1	AR363387	ACCESSION:AR363387
994	11.6	0.3	19	1	AX080722	ACCESSION:AX080722
995	11.6	0.3	19	1	BD064203	ACCESSION:BD064203
996	11.4	0.3	14	1	AR029886	ACCESSION:AR029886
c 997	11.4	0.3	14	1	AR029887	ACCESSION:AR029887
c 998	11.4	0.3	14	1	BD132850	ACCESSION:BD132850
999	11.4	0.3	14	1	BD176795	ACCESSION:BD176795
c1000	11.4	0.3	14	1	BD176803	ACCESSION:BD176803
c1001	11.4	0.3	14	1	BD176804	ACCESSION:BD176804
1002	11.4	0.3	14	1	BD237464	ACCESSION:BD237464
1003	11.4	0.3	14	1	CQ827692	ACCESSION:CQ827692
1004	11.4	0.3	14	1	AR222460	ACCESSION:AR222460
c1005	11.4	0.3	14	1	AR364948	ACCESSION:AR364948
1006	11.4	0.3	14	1	AR364949	ACCESSION:AR364949
c1007	11.4	0.3	14	1	AX048406	ACCESSION:AX048406
1008	11.4	0.3	14	1	AX827014	ACCESSION:AX827014
1009	11.4	0.3	14	1	AX839906	ACCESSION:AX839906
1010	11.4	0.3	14	1	BD084127	ACCESSION:BD084127
c1011	11.4	0.3	14	1	BD096963	ACCESSION:BD096963
c1012	11.4	0.3	14	1	BD096965	ACCESSION:BD096965

ALIGNMENTS

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RESULT 1
AR003340
LOCUS       AR003340                  39 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 62 from patent US 5744300.
ACCESSION   AR003340
VERSION     AR003340.1  GI:3964599
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 62 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 39;  DB 1;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.00088;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1412 AGATGATGATGTTAACCCATTCCAGTACAGTATTCTTTT 1450
              |||||||||||||||||||||||||||||||||||||||
Db          1 AGATGATGATGTTAACCCATTCCAGTACAGTATTCTTTT 39


RESULT 2
AX662645
LOCUS       AX662645                  27 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 327 from Patent WO02062999.
ACCESSION   AX662645
VERSION     AX662645.1  GI:29163314
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Spytek,K.A., Li,L., Wolenc,A.R., Vernet,C.A., Eisen,A., Liu,X.,
            Malyankar,U., Shimkets,R.A., Tchernev,V.T., Spaderna,S.K.,
            Gorman,L., Kekuda,R., Patturajan,M., Gusev,V., Gangolli,E.A.,
            Guo,X., Shenoy,S., Rastelli,L., Casman,S.J., Boldog,F.,
            Burgess,C.E., Edinger,S., Ellerman,K., Gunther,E., Smithson,G.,
            Millet,I. and Macdougall,J.R.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02062999-A 327 15-AUG-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically synthesized"

  Query Match             0.6%;  Score 23.8;  DB 1;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 3.3;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1143 CCTTTCCCTATGACTACTCTGCCAGTG 1169
              ||||||||| |||||||||||| ||||
Db          1 CCTTTCCCTTTGACTACTCTGCGAGTG 27


RESULT 3
AX662648
LOCUS       AX662648                  27 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 330 from Patent WO02062999.
ACCESSION   AX662648
VERSION     AX662648.1  GI:29163317
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Spytek,K.A., Li,L., Wolenc,A.R., Vernet,C.A., Eisen,A., Liu,X.,
            Malyankar,U., Shimkets,R.A., Tchernev,V.T., Spaderna,S.K.,
            Gorman,L., Kekuda,R., Patturajan,M., Gusev,V., Gangolli,E.A.,
            Guo,X., Shenoy,S., Rastelli,L., Casman,S.J., Boldog,F.,
            Burgess,C.E., Edinger,S., Ellerman,K., Gunther,E., Smithson,G.,
            Millet,I. and Macdougall,J.R.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02062999-A 330 15-AUG-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically synthesized"

  Query Match             0.6%;  Score 23.8;  DB 1;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 3.3;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1143 CCTTTCCCTATGACTACTCTGCCAGTG 1169
              ||||||||| |||||||||||| ||||
Db          1 CCTTTCCCTTTGACTACTCTGCGAGTG 27


RESULT 4
AR228739/c
LOCUS       AR228739                  26 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6448055.
ACCESSION   AR228739
VERSION     AR228739.1  GI:27267842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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           Unclassified.
REFERENCE  1  (bases 1 to 26)
  AUTHORS  Shimizu,S. and Kobayashi,M.
  TITLE    .DELTA.9-desaturase gene
  JOURNAL  Patent: US 6448055-A 2 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 20.8;  DB 1;  Length 26;
  Best Local Similarity   61.5%;  Pred. No. 18;
  Matches   16;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1115 GGTGAGGGCTTCCACAACTACCACCA 1140
              || ||:|| |::||:||:|::||:||
Db         26 GGNGARGGNTWYCAYAAYTWYCAYCA 1


RESULT 5
AX043066
LOCUS       AX043066                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 632 from Patent WO0065088.
ACCESSION   AX043066
VERSION     AX043066.1  GI:11341674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 632 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 24;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGGTTAAAAGATG 4528
              ||||||||||||  | |||||||||
Db          1 TTTTTTTTTTTTACGGTAAAAGATG 25


RESULT 6
AR373540/c
LOCUS       AR373540                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 110 from patent US 6602713.
ACCESSION   AR373540
VERSION     AR373540.1  GI:40075669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 110 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATATA 2410
              ||||||||||||||||||||
Db         20 AAAATATATATACATATATA 1


RESULT 7
AR299686/c
LOCUS       AR299686                  21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 11421 from patent US 6537751.
ACCESSION   AR299686
VERSION     AR299686.1  GI:31686970
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 11421 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 30;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4688 CACTGACTTGCTGTGTGACCC 4708
              || ||||||||||||||||||
Db         21 CATTGACTTGCTGTGTGACCC 1


RESULT 8
S61964/c
LOCUS       S61964                    23 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  (beta C)=beta-globin (5'region) [human, Genomic Mutant, 23 nt].
ACCESSION   S61964
VERSION     S61964.1  GI:236198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Trabuchet,G., Elion,J., Dunda,O., Lapoumeroulie,C., Ducrocq,R.,
            Nadifi,S., Zohoun,I., Chaventre,A., Carnevale,P., Nagel,R.L. et,al.
  TITLE     Nucleotide sequence evidence of the unicentric origin of the beta C
            mutation in Africa
  JOURNAL   Hum. Genet. 87 (5), 597-601 (1991)
  MEDLINE   92009838
   PUBMED   1680789
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 61964] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1. .23
                     /gene="beta-globin"
                     /allele="beta C"

  Query Match             0.4%;  Score 18.8;  DB 1;  Length 23;
  Best Local Similarity   90.9%;  Pred. No. 47;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2387 AAATAAAATATATATACATATA 2408
              ||| |||||||||||| |||||
Db         22 AAAAAAAATATATATATATATA 1
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RESULT 9
S61969/c
LOCUS       S61969                    23 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  (A3 beta C)=beta-globin {5'region} [human, Genomic Mutant, 23 nt].
ACCESSION   S61969
VERSION     S61969.1  GI:236199
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Trabuchet,G., Elion,J., Dunda,O., Lapoumeroulie,C., Ducrocq,R.,
            Nadifi,S., Zohoun,I., Chaventre,A., Carnevale,P., Nagel,R.L. et,al.
  TITLE     Nucleotide sequence evidence of the unicentric origin of the beta C
            mutation in Africa
  JOURNAL   Hum. Genet. 87 (5), 597-601 (1991)
  MEDLINE   92009838
   PUBMED   1680789
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 61969] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1. .23
                     /gene="beta-globin"
                     /allele="A3 beta C"

  Query Match             0.4%;  Score 18.8;  DB 1;  Length 23;
  Best Local Similarity   90.9%;  Pred. No. 47;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACATA 2406
             ||||| |||||||||||| |||
Db         22 AAAAAAAAAATATATATATATA 1


RESULT 10
E32451
LOCUS       E32451                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32451
VERSION     E32451.1  GI:13018687
KEYWORDS    JP 2000037190-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/11
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||||
Db          1 GTTTTTTTTTTTTTTGG 18


RESULT 11
AX825124
LOCUS       AX825124                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 22 from Patent WO03072818.
ACCESSION   AX825124
VERSION     AX825124.1  GI:39750853
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 22 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 65;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          4 TTTTTTTTTTTTTTGGG 21


RESULT 12
AX104716
LOCUS       AX104716                  22 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 908 from Patent WO0122972.
ACCESSION   AX104716
VERSION     AX104716.1  GI:13920913
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
```

```
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 908 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 77;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTC 21


RESULT 13
AX547769
LOCUS       AX547769                  22 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 908 from Patent WO02053141.
ACCESSION   AX547769
VERSION     AX547769.1  GI:25812913
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 908 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 77;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTC 21


RESULT 14
CQ759632/c
LOCUS       CQ759632                  19 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 62 from Patent WO2003106672.
ACCESSION   CQ759632
VERSION     CQ759632.1  GI:44849582
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hayashizaki,Y., Carninci,P. and Harbers,M.T.
  TITLE     Method of utilizing the 5' end of transcribed nucleic acid regions
            for cloning and analysis
  JOURNAL   Patent: WO 2003106672-A 62 24-DEC-2003;
            Riken (JP) ; Kabushiki Kaisha Dnaform (JP)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="tag3"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 81;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||  |
Db         19 AGTTTTTTTTTTTTTTTG 1


RESULT 15
I19906
LOCUS       I19906                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 3 from patent US 5512462.
ACCESSION   I19906
VERSION     I19906.1  GI:1600261
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cheng,S.
  TITLE     Methods and reagents for the polymerase chain reaction
            amplification of long DNA sequences
  JOURNAL   Patent: US 5512462-A 3 30-APR-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 86;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2269 CTCTTTCTGCTCTGCCATC 2287
              ||||||| ||||||||||||
Db          2 CTCTTTCCGCTCTGCCATC 20


RESULT 16
BD089857
LOCUS       BD089857                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089857
VERSION     BD089857.1  GI:22635467
KEYWORDS    JP 2001321190-A/2101.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2101 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2101
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 86;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4705 ACCCTGGGCAAGTCACTTA 4723
              ||||||||||| |||||||
Db          2 ACCCTGGGCAACTCACTTA 20


RESULT 17
AB068200
LOCUS       AB068200                  20 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-D1S1297
            at 1p36.
ACCESSION   AB068200
VERSION     AB068200.1  GI:15129004
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="forward primer for human STS sts-D1S1297 at 1p36
                     sts-D1S1297 obtained from clones B279HN/6, B332E8,
                     B156C13, B370L6, B185M23, B359J17, B45N15, B63P6, Human
                     BAC library RPCI-11"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 86;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4705 ACCCTGGGCAAGTCACTTA 4723
              ||||||||||| |||||||
Db          2 ACCCTGGGCAACTCACTTA 20


RESULT 18
A23592
LOCUS       A23592                    21 bp    DNA     linear   PAT 23-JUN-1995
DEFINITION  CE gene mutagenic primer.
ACCESSION   A23592
VERSION     A23592.1  GI:1247969
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   .
  JOURNAL   Patent: DE 4018152-A 4 12-DEC-1991;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 91;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1216 GGCCGCCCTCGGTCTGGCC 1234
              ||||||||||| |||||||
Db          3 GGCCGCCCTCGCTCTGGCC 21


RESULT 19
AR074334
LOCUS       AR074334                  21 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 142 from patent US 5952490.
ACCESSION   AR074334
VERSION     AR074334.1  GI:10001089
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
            Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
            Imbach,J.Louis.
  TITLE     Oligonucleotides having a conserved G4 core sequence
  JOURNAL   Patent: US 5952490-A 142 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 91;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTTGGGGTT 19


RESULT 20
I21708
LOCUS       I21708                    21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 4 from patent US 5523389.
ACCESSION   I21708
VERSION     I21708.1  GI:1602062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ecker,D.J., Wyatt,J.R. and Imbach,J.L.
  TITLE     Inhibitors of human immunodeficiency virus
  JOURNAL   Patent: US 5523389-A 4 04-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 91;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTTGGGGTT 19


RESULT 21
AX032696
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LOCUS       AX032696                 21 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 142 from Patent EP1016715.
ACCESSION   AX032696
VERSION     AX032696.1  GI:10279634
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
  TITLE     Oligonucleotides having a conserved g4 core sequence
  JOURNAL   Patent: EP 1016715-A 142 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 91;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTGGGGTT 19


RESULT 22
AX825126
LOCUS       AX825126                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 24 from Patent WO03072818.
ACCESSION   AX825126
VERSION     AX825126.1  GI:39750855
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 24 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 91;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||| |||
Db          3 TTTTTTTTTTTTTTTGGT 21


RESULT 23
BD142810
LOCUS       BD142810                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142810
VERSION     BD142810.1  GI:23237755
KEYWORDS    WO 0224903-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 4 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/4
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 24
BD143836
LOCUS       BD143836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143836
VERSION     BD143836.1  GI:27849594
KEYWORDS    JP 2002095500-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
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REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 4 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/4
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 25
BD167837
LOCUS       BD167837                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167837
VERSION     BD167837.1  GI:27873649
KEYWORDS    WO 0233122-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 4 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/4
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized
            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 26
BD167909
LOCUS       BD167909                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167909
VERSION     BD167909.1  GI:27873721
KEYWORDS    WO 0226962-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 8 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/8
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

```
RESULT 27
BD168113
LOCUS       BD168113                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168113
VERSION     BD168113.1  GI:27873925
KEYWORDS    WO 0233069-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 20 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/20
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 28
BD171179
LOCUS       BD171179                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171179
VERSION     BD171179.1  GI:27876991
KEYWORDS    WO 0250269-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 4 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/4
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15G', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 29
E34260
LOCUS       E34260                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34260
VERSION     E34260.1  GI:18624265
KEYWORDS    JP 2000106879-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 4 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/4
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
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              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 30
E59657
LOCUS       E59657                    17 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
             for using the same.
ACCESSION   E59657
VERSION     E59657.1  GI:13019451
KEYWORDS    JP 2000037193-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
  TITLE     Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
            for using the same
  JOURNAL   Patent: JP 2000037193-A 3 08-FEB-2000;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 2000037193-A/3
            PD   08-FEB-2000
            PF   19-MAY-1999 JP 1999138051
            PR
            PI   TAKAMICHI MATSUMURA,TSUYOSHI FUJITA,MASAHARU KIYAMA, PI
            TAKASHI IRIE,
            PI   KAZUNORI OKANO
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 31
AR256849
LOCUS       AR256849                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6485916.
ACCESSION   AR256849
VERSION     AR256849.1  GI:27306475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
  TITLE     Preparation method of nucleic acid sample for rare expressed genes
            and analyzing method using the prepared nucleic acid samples
            thereby
  JOURNAL   Patent: US 6485916-A 3 26-NOV-2002;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 32
AR266626
LOCUS       AR266626                  17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 64 from patent US 6495319.
ACCESSION   AR266626
VERSION     AR266626.1  GI:29695690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 64 17-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 33
AX671929
LOCUS       AX671929                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 374 from Patent WO03004526.
ACCESSION   AX671929
VERSION     AX671929.1  GI:29330277
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 374 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3865 GATCACTGTAGTTTAGT 3881
              ||||||||||||||||
Db          1 GATCACTGTAGTTTAGT 17


RESULT 34
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AX673524
LOCUS       AX673524                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1969 from Patent WO03004526.
ACCESSION   AX673524
VERSION     AX673524.1  GI:29331872
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1969 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGGA 4848
              |||||||||||||||||
Db          1 GATCCTTCAGCACAGGA 17


RESULT 35
AX737809
LOCUS       AX737809                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3399 from Patent WO03025177.
ACCESSION   AX737809
VERSION     AX737809.1  GI:30517097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3399 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3865 GATCACTGTAGTTTAGT 3881
              |||||||||||||||||
Db          1 GATCACTGTAGTTTAGT 17


RESULT 36
AX759616/c
LOCUS       AX759616                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 2937 from Patent WO03040369.
ACCESSION   AX759616
VERSION     AX759616.1  GI:32254232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 2937 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4819 GAAAGCATTTTGGGATC 4835
              |||||||||||||||||
Db         17 GAAAGCATTTTGGGATC 1


RESULT 37
AX761072
LOCUS       AX761072                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 4393 from Patent WO03040369.
ACCESSION   AX761072
VERSION     AX761072.1  GI:32255688
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 4393 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1926 GATCAGACATACAGCTG 1942
              |||||||||||||||||
Db          1 GATCAGACATACAGCTG 17


RESULT 38
BD011732
LOCUS       BD011732                 17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011732
VERSION     BD011732.1  GI:22091921
KEYWORDS    WO 0065050-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
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  JOURNAL   Patent: WO 0065050-A 4 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/4
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 39
BD091744
LOCUS       BD091744                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091744
VERSION     BD091744.1  GI:22637355
KEYWORDS    WO 0073435-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 40
BD091752
LOCUS       BD091752                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091752
VERSION     BD091752.1  GI:22637363
KEYWORDS    WO 0073439-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 41
BD091775
LOCUS       BD091775                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091775
VERSION     BD091775.1  GI:22637386
KEYWORDS    WO 0073440-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
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            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 42
BD097336
LOCUS       BD097336                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097336
VERSION     BD097336.1  GI:22642910
KEYWORDS    WO 0165259-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 7 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/7
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 43
E32454
LOCUS       E32454                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32454
VERSION     E32454.1  GI:13018690
KEYWORDS    JP 2000037190-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 14 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/14
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 44
E32457
LOCUS       E32457                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32457
VERSION     E32457.1  GI:13018693
KEYWORDS    JP 2000037190-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 17 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/17
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
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           CC
           FH   Key             Location/Qualifiers
           FT   primer_bind      (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 45
E32460
LOCUS       E32460                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32460
VERSION     E32460.1  GI:13018696
KEYWORDS    JP 2000037190-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 20 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/20
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 46
AR139960
LOCUS       AR139960                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207417.
ACCESSION   AR139960
VERSION     AR139960.1  GI:14482456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 47
AR140279
LOCUS       AR140279                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207454.
ACCESSION   AR140279
VERSION     AR140279.1  GI:14482775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 48
AR140557
LOCUS       AR140557                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207802.
ACCESSION   AR140557
VERSION     AR140557.1  GI:14483053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20
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RESULT 49
AR142677/c
LOCUS       AR142677                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6203988.
ACCESSION   AR142677
VERSION     AR142677.1  GI:15103963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 7 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         20 TTTTTTTTTTTTTTTGG 4

RESULT 50
E15159
LOCUS       E15159                    20 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Phosphorothioate antisence oligo DNA for human VEGF mRNA.
ACCESSION   E15159
VERSION     E15159.1  GI:5709842
KEYWORDS    JP 1998052285-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K.
  TITLE     PREPARATION OF ANTISENSE NUCLEIC ACID
  JOURNAL   Patent: JP 1998052285-A 4 24-FEB-1998;
            TOAGOSEI CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1998052285-A/4
            PD   24-FEB-1998
            PF   20-MAY-1997 JP 1997129767
            PR   23-MAY-1996 JP 96P   128192
            PI   UCHIDA KIYOSHI
            PC   C12N15/09,C07H21/02,C07H21/04;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGCT 2279
              |||||||||||||||||
Db          4 TCTTTCCTCTTTCTGCT 20

RESULT 51
E22402/c
LOCUS       E22402                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Antisense nucleic acid compound.
ACCESSION   E22402
VERSION     E22402.1  GI:13024045
KEYWORDS    JP 1999042091-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kinya,K., Yoko,M. and Kiyoshi,U.
  TITLE     Antisense nucleic acid compound
  JOURNAL   Patent: JP 1999042091-A 4 16-FEB-1999;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999042091-A/4
            PD   16-FEB-1999
            PF   25-JUL-1997 JP 1997213838
            PR
            PI   KINYA KAMIYA,YOKO MATSUDA,KIYOSHI UCHIDA
            PC   C12N15/09,A61K31/70,A61K48/00,C12Q1/68,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGCT 2279
              |||||||||||||||||
Db         17 TCTTTCCTCTTTCTGCT 1

RESULT 52
E28096/c
LOCUS       E28096                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28096
VERSION     E28096.1  GI:13018321
KEYWORDS    JP 1999196874-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 7 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/7
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         20 TTTTTTTTTTTTTTTGG 4


RESULT 53
AR562156
LOCUS       AR562156                  20 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 32 from patent US 6759215.
ACCESSION   AR562156
VERSION     AR562156.1  GI:53976019
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method of preparing human stem cell factor polypeptide
  JOURNAL   Patent: US 6759215-A 32 06-JUL-2004;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 54
AX498246/c
LOCUS       AX498246                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from Patent WO0218951.
ACCESSION   AX498246
VERSION     AX498246.1  GI:23343165
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 2 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         17 AGTTTTTTTTTTTTTTT 1


RESULT 55
AX498247/c
LOCUS       AX498247                  21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from Patent WO0218951.
ACCESSION   AX498247
VERSION     AX498247.1  GI:23343166
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 3 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         18 AGTTTTTTTTTTTTTTT 2


RESULT 56
AX825123
LOCUS       AX825123                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 21 from Patent WO03072818.
ACCESSION   AX825123
VERSION     AX825123.1  GI:39750852
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 21 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 57
AX825125
LOCUS       AX825125                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 23 from Patent WO03072818.
ACCESSION   AX825125
VERSION     AX825125.1  GI:39750854
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 23 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 58
AX825156
LOCUS       AX825156                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 54 from Patent WO03072818.
ACCESSION   AX825156
VERSION     AX825156.1  GI:39750885
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 54 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTGG 21


RESULT 59
DOGP18802
LOCUS       DOGP18802                 20 bp    DNA     linear   MAM 11-MAR-1996
DEFINITION  Dog (Clone: CXX.188) primer for STS 188, 3' end.
ACCESSION   L24215
VERSION     L24215.1  GI:401865
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     2 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  TITLE     One hundred and one new simple sequence repeat-based markers for
            the canine genome
  JOURNAL   Mamm. Genome 6 (3), 192-195 (1995)
  MEDLINE   95268214
   PUBMED   7749226
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EAOstrander@lbl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile:  Denaturation:    94 degrees C for 1.00 minute
            Annealing:       55 or 59 degrees C for 0.45 minutes
            Polymerization:  74 degrees C for 1.00 minutes
            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     complement(1. .20)

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              || ||||||||| ||||||||
Db          1 TCCCTCTCCCTTCCTCTCTC 20


RESULT 60
AR084583/c
LOCUS       AR084583                  20 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 72 from patent US 5981185.
ACCESSION   AR084583
VERSION     AR084583.1  GI:10011354
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 72 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 61
AR084604
LOCUS       AR084604                  20 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 93 from patent US 5981185.
ACCESSION   AR084604
VERSION     AR084604.1  GI:10011375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 93 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db          1 CTCTCTCTCTCTCTCTCTCT 20


RESULT 62
BD145051/c
LOCUS       BD145051                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145051
VERSION     BD145051.1  GI:27850809
KEYWORDS    JP 2002119291-A/32.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 32 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/32
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 63
BD145062
LOCUS       BD145062                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145062
VERSION     BD145062.1  GI:27850820
KEYWORDS    JP 2002119291-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 43 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
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            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/43
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db          1 AAAAAAAAAATATATATATA 20


RESULT 64
BD166051/c
LOCUS       BD166051                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166051
VERSION     BD166051.1  GI:27871863
KEYWORDS    JP 2002191372-A/31.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 31 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/31
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 65
BD166062
LOCUS       BD166062                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166062
VERSION     BD166062.1  GI:27871874
KEYWORDS    JP 2002191372-A/42.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 42 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/42
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
```

```
Db          1 AAAAAAAAAATATATATATA 20


RESULT 66
BD228445
LOCUS       BD228445                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  IL-17 homologous polypeptide and its application to remedy.
ACCESSION   BD228445
VERSION     BD228445.1  GI:33038215
KEYWORDS    JP 2002515246-A/40.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Chen,J., Filvaroff,E., Goddard,A., Gurney,A.L., Li,H. and Wood,W.I.
  TITLE     IL-17 homologous polypeptide and its application to remedy
  JOURNAL   Patent: JP 2002515246-A 40 28-MAY-2002;
            GENENTECH INC
COMMENT     OS   Unidentified
            PN   JP 2002515246-A/40
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549734
            PR   15-MAY-1998 US    60/085579,23-DEC-1998 US    60/113621 PI
            JIAN CHEN,ELLEN FILVAROFF,AUDLEY GODDARD,AUSTIN L GURNEY, PI
            HANZHONG LI,
            PI   WILLIAM I WOOD
            PC   C12N15/09,A61K38/21,A61K45/00,A61P19/00,C07K14/52,C07K16/24,
            PC   C07K19/00,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/00 PC
            ,C12Q1/68,C12N15/00,
            PC   A61K37/66,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   IL-17 homologous polypeptide and its application to remedy FH
             Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20


RESULT 67
BD230765
LOCUS       BD230765                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes.
ACCESSION   BD230765
VERSION     BD230765.1  GI:33040535
KEYWORDS    JP 2002530091-A/634.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Galibert,F. and Andre,C.
  TITLE     Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes
  JOURNAL   Patent: JP 2002530091-A 634 17-SEP-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002530091-A/634
            PD   17-SEP-2002
            PF   15-NOV-1999 JP 2000582596
            PR   13-NOV-1998 US    60/108193
            PI   FRANCIS GALIBERT,CATHERINE ANDRE
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   CXX188
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Canis familiaris (dog)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              || |||||||| ||||||||
Db          1 TCCCTCTCCCTTCCTCTCTC 20


RESULT 68
I16926
LOCUS       I16926                    20 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 1 from patent US 5482836.
ACCESSION   I16926
VERSION     I16926.1  GI:1251834
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cantor,C.R., Ito,T. and Smith,C.L.
  TITLE     DNA purification by triplex-affinity capture and affinity capture
            electrophoresis
  JOURNAL   Patent: US 5482836-A 1 09-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 69
AR264947/c
LOCUS       AR264947                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 31 from patent US 6492121.
ACCESSION   AR264947
VERSION     AR264947.1  GI:29693334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 31 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 70
AR350279/c
LOCUS       AR350279                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 56 from patent US 6586245.
ACCESSION   AR350279
VERSION     AR350279.1  GI:33751250
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.F., Baker,B.F., Wyatt,J. and Davis,S.E.
  TITLE     Antisense modulation of CD40 ligand expression
  JOURNAL   Patent: US 6586245-A 56 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4482 AATGTATTTGATTTATAAGT 4501
              |||| |||||||||||| |||
Db         20 AATGCATTTGATTTATCAGT 1


RESULT 71
AR359670
LOCUS       AR359670                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 40 from patent US 6593456.
ACCESSION   AR359670
VERSION     AR359670.1  GI:33766414
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Gatanaga,T. and Granger,G.A.
  TITLE     Tumor necrosis factor receptor releasing enzyme
  JOURNAL   Patent: US 6593456-A 40 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20


RESULT 72
AR437004
LOCUS       AR437004                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 56 from patent US 6656732.
ACCESSION   AR437004
VERSION     AR437004.1  GI:40200088
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.F. and Watt,A.T.
  TITLE     Antisense inhibition of src-c expression
  JOURNAL   Patent: US 6656732-A 56 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3229 TGTTGAGCCAGTGGGCCAGC 3248
              || ||||| ||||||||||
Db          1 TGCTGAGCGAGTGGGCCAGC 20


RESULT 73
AR478228/c
LOCUS       AR478228                  20 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 31 from patent US 6699661.
ACCESSION   AR478228
VERSION     AR478228.1  GI:47236876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 31 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 74
BD072892/c
LOCUS       BD072892                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072892
VERSION     BD072892.1  GI:22618495
KEYWORDS    JP 2001286300-A/30.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 30 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
```

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            PN   JP 2001286300-A/30
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 75
BD072903
LOCUS       BD072903                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072903
VERSION     BD072903.1  GI:22618506
KEYWORDS    JP 2001286300-A/41.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 41 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/41
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db          1 AAAAAAAAAATATATATATA 20


RESULT 76
BD084130
LOCUS       BD084130                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084130
VERSION     BD084130.1  GI:22629740
KEYWORDS    JP 2001525663-A/18.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 18 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/18
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
              |||||||| ||||||| ||
Db          1 ATATATATATATATATATAT 20


RESULT 77
BD084130/c
LOCUS       BD084130                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084130
VERSION     BD084130.1  GI:22629740
KEYWORDS    JP 2001525663-A/18.
SOURCE      Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 18 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/18
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
              ||||||||| ||||||| ||
Db         20 ATATATATATATATATATAT 1


RESULT 78
BD107519/c
LOCUS       BD107519                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107519
VERSION     BD107519.1  GI:23202337
KEYWORDS    JP 2002000275-A/28.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 28 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/28
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 79
BD107530
LOCUS       BD107530                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107530
VERSION     BD107530.1  GI:23202348
KEYWORDS    JP 2002000275-A/39.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 39 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/39
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db          1 AAAAAAAAAATATATATATA 20


RESULT 80
A64735
LOCUS       A64735                    21 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 1 from Patent WO9729116.
ACCESSION   A64735
VERSION     A64735.1  GI:4530771
KEYWORDS    .
```

```
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Reese,C.B. and Rao,M.V.
  TITLE     SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
  JOURNAL   Patent: WO 9729116-A 1 14-AUG-1997;
            CRUACHEM LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 81
A64736
LOCUS       A64736                    21 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 2 from Patent WO9729116.
ACCESSION   A64736
VERSION     A64736.1  GI:4530772
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Reese,C.B. and Rao,M.V.
  TITLE     SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
  JOURNAL   Patent: WO 9729116-A 2 14-AUG-1997;
            CRUACHEM LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              |||||||| ||| ||||||
Db          1 CTCTCTCTCTCTCTCTCTCT 20


RESULT 82
A64738
LOCUS       A64738                    21 bp    DNA     linear   PAT 16-OCT-1999
DEFINITION  Sequence 4 from Patent WO9729116.
ACCESSION   A64738
VERSION     A64738.1  GI:4530774
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Reese,C.B. and Rao,M.V.
  TITLE     SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
  JOURNAL   Patent: WO 9729116-A 4 14-AUG-1997;
            CRUACHEM LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     modified_base   2
                     /mod_base=OTHER
     modified_base   4
                     /mod_base=OTHER
     modified_base   6
                     /mod_base=OTHER
     modified_base   8
                     /mod_base=OTHER
     modified_base   10
                     /mod_base=OTHER
     modified_base   12
                     /mod_base=OTHER
     modified_base   14
                     /mod_base=OTHER
     modified_base   16
                     /mod_base=OTHER
     modified_base   18
                     /mod_base=OTHER
     modified_base   20
                     /mod_base=OTHER

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 83
A64739
LOCUS       A64739                    21 bp    DNA     linear   PAT 16-OCT-1999
DEFINITION  Sequence 5 from Patent WO9729116.
ACCESSION   A64739
VERSION     A64739.1  GI:4530775
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Reese,C.B. and Rao,M.V.
  TITLE     SULPHUR CONTAINING DINUCLEOTIDE PHOSPHORAMIDITES
  JOURNAL   Patent: WO 9729116-A 5 14-AUG-1997;
            CRUACHEM LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     modified_base   2
                     /mod_base=OTHER
     modified_base   4
                     /mod_base=OTHER
     modified_base   6
                     /mod_base=OTHER
     modified_base   8
                     /mod_base=OTHER
     modified_base   10
                     /mod_base=OTHER
     modified_base   12
                     /mod_base=OTHER
     modified_base   14
                     /mod_base=OTHER
     modified_base   16
                     /mod_base=OTHER
     modified_base   18
                     /mod_base=OTHER
     modified_base   20
                     /mod_base=OTHER

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
```

```
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db          1 CTCTCTCTCTCTCTCTCTCT 20


RESULT 84
AR540710
LOCUS       AR540710                  21 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 2 from patent US 6737253.
ACCESSION   AR540710
VERSION     AR540710.1  GI:53932035
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Tillett,D.
  TITLE     Method of amplification of nucleic acids
  JOURNAL   Patent: US 6737253-A 2 18-MAY-2004;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1423 TTAACCCATTCCAGTACAGT 1442
              ||||||||| |||||||| |
Db          2 TTAACCCATACCAGTACAAT 21


RESULT 85
AX825134
LOCUS       AX825134                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 32 from Patent WO03072818.
ACCESSION   AX825134
VERSION     AX825134.1  GI:39750863
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 32 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||  |||
Db          2 TTTTTTTTTTTTTTTTGTT 21


RESULT 86
AX825150
LOCUS       AX825150                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 48 from Patent WO03072818.
ACCESSION   AX825150
VERSION     AX825150.1  GI:39750879
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 48 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTT 2143
              |||| |||| ||||||||||
Db          2 TTTTTTTTTTTTTTTTTCTT 21


RESULT 87
BD056566
LOCUS       BD056566                  21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method to diagnose and treat pathological conditions resulting from
            deficient ion transport.
ACCESSION   BD056566
VERSION     BD056566.1  GI:22602172
```

```
KEYWORDS    JP 2001508291-A/23.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lifton,R.P. and Simon,D.B.
  TITLE     Method to diagnose and treat pathological conditions resulting from
            deficient ion transport
  JOURNAL   Patent: JP 2001508291-A 23 26-JUN-2001;
            YALE UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2001508291-A/23
            PD   26-JUN-2001
            PF   19-DEC-1997 JP 1998530123
            PR   31-DEC-1996 US    08/778052
            PI   RICHARD P LIFTON,DAVID B SIMON
            PC   C12N15/09,C07K14/435,C07K16/00,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00 CC   Primer
            for analysis of human TSC gene
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3183 CTCTCTCCCTCCCTCTCTCA 3202
              ||||||||||||||||  |||
Db          1 CTCTCTCCCTCCCTCCTTCA 20


RESULT 88
BD145036
LOCUS       BD145036                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145036
VERSION     BD145036.1  GI:27850794
KEYWORDS    JP 2002119291-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 17 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/17
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 89
BD166036
LOCUS       BD166036                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166036
VERSION     BD166036.1  GI:27871848
KEYWORDS    JP 2002191372-A/16.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 16 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/16
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC          nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18
```

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RESULT 90
E32450
LOCUS       E32450                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32450
VERSION     E32450.1  GI:13018686
KEYWORDS    JP 2000037190-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 10 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/10
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||| |
Db          1 GTTTTTTTTTTTTTTTAG 18


RESULT 91
E32452
LOCUS       E32452                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32452
VERSION     E32452.1  GI:13018688
KEYWORDS    JP 2000037190-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 12 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/12
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||| |
Db          1 GTTTTTTTTTTTTTTTCG 18


RESULT 92
AR241816/c
LOCUS       AR241816                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 104 from patent US 6472154.
ACCESSION   AR241816
VERSION     AR241816.1  GI:27287628
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 104 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATAC 2411
              ||||||||| ||||||||
Db         18 ATATATATATATATATAC 1


RESULT 93
AR264932
LOCUS       AR264932                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 16 from patent US 6492121.
ACCESSION   AR264932
VERSION     AR264932.1  GI:29693319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 16 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18
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RESULT 94
AR478213
LOCUS       AR478213                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 16 from patent US 6699661.
ACCESSION   AR478213
VERSION     AR478213.1  GI:47236861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 16 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 95
BD072877
LOCUS       BD072877                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072877
VERSION     BD072877.1  GI:22618480
KEYWORDS    JP 2001286300-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 15 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/15
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 96
BD107504
LOCUS       BD107504                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107504
VERSION     BD107504.1  GI:23202322
KEYWORDS    JP 2002000275-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 13 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/13
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 97
AB175211
LOCUS       AB175211                 18 bp    DNA     linear   SYN 26-MAR-2004
DEFINITION  Synthetic construct DNA, forward primer for Japanese flounder
            microsatellite sequence Poli21HFS-M.
ACCESSION   AB175211
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```
VERSION     AB175211.1  GI:45752534
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fuji,K., Kobayashi,K., Mizuta,A., Hasegawa,O., Tabata,K.,
            Sakamoto,T. and Okamoto,N.
  TITLE     A genetic linkage map of the Japanease Flounder, (Paralichthys
            olivaceus)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Mizuta,A., Tabata,K., Kobayashi,K., Fuji,K., Sakamoto,T. and
            Okamoto,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2004) Nobuaki Okamoto, Tokyo University of Marine
            Science and Technology, Department of Marine Biosciences; 4-5-7
            Konan, Minato-ku, Tokyo 108-8477, Japan
            (E-mail:nokamoto@s.kaiyodai.ac.jp, Tel:81-3-5463-0547,
            Fax:81-3-5463-0552)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="other DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .18
                     /note="forward primer for Japanese flounder microsatellite
                     sequence Poli21MHFS"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5165 ATCTGAGATTGTGTTTGT 5182
              || ||||||||||||||||
Db          1 ATTTGAGATTGTGTTTGT 18


RESULT 98
AX129706
LOCUS       AX129706                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 924 from Patent WO0130362.
ACCESSION   AX129706
VERSION     AX129706.1  GI:14136011
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 924 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk8 ribozyme binding site"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1830 CACAAAGCTTCTAAAGCA 1847
              |||| ||||||||||||||
Db          1 CACAGAGCTTCTAAAGCA 18


RESULT 99
BD143136
LOCUS       BD143136                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel testis-specific gene.
ACCESSION   BD143136
VERSION     BD143136.1  GI:27848894
KEYWORDS    JP 2002112777-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Novel testis-specific gene
  JOURNAL   Patent: JP 2002112777-A 3 16-APR-2002;
            KACHIKU KAIRYO JIGYODAN,PRESIDENT OF GUNMA UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002112777-A/3
            PD   16-APR-2002
            PF   03-OCT-2000 JP 2000303994
            PI   AKIRA AIZAWA,AKIKO KAWAKAMI,TOSHIHIKO KONDO
            PC   C12N15/09,C07K14/47,C12N15/00
            CC   Novel testis-specific gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTTT 4515
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTTT 18


RESULT 100
BD161924
LOCUS       BD161924                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161924
VERSION     BD161924.1  GI:27867682
KEYWORDS    JP 2002191369-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 1 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/1
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTTT 4515
              || |||||||||||||||
Db          1 AAATTTTTTTTTTTTTTT 18


RESULT 101
AR309844
LOCUS       AR309844                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4 from patent US 6555670.
ACCESSION   AR309844
VERSION     AR309844.1  GI:31701953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: US 6555670-A 4 29-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTTT 4515
              ||| |||||||||||||||
Db          1 AAGCTTTTTTTTTTTTTT 18


RESULT 102
AX296109/c
LOCUS       AX296109                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7871 from Patent WO0179548.
ACCESSION   AX296109
VERSION     AX296109.1  GI:17057798
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7871 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2527 CATGAGATGGAGAGGCTG 2544
              |||||||||| ||||||
Db         18 CATGAGATGGACAGGCTG 1


RESULT 103
AX404077
LOCUS       AX404077                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 4 from Patent EP1195382.
ACCESSION   AX404077
VERSION     AX404077.1  GI:21437393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: EP 1195382-A 4 10-APR-2002;
            Livestock Improvement Association of Japan, Inc. (JP) ; President
            of Gunma University (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTTT 4515
              ||| |||||||||||||||
Db          1 AAGCTTTTTTTTTTTTTT 18


RESULT 104
BD142808
LOCUS       BD142808                  17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142808
VERSION     BD142808.1  GI:23237753
KEYWORDS    WO 0224903-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 2 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/2
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
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  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 105
BD142809
LOCUS       BD142809                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142809
VERSION     BD142809.1  GI:23237754
KEYWORDS    WO 0224903-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 3 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/3
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 106
BD143834
LOCUS       BD143834                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143834
VERSION     BD143834.1  GI:27849592
KEYWORDS    JP 2002095500-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 2 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/2
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 107
BD143835
LOCUS       BD143835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143835
VERSION     BD143835.1  GI:27849593
KEYWORDS    JP 2002095500-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 3 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/3
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized
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           CC            primer
           CC   sequence
           FH   Key             Location/Qualifiers
           FT   source          1. .17
           FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 108
BD167835
LOCUS       BD167835                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167835
VERSION     BD167835.1  GI:27873647
KEYWORDS    WO 0233122-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 2 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/2
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 109
BD167836
LOCUS       BD167836                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167836
VERSION     BD167836.1  GI:27873648
KEYWORDS    WO 0233122-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 3 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/3
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 110
BD167907
LOCUS       BD167907                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167907
VERSION     BD167907.1  GI:27873719
KEYWORDS    WO 0226962-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 6 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/6
            PD   04-APR-2002
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            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
           TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 111
BD167908
LOCUS       BD167908                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167908
VERSION     BD167908.1  GI:27873720
KEYWORDS    WO 0226962-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 7 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/7
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 112
BD168111
LOCUS       BD168111                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168111
VERSION     BD168111.1  GI:27873923
KEYWORDS    WO 0233069-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 18 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/18
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630" .

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 113
BD168112
LOCUS       BD168112                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168112
VERSION     BD168112.1  GI:27873924
KEYWORDS    WO 0233069-A/19.
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 19 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/19
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 114
BD171177
LOCUS       BD171177                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171177
VERSION     BD171177.1  GI:27876989
KEYWORDS    WO 0250269-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 2 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/2
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15A', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 115
BD171178
LOCUS       BD171178                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171178
VERSION     BD171178.1  GI:27876990
KEYWORDS    WO 0250269-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 3 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/3
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15C', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16
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RESULT 116
E34258
LOCUS       E34258                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34258
VERSION     E34258.1  GI:18624263
KEYWORDS    JP 2000106879-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 2 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/2
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 117
E34259
LOCUS       E34259                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34259
VERSION     E34259.1  GI:18624264
KEYWORDS    JP 2000106879-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 3 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/3
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 118
AX673525
LOCUS       AX673525                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1970 from Patent WO03004526.
ACCESSION   AX673525
VERSION     AX673525.1  GI:29331873
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1970 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 119
AX692526
LOCUS       AX692526                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5258 from Patent EP1281758.
ACCESSION   AX692526
VERSION     AX692526.1  GI:29415484
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5258 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 120
AX692527
LOCUS       AX692527                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5259 from Patent EP1281758.
ACCESSION   AX692527
VERSION     AX692527.1  GI:29415485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5259 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 121
AX735811
LOCUS       AX735811                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1401 from Patent WO03025177.
ACCESSION   AX735811
VERSION     AX735811.1  GI:30515088
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 1401 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 122
AX758271
LOCUS       AX758271                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1592 from Patent WO03040369.
ACCESSION   AX758271
VERSION     AX758271.1  GI:32252887
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1592 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 123
AX762966
LOCUS       AX762966                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 6287 from Patent WO03040369.
ACCESSION   AX762966
VERSION     AX762966.1  GI:32257582
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 6287 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 124
BD011730
LOCUS       BD011730                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011730
VERSION     BD011730.1  GI:22091919
```

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KEYWORDS    WO 0065050-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 2 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/2
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 125
BD011731
LOCUS       BD011731                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011731
VERSION     BD011731.1  GI:22091920
KEYWORDS    WO 0065050-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 3 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/3
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 126
BD091742
LOCUS       BD091742                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091742
VERSION     BD091742.1  GI:22637353
KEYWORDS    WO 0073435-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 127
BD091743
LOCUS       BD091743                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091743
VERSION     BD091743.1  GI:22637354
KEYWORDS    WO 0073435-A/3.
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 128
BD091750
LOCUS       BD091750                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091750
VERSION     BD091750.1  GI:22637361
KEYWORDS    WO 0073439-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 129
BD091751
LOCUS       BD091751                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091751
VERSION     BD091751.1  GI:22637362
KEYWORDS    WO 0073439-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 130
BD091773
LOCUS       BD091773                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091773
VERSION     BD091773.1  GI:22637384
KEYWORDS    WO 0073440-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
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            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 131
BD091774
LOCUS       BD091774                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091774
VERSION     BD091774.1  GI:22637385
KEYWORDS    WO 0073440-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 132
BD097334
LOCUS       BD097334                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097334
VERSION     BD097334.1  GI:22642908
KEYWORDS    WO 0165259-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 5 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/5
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 133
BD097335
LOCUS       BD097335                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097335
VERSION     BD097335.1  GI:22642909
KEYWORDS    WO 0165259-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 6 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
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            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/6
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 134
A14689/c
LOCUS       A14689                    18 bp    DNA     linear   PAT 28-MAR-1994
DEFINITION  Nucleotide sequence 9 from patent number WO8303623.
ACCESSION   A14689
VERSION     A14689.1  GI:513760
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE
            ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a
            HPV TYPE AND CORRESPONDING POLYPEPTIDES
  JOURNAL   Patent: WO 8303623-A 9 27-OCT-1983;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         17 TTTTTTTTTTTTTTTG 2


RESULT 135
E32453
LOCUS       E32453                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32453
VERSION     E32453.1  GI:13018689
KEYWORDS    JP 2000037190-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 13 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/13
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 136
E32455
LOCUS       E32455                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32455
VERSION     E32455.1  GI:13018691
KEYWORDS    JP 2000037190-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 15 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/15
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
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```
Db          1 GTTTTTTTTTTTTTT 16


RESULT 137
E32456
LOCUS       E32456                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32456
VERSION     E32456.1  GI:13018692
KEYWORDS    JP 2000037190-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 16 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/16
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 GTTTTTTTTTTTTTT 16


RESULT 138
E32458
LOCUS       E32458                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32458
VERSION     E32458.1  GI:13018694
KEYWORDS    JP 2000037190-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 18 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/18
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 GTTTTTTTTTTTTTT 16


RESULT 139
E32459
LOCUS       E32459                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32459
VERSION     E32459.1  GI:13018695
KEYWORDS    JP 2000037190-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 19 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/19
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 GTTTTTTTTTTTTTT 16


RESULT 140
E32461
LOCUS       E32461                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32461
VERSION     E32461.1  GI:13018697
KEYWORDS    JP 2000037190-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
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  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 21 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/21
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 141
AR208425
LOCUS       AR208425                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6383754.
ACCESSION   AR208425
VERSION     AR208425.1  GI:21509576
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 5 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 142
AR208426
LOCUS       AR208426                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6383754.
ACCESSION   AR208426
VERSION     AR208426.1  GI:21509577
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 6 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 143
AX028845
LOCUS       AX028845                  18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 29 from Patent WO9732023.
ACCESSION   AX028845
VERSION     AX028845.1  GI:10189948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 29 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 144
AX085251
LOCUS       AX085251                  18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 5 from Patent WO0112855.
ACCESSION   AX085251
VERSION     AX085251.1  GI:13275309
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 5 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
```

```
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTG 17


RESULT 145
AX085252
LOCUS       AX085252                  18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 6 from Patent WO0112855.
ACCESSION   AX085252
VERSION     AX085252.1  GI:13275310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 6 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTG 17


RESULT 146
AX224044
LOCUS       AX224044                  18 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 3 from Patent WO0160993.
ACCESSION   AX224044
VERSION     AX224044.1  GI:15554357
KEYWORDS    .
SOURCE      Klebsiella singaporensis
  ORGANISM  Klebsiella singaporensis
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Zhang,L.H., Li,X. and Zhang,D.
  TITLE     Bacterial isolates of the genus klebsiella, and an isomaltulose
            synthase gene isolated therefrom
  JOURNAL   Patent: WO 0160993-A 3 23-AUG-2001;
            Institute of Molecular Agrobiology (SG)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Klebsiella singaporensis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:157589"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2137 TTTTCTTTAATAACAA 2152
              ||||||||||||||||
Db          1 TTTTCTTTAATAACAA 16


RESULT 147
AX643396/c
LOCUS       AX643396                  19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 262 from Patent WO02099099.
ACCESSION   AX643396
VERSION     AX643396.1  GI:28551047
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 262 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||||||||||||||
Db         18 TATACATATATACATT 3


RESULT 148
AX643399
LOCUS       AX643399                  19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 265 from Patent WO02099099.
ACCESSION   AX643399
VERSION     AX643399.1  GI:28551051
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 265 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||||||||||||||
Db          2 TATACATATATACATT 17


RESULT 149
AR162375
LOCUS       AR162375                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 55 from patent US 6258600.
ACCESSION   AR162375
VERSION     AR162375.1  GI:16229549
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 8 expression
  JOURNAL   Patent: US 6258600-A 55 10-JUL-2001;
```

```
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1772 GTTGATTATCTTCAGC 1787
              ||||||||||||||||
Db          3 GTTGATTATCTTCAGC 18


RESULT 150
BD196130/c
LOCUS       BD196130                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide sequences as inhibitors of
            microorganisms.
ACCESSION   BD196130
VERSION     BD196130.1  GI:33005900
KEYWORDS    JP 2002514093-A/161.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences as inhibitors of microorganisms
  JOURNAL   Patent: JP 2002514093-A 161 14-MAY-2002;
            GENESENSE TECHNOLOGIES INC
COMMENT     OS   Escherichia coli
            PN   JP 2002514093-A/161
            PD   14-MAY-2002
            PF   10-JUL-1998 JP 1999507930
            PR   10-JUL-1997 US    60/052160
            PI   JIM A WRIGHT,AIPING H YOUNG,DOMINIQUE DUGOURD PC
            C12N15/11,C12N15/31
            CC   Antisense oligonucleotide sequences as inhibitors of  CC
                 microorganisms
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Escherichia coli'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"

  Query Match              0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1284 GAACCGGAGATGGAAA 1299
              ||||||||||||||||
Db         18 GAACCGGAGATGGAAA 3


RESULT 151
BD234126/c
LOCUS       BD234126                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION   BD234126
VERSION     BD234126.1  GI:33043896
KEYWORDS    JP 2002532072-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipovsek,D.
  TITLE     Protein skeleton of antibody mimetics and other binding proteins
  JOURNAL   Patent: JP 2002532072-A 14 02-OCT-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002532072-A/14
            PD   02-OCT-2002
            PF   09-DEC-1999 JP 2000587187
            PR   10-DEC-1998 US    60/111737
            PI   DASA LIPOVSEK
            PC   C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC
              C12P21/02,
            PC   C12N15/00
            CC   Puromycin linker oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db         19 GTTTTTTTTTTTTTTT 4


RESULT 152
AR382921/c
LOCUS       AR382921                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 161 from patent US 6610539.
ACCESSION   AR382921
VERSION     AR382921.1  GI:40091734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences as inhibitors of microorganisms
  JOURNAL   Patent: US 6610539-A 161 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1284 GAACCGGAGATGGAAA 1299
              ||||||||||||||||
Db         18 GAACCGGAGATGGAAA 3


RESULT 153
AX067205
LOCUS       AX067205                  20 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 57 from Patent WO0100669.
ACCESSION   AX067205
VERSION     AX067205.1  GI:12544870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Barry,C., Bougueleret,L., Chumakov,I. and Cohen-Akenine,A.
  TITLE     A bap28 gene and protein
  JOURNAL   Patent: WO 0100669-A 57 04-JAN-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide BAP28polyTcourt"

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 154
AR072539/c
LOCUS       AR072539                 19 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 10 from patent US 5948622.
ACCESSION   AR072539
VERSION     AR072539.1  GI:9999303
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S., Goryshin,I.Yu., York,D.L. and Zhou,H.
  TITLE     System for in vitro transposition
  JOURNAL   Patent: US 5948622-A 10 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 155
AR121569/c
LOCUS       AR121569                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6159736.
ACCESSION   AR121569
VERSION     AR121569.1  GI:14105145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S. and Goryshin,I.Y.
  TITLE     Method for making insertional mutations using a Tn5 synaptic
            complex
  JOURNAL   Patent: US 6159736-A 2 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 156
BD251066/c
LOCUS       BD251066                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method for making insertional mutations.
ACCESSION   BD251066
VERSION     BD251066.1  GI:33060836
KEYWORDS    JP 2002531062-A/2.
SOURCE      Transposon Tn5
  ORGANISM  Transposon Tn5
            other sequences; transposons.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S. and Goryshin,I.Y.
  TITLE     Method for making insertional mutations
  JOURNAL   Patent: JP 2002531062-A 2 24-SEP-2002;
            WISCONSIN ALUMNI RESEARCH FOUNDATION
COMMENT     OS   Transposon Tn5
            PN   JP 2002531062-A/2
            PD   24-SEP-2002
            PF   21-SEP-1999 JP 2000574243
            PR   23-SEP-1998 US    09/159363
            PI   WILLIAM S REZNIKOFF,IGOR Y GORYSHIN
            PC   C12N15/09,C12N9/00,C12N15/01,C12Q1/02//G01N33/15,G01N33/50, PC
              G01N33/566,
            PC   C12N15/00,C12N15/00
            CC   Method for making insertional mutations
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Transposon Tn5'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Transposon Tn5"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:2411"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 157
CQ798891
LOCUS       CQ798891                 19 bp    DNA     linear   PAT 28-APR-2004
DEFINITION  Sequence 30 from Patent EP1410803.
ACCESSION   CQ798891
VERSION     CQ798891.1  GI:46847926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bosserhoff,A., Hellerbrand,C. and Buettner,R.
  TITLE     MIA-2 proteins
  JOURNAL   Patent: EP 1410803-A 30 21-APR-2004;
            Scil proteins GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2317 AATAAGATGGCTGTGGCAT 2335
              || |||||||| |||||||
Db          1 AAGAAGATGGCGGTGGCAT 19


RESULT 158
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AR214207/c
LOCUS       AR214207                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6406896.
ACCESSION   AR214207
VERSION     AR214207.1  GI:23311737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S. and Naumann,T.A.
  TITLE     Transposase enzyme and method for use
  JOURNAL   Patent: US 6406896-A 4 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 159
AR360576
LOCUS       AR360576                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3 from patent US 6596509.
ACCESSION   AR360576
VERSION     AR360576.1  GI:33767641
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bauer,D.W., Beer,S.V., Bogdanove,A.J., Collmer,A. and Ham,J.H.
  TITLE     Recombinant constructs and systems for secretion of proteins via
            type III secretion systems
  JOURNAL   Patent: US 6596509-A 3 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db          1 AGATCTGATCAAGAGACAG 19


RESULT 160
AR363387/c
LOCUS       AR363387                  19 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 3 from patent US 5212080.
ACCESSION   AR363387
VERSION     AR363387.1  GI:34424883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Nag,D.K., Huang,H.V. and Berg,D.E.
  TITLE     Method of DNA sequencing using DNA transposon Tn5seql
  JOURNAL   Patent: US 5212080-A 3 18-MAY-1993;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 161
AX080722/c
LOCUS       AX080722                  19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 4 from Patent WO0109363.
ACCESSION   AX080722
VERSION     AX080722.1  GI:13169711
KEYWORDS    .
SOURCE      Transposon Tn5
  ORGANISM  Transposon Tn5
            other sequences; transposons.
REFERENCE   1
  AUTHORS   Reznikoff,W.S. and Naumann,T.A.
  TITLE     Mutant tn5 transposase enzymes and method for their use
  JOURNAL   Patent: WO 0109363-A 4 08-FEB-2001;
            WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Transposon Tn5"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:2411"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 162
AX132689
LOCUS       AX132689                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3907 from Patent WO0130362.
ACCESSION   AX132689
VERSION     AX132689.1  GI:14138994
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3907 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1117 TGAGGGCTTCCACAACTAC 1135
              |||||||||| ||| ||||
Db          1 TGAGGGCTTCGACACCTAC 19
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RESULT 163
BD064203/c
LOCUS       BD064203                19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  System for in vitro transposition using modified TN5 transposase.
ACCESSION   BD064203
VERSION     BD064203.1  GI:22609806
KEYWORDS    JP 2001507565-A/6.
SOURCE      Conus quercinus
  ORGANISM  Conus quercinus
            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
            Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
            Neogastropoda; Conoidea; Conidae; Conus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S., Goryshin,I.Y. and Zhou,H.
  TITLE     System for in vitro transposition using modified TN5 transposase
  JOURNAL   Patent: JP 2001507565-A 6 12-JUN-2001;
            WISCONSIN ALUMNI RESEARCH FOUNDATION
COMMENT     PN   JP 2001507565-A/6
            PD   12-JUN-2001
            PF   09-SEP-1997 JP 1998512997
            PR   09-SEP-1996 US    08/814877,02-MAY-1997 US    08/850880 PI
            WILLIAM S REZNIKOFF,IGOR YU GORYSHIN,HONG ZHOU PC
            C12N15/55,C12N9/22,C12N15/90,C12N15/85
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc= Tn5 wild inner end
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="Conus quercinus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:101313"

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 164
BD217905
LOCUS       BD217905                17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same.
ACCESSION   BD217905
VERSION     BD217905.1  GI:33027675
KEYWORDS    JP 2002516564-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Umansky,S. and Melkonyan,H.
  TITLE     Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same
  JOURNAL   Patent: JP 2002516564-A 6 04-JUN-2002;
            TANOX INC
COMMENT     OS   Unidentified
            PN   JP 2002516564-A/6
            PD   04-JUN-2002
            PF   24-SEP-1997 JP 1998515877
            PR   24-SEP-1996 US    60/026603,11-OCT-1996 US    60/028363 PI
            SAMUIL UMANSKY,HOVSEP MELKONYAN
            PC   C12N15/12,C12N15/62,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
              G01N33/68,
            PC   A61K38/17
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Gene family encoding apoptosis-associated peptides, peptides
            CC            encoded
            CC   thereby and method of using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.4%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  :
Db          1 TTTTTTTTTTTTTTNS 17


RESULT 165
AX643397/c
LOCUS       AX643397                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 263 from Patent WO02099099.
ACCESSION   AX643397
VERSION     AX643397.1  GI:28551049
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 263 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="r=g or a"

  Query Match             0.4%;  Score 15.6;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||||||:|||||||
Db         18 TATACATAYATACATT 3


RESULT 166
AX643400
LOCUS       AX643400                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 266 from Patent WO02099099.
ACCESSION   AX643400
VERSION     AX643400.1  GI:28551052
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 266 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="y=t or c"
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  Query Match             0.4%;  Score 15.6;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||||||:|||||||
Db          2 TATACATAYATACATT 17


RESULT 167
AR047358/c
LOCUS       AR047358                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2151 from patent US 5817796.
ACCESSION   AR047358
VERSION     AR047358.1  GI:5968823
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2151 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAA 3979
              |||||||| ||||||||
Db         17 TATATAAAAAATAAAA 1


RESULT 168
AR047360/c
LOCUS       AR047360                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2153 from patent US 5817796.
ACCESSION   AR047360
VERSION     AR047360.1  GI:5968825
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2153 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAA 3978
              |||||||| |||||||
Db         17 ATATATAAAAAATAAA 1


RESULT 169
I54410/c
LOCUS       I54410                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2151 from patent US 5646042.
ACCESSION   I54410
VERSION     I54410.1  GI:2475613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2151 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAA 3979
              |||||||| ||||||||
Db         17 TATATAAAAAATAAAA 1


RESULT 170
I54412/c
LOCUS       I54412                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2153 from patent US 5646042.
ACCESSION   I54412
VERSION     I54412.1  GI:2475615
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2153 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAA 3978
              |||||||| |||||||
Db         17 ATATATAAAAAATAAA 1


RESULT 171
AR187061
LOCUS       AR187061                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2549 from patent US 6346398.
ACCESSION   AR187061
VERSION     AR187061.1  GI:20233026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ||||||||||||||||
Db          1 ACTTTTTTTTTTTTTTT 17


RESULT 172
AR323671
LOCUS       AR323671                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1073 from patent US 6566127.
ACCESSION   AR323671
VERSION     AR323671.1  GI:33709479
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1073 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ||||||||||||||||
Db          1 ACTTTTTTTTTTTTTTT 17


RESULT 173
AX672990/c
LOCUS       AX672990                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1435 from Patent WO03004526.
ACCESSION   AX672990
VERSION     AX672990.1  GI:29331338
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1435 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2582 TCACATAGGAAGGGATC 2598
              ||||||||| ||||||
Db         17 TCACATAGGATGGGATC 1


RESULT 174
AX692528
LOCUS       AX692528                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5260 from Patent EP1281758.
ACCESSION   AX692528
VERSION     AX692528.1  GI:29415486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGG 4518
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTTGAG 17


RESULT 175
AX729110/c
LOCUS       AX729110                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 744 from Patent WO03025175.
ACCESSION   AX729110
VERSION     AX729110.1  GI:30508453
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 744 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4170 AATGATAAACTCAGATC 4186
              |||||||||| ||||||
Db         17 AATGATAAACACAGATC 1


RESULT 176
HSDNA2128
LOCUS       HSDNA2128                 17 bp    DNA     linear   PRI 09-SEP-2004
DEFINITION  Homo sapiens Solid-phase minisequencing detection primer for PBGD
            gene in exon 10.
ACCESSION   AJ002128
VERSION     AJ002128.1  GI:2546967
KEYWORDS    PBGD gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Mustajoki,S., Kauppinen,R., Mustajoki,P., Suomalainen,A. and
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            Peltonen,L.
  TITLE     Steady-state transcript levels of the porphobilinogen deaminase
            gene in patients with acute intermittent porphyria
  JOURNAL   Genome Res. 7 (11), 1054-1060 (1997)
  MEDLINE   98041951
   PUBMED   9371741
REFERENCE   2  (bases 1 to 17)
  AUTHORS   Mustajoki,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-OCT-1997) Mustajoki S., Department of Medicine,
            Division of Endocrinology, Helsinki University Central Hsopital,
            Meilahti Hospital, 1 st floor, room P0155, FIN-00290 Helsinki,
            FINLAND
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="q24"
     gene            1. .17
                     /gene="PBGD"
     misc_feature    1. .17
                     /gene="PBGD"
                     /note="Solid-phase minisequencing detection primer"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1626 GTCCAGCTTCCAAAGCC 1642
              ||||||||||| |||||
Db          1 GTCCAGCTTCCGAAGCC 17


RESULT 177
BD145037
LOCUS       BD145037                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145037
VERSION     BD145037.1  GI:27850795
KEYWORDS    JP 2002119291-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 18 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/18
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 178
BD145040
LOCUS       BD145040                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145040
VERSION     BD145040.1  GI:27850798
KEYWORDS    JP 2002119291-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 21 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/21
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 179
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```
BD166037
LOCUS       BD166037                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166037
VERSION     BD166037.1  GI:27871849
KEYWORDS    JP 2002191372-A/17.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 17 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/17
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 180
BD166040
LOCUS       BD166040                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166040
VERSION     BD166040.1  GI:27871852
KEYWORDS    JP 2002191372-A/20.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 20 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/20
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 181
BD267708
LOCUS       BD267708                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of amplifying nucleic acid.
ACCESSION   BD267708
VERSION     BD267708.1  GI:33077476
KEYWORDS    JP 2002542837-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Tillett,D.
  TITLE     Method of amplifying nucleic acid
  JOURNAL   Patent: JP 2002542837-A 2 17-DEC-2002;.
            TAKARA HOLDINGS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002542837-A/2
            PD   17-DEC-2002
            PF   01-MAY-2000 JP 2000615790
            PR   30-APR-1999 AU      PQ 0087
            PI   DANIEL TILLETT
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Method of amplifying nucleic acid
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       1423 TTAACCCATTCCAGTAC 1439
              ||||||||| |||||||
Db          2 TTAACCCATACCAGTAC 18
```

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RESULT 182
E28534
LOCUS       E28534                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28534
VERSION     E28534.1  GI:13025386
KEYWORDS    JP 1999075880-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 1 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/1
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          2 ATATATATATATATATA 18
```

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RESULT 183
E28534/c
LOCUS       E28534                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28534
VERSION     E28534.1  GI:13025386
KEYWORDS    JP 1999075880-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 1 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/1
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         17 ATATATATATATATATA 1
```

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RESULT 184
AR264933
LOCUS       AR264933                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6492121.
ACCESSION   AR264933
VERSION     AR264933.1  GI:29693320
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 17 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18
```

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RESULT 185
AR264936
LOCUS       AR264936                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 20 from patent US 6492121.
ACCESSION   AR264936
VERSION     AR264936.1  GI:29693323
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 20 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 186
AR478214
LOCUS       AR478214                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 17 from patent US 6699661.
ACCESSION   AR478214
VERSION     AR478214.1  GI:47236862
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 17 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 187
AR478217
LOCUS       AR478217                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 20 from patent US 6699661.
ACCESSION   AR478217
VERSION     AR478217.1  GI:47236865
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 20 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 188
AX355057
LOCUS       AX355057                 18 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 85 from Patent WO0197843.
ACCESSION   AX355057
VERSION     AX355057.1  GI:18619724
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 85 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          1 ATATATATATATATATA 17


RESULT 189
AX355057/c
LOCUS       AX355057                 18 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 85 from Patent WO0197843.
ACCESSION   AX355057
VERSION     AX355057.1  GI:18619724
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 85 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         18 ATATATATATATATATA 2


RESULT 190
AX361600
LOCUS       AX361600                 18 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 18 from Patent WO0208461.
ACCESSION   AX361600
VERSION     AX361600.1  GI:18694219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
```

```
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 18 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Double-stranded product DNA"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 191
AX814932
LOCUS       AX814932                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 18 from Patent WO03064691.
ACCESSION   AX814932
VERSION     AX814932.1  GI:39104070
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 18 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 192
AX837956/c
LOCUS       AX837956                  18 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 5080 from Patent EP1347046.
ACCESSION   AX837956
VERSION     AX837956.1  GI:39921648
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1347046-A 5080 24-SEP-2003;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="Description of Artificial Sequence: an artificially
                     synthesized primer se q"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3812 AGGCATCCTTGTCTTTT 3828
              ||||||| |||||||||
Db         17 AGGCATCGTTGTCTTTT 1


RESULT 193
BD072878
LOCUS       BD072878                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072878
VERSION     BD072878.1  GI:22618481
KEYWORDS    JP 2001286300-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 16 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/16
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key                Location/Qualifiers
            FT   source             1. .18
            FT                      /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 194
BD072881
LOCUS       BD072881                  18 bp    DNA     linear   PAT 27-AUG-2002
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```
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072881
VERSION     BD072881.1  GI:22618484
KEYWORDS    JP 2001286300-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 19 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/19
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 195
BD096968
LOCUS       BD096968                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  SAG:apoptosis sensitivity gene.
ACCESSION   BD096968
VERSION     BD096968.1  GI:22642556
KEYWORDS    JP 2001526063-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sun,Y.
  TITLE     SAG:apoptosis sensitivity gene
  JOURNAL   Patent: JP 2001526063-A 3 18-DEC-2001;
            WARNER LAMBERT CO
COMMENT     OS   Unidentified
            PN   JP 2001526063-A/3
            PD   18-DEC-2001
            PF   15-DEC-1998 JP 2000525451
            PR   19-DEC-1997 US    60/068179,11-SEP-1998 US    60/099840 PI
            YI SUN
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
            PC   A61P39/06,
            PC   A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'oligonucleotide P1 downstream primer' FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 196
BD104774/c
LOCUS       BD104774                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104774
VERSION     BD104774.1  GI:22650348
KEYWORDS    WO 0192572-A/878.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 878 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/878
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4390 TGCAGGATTCCCTTCTG 4406
              | ||||||||||||||||
Db         17 TCCAGGATTCCCTTCTG 1
```

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RESULT 197
BD107505
LOCUS       BD107505                  18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107505
VERSION     BD107505.1  GI:23202323
KEYWORDS    JP 2002000275-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 14 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/14
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 198
BD107508
LOCUS       BD107508                  18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107508
VERSION     BD107508.1  GI:23202326
KEYWORDS    JP 2002000275-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 17 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/17
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 199
AB069500
LOCUS       AB069500                  18 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-stSG54900
            at 1p36.
ACCESSION   AB069500
VERSION     AB069500.1  GI:15130304
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .18
                     /note="forward primer for human STS sts-stSG54900 at 1p36
                     sts-stSG54900 obtained from clones B382K11, Human BAC
                     library RPCI-11"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4047 GCTGGATGGCACCTCAG 4063
              ||||| ||||||||||
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```
Db          2 GCTGGTTGGCACCTCAG 18


RESULT 200
AX129035
LOCUS       AX129035                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 253 from Patent WO0130362.
ACCESSION   AX129035
VERSION     AX129035.1  GI:14135340
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 253 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk2 ribozyme binding site"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
              ||||||  ||||||||||
Db          2 GGCCCTATTCCCTGGAG 18


RESULT 201
AX129036
LOCUS       AX129036                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 254 from Patent WO0130362.
ACCESSION   AX129036
VERSION     AX129036.1  GI:14135341
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 254 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk2 ribozyme binding site"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
              ||||||  ||||||||||
Db          1 GGCCCTATTCCCTGGAG 17


RESULT 202
AX129707
LOCUS       AX129707                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 925 from Patent WO0130362.
ACCESSION   AX129707
VERSION     AX129707.1  GI:14136012
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 925 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk8 ribozyme binding site"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1831 ACAAAGCTTCTAAAGCA 1847
              |||  ||||||||||||||
Db          1 ACAGAGCTTCTAAAGCA 17


RESULT 203
AX188729/c
LOCUS       AX188729                 19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 40 from Patent WO0148015.
ACCESSION   AX188729
VERSION     AX188729.1  GI:15142293
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lind,P., Parodi,L.A., Lindberg,E., Vogeli,G., Wood,L.S.,
            Hiebsch,R.R. and Ruff,V.
  TITLE     Novel g protein-coupled receptors
  JOURNAL   Patent: WO 0148015-A 40 05-JUL-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Novel Sequence"

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3422 GGGCAAGAACCCAAGTG 3438
              ||||||||||  ||||||
Db         19 GGGCAAGAACACAAGTG 3


RESULT 204
AR183909
LOCUS       AR183909                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6342376.
ACCESSION   AR183909
VERSION     AR183909.1  GI:20227878
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
```

```
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6342376-A 2 29-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 16


RESULT 205
AR429726
LOCUS       AR429726                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6645741.
ACCESSION   AR429726
VERSION     AR429726.1  GI:40190064
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6645741-A 2 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 16


RESULT 206
AR163080/c
LOCUS       AR163080                  19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6270966.
ACCESSION   AR163080
VERSION     AR163080.1  GI:16233563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weinstein,J.N. and Buolamwini,J.
  TITLE     Restriction display (RD-PCR) of differentially expressed mRNAs
  JOURNAL   Patent: US 6270966-A 1 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db         17 TTTTTTTTTTTTTTV 2


RESULT 207
E08331
LOCUS       E08331                    19 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08331
VERSION     E08331.1  GI:2176448
KEYWORDS    JP 1994303997-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 2 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/2
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .19
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          3 TTTTTTTTTTTTTTV 18


RESULT 208
AR491869/c
LOCUS       AR491869                  19 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 4 from patent US 6716585.
ACCESSION   AR491869
VERSION     AR491869.1  GI:47260090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Al-Mahmood,S.
  TITLE     Method for identifying novel genes involved in the regulation of
            angiogenesis, study of said genes and use thereof for therapeutic
            purposes
  JOURNAL   Patent: US 6716585-A 4 06-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
```

```
Db         17 TTTTTTTTTTTTTTTB 2


RESULT 209
AR528447
LOCUS       AR528447                 19 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 85 from patent US 6723897.
ACCESSION   AR528447
VERSION     AR528447.1  GI:53916512
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Brown,S.M., Elich,T.D., Heck,G.R., Kishore,G.M., Logusch,E.W.,
            Logusch,S.J., Piller,K.J., Rao,S., Ream,J.E. and Baerson,S.R.
  TITLE     Methods for controlling gibberellin levels
  JOURNAL   Patent: US 6723897-A 85 20-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 210
BD161924/c
LOCUS       BD161924                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161924
VERSION     BD161924.1  GI:27867682
KEYWORDS    JP 2002191369-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 1 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/1
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAATTT 3625
              |||||| ||||| | |||||
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```
Db         20 AAAAAAAAAAAAAAAATTT 1


RESULT 211
AR029402
LOCUS       AR029402                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5859233.
ACCESSION   AR029402
VERSION     AR029402.1  GI:5941375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 212
AR029403/c
LOCUS       AR029403                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5859233.
ACCESSION   AR029403
VERSION     AR029403.1  GI:5941376
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 4 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 213
AR034895
LOCUS       AR034895                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5869643.
ACCESSION   AR034895
VERSION     AR034895.1  GI:5950500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
```

```
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 10 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 214
AR034898/c
LOCUS       AR034898                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5869643.
ACCESSION   AR034898
VERSION     AR034898.1  GI:5950503
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 16 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 215
AR048768/c
LOCUS       AR048768                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5821354.
ACCESSION   AR048768
VERSION     AR048768.1  GI:5971111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Leclerc,G. and Martel,R.
  TITLE     Radiolabeled DNA oligonucleotide and method of preparation
  JOURNAL   Patent: US 5821354-A 2 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 216
AR049970
LOCUS       AR049970                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5824793.
ACCESSION   AR049970
VERSION     AR049970.1  GI:5971962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 3 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 217
AR049971/c
LOCUS       AR049971                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5824793.
ACCESSION   AR049971
VERSION     AR049971.1  GI:5971963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 4 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 218
AR056157
LOCUS       AR056157                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 361 from patent US 5837542.
ACCESSION   AR056157
VERSION     AR056157.1  GI:5981734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
```

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  JOURNAL   Patent: US 5837542-A 361 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 219
AR056158
LOCUS       AR056158                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 362 from patent US 5837542.
ACCESSION   AR056158
VERSION     AR056158.1  GI:5981735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 362 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 220
AR080676
LOCUS       AR080676                 15 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 5 from patent US 5968822.
ACCESSION   AR080676
VERSION     AR080676.1  GI:10007406
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in transduced cells
  JOURNAL   Patent: US 5968822-A 5 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 221
AR084516/c
LOCUS       AR084516                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 5 from patent US 5981185.
ACCESSION   AR084516
VERSION     AR084516.1  GI:10011287
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 5 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 222
AR084520
LOCUS       AR084520                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 9 from patent US 5981185.
ACCESSION   AR084520
VERSION     AR084520.1  GI:10011291
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 9 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 223
AR105981
LOCUS       AR105981                 15 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6103474.
ACCESSION   AR105981
VERSION     AR105981.1  GI:12820046
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 4 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
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/mol_type="unassigned DNA"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 224
AR113915
LOCUS AR113915 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 361 from patent US 6132967.
ACCESSION AR113915
VERSION AR113915.1 GI:14094237
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 361 17-OCT-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 225
AR113916
LOCUS AR113916 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 362 from patent US 6132967.
ACCESSION AR113916
VERSION AR113916.1 GI:14094238
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 362 17-OCT-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 226
AR132213/c
LOCUS AR132213 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 638 from patent US 6194150.
ACCESSION AR132213
VERSION AR132213.1 GI:14121118
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 638 27-FEB-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 GATGCTAAAGATGAT 1418
||||||||||||||||
Db 15 GATGCTAAAGATGAT 1

RESULT 227
AR170375/c
LOCUS AR170375 15 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6291438.
ACCESSION AR170375
VERSION AR170375.1 GI:17908334
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Wang,J.H.
TITLE Antiviral anticancer poly-substituted phenyl derivatized oligoribonucleotides and methods for their use
JOURNAL Patent: US 6291438-A 1 18-SEP-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 15 TTTTTTTTTTTTTTT 1

RESULT 228
BD184668
LOCUS BD184668 15 bp DNA linear PAT 17-JUN-2003
DEFINITION Method and detector for identifying subtypes of human papiloma viruses.
ACCESSION BD184668
VERSION BD184668.1 GI:31876868
KEYWORDS JP 2002360271-A/647.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y., Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
TITLE Method and detector for identifying subtypes of human papiloma
JOURNAL Patent: JP 2002360271-A 647 17-DEC-2002;
KING CAR FOOD INDUSTRIAL CO LTD
COMMENT OS Artificial Sequence

```
            PN   JP 2002360271-A/647
            PD   17-DEC-2002
            PF   28-NOV-2001 JP 2001362595
            PR   04-MAY-2001 TW     90110785
            PI   CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
            PI   HAENG LEE,
            PI   SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
            PI   WEN SHI,
            PI   CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
            PC   C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
            ,C12Q1/70,G01N21/64,
            PC   G01N33/53,G01N33/574,G01N33/58,G01N37/00//(C12M1/34,C12R1:93),
            PC   (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
            CC   Added sequence for 3' end labeling of oligonucleic acid. FH
            Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 229
BD206432
LOCUS       BD206432                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD206432
VERSION     BD206432.1  GI:33016202
KEYWORDS    JP 2002512791-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 22 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/22
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                      related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                           virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 230
BD209488
LOCUS       BD209488                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD209488
VERSION     BD209488.1  GI:33019258
KEYWORDS    JP 2002512791-A/3078.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 3078 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/3078
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                      related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                           virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 231
CQ832330
LOCUS       CQ832330                 15 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 13 from Patent WO2004058794.
ACCESSION   CQ832330
VERSION     CQ832330.1  GI:50831954
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Arar,K.
```

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  TITLE     Methods and compositions for the tandem synthesis of two or more
            oligonuleotides on the same solid support
  JOURNAL   Patent: WO 2004058794-A 13 15-JUL-2004;
            Proligo LLC (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Nucleic Acid Ligand"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 232
CQ840762
LOCUS       CQ840762                  15 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 5 from Patent EP1439193.
ACCESSION   CQ840762
VERSION     CQ840762.1  GI:50838367
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Antibody directed to polypeptide having heparanase activity
  JOURNAL   Patent: EP 1439193-A 5 21-JUL-2004;
            Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH
            SERVICES AND DEVELOPMENT LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 233
CQ840854
LOCUS       CQ840854                  15 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 5 from Patent EP1439226.
ACCESSION   CQ840854
VERSION     CQ840854.1  GI:50838429
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     A nucleic acid antisense sequence to a polynucleotide encoding a
            polypeptide having heparanese activity
  JOURNAL   Patent: EP 1439226-A 5 21-JUL-2004;
            Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH
            SERVICES AND DEVELOPMENT LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Single strand DNA oligonucleotide"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 234
E08522
LOCUS       E08522                    15 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
  TITLE     S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
  JOURNAL   Patent: JP 1994335389-A 7 06-DEC-1994;
            KAGOME CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993 JP 1993126286
            PI   TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 235
E12591
LOCUS       E12591                    15 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  pRIMER.
ACCESSION   E12591
VERSION     E12591.1  GI:3251423
KEYWORDS    JP 1997028381-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Minami,K. and Takagi,M.
  TITLE     S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE
  JOURNAL   Patent: JP 1997028381-A 8 04-FEB-1997;
            TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
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COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997028381-A/8
            PD   04-FEB-1997
            PF   24-JUL-1995 JP 1995187557
            PI   TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 236
I29068/c
LOCUS       I29068                  15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5576427.
ACCESSION   I29068
VERSION     I29068.1  GI:1819859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 6 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 237
I38641
LOCUS       I38641                  15 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5614617.
ACCESSION   I38641
VERSION     I38641.1  GI:2084695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 1 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 238
AR200476
LOCUS       AR200476                15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 19 from patent US 6357163.
ACCESSION   AR200476
VERSION     AR200476.1  GI:20251364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 19 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 239
AR200477/c
LOCUS       AR200477                15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 20 from patent US 6357163.
ACCESSION   AR200477
VERSION     AR200477.1  GI:20251365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 20 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1
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RESULT 240
AR222461/c
LOCUS       AR222461                 15 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 21 from patent US 6429300.
ACCESSION   AR222461
VERSION     AR222461.1  GI:23329992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 21 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 241
AR266630
LOCUS       AR266630                 15 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 68 from patent US 6495319.
ACCESSION   AR266630
VERSION     AR266630.1  GI:29695694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 68 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 242
AR371280
LOCUS       AR371280                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 17 from patent US 6395474.
ACCESSION   AR371280
VERSION     AR371280.1  GI:34608212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 17 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 243
AR371281/c
LOCUS       AR371281                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 18 from patent US 6395474.
ACCESSION   AR371281
VERSION     AR371281.1  GI:34608213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 18 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 244
AR410213
LOCUS       AR410213                 15 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 9 from patent US 6635452.
ACCESSION   AR410213
VERSION     AR410213.1  GI:40161460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass label molecules
  JOURNAL   Patent: US 6635452-A 9 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 245
AR438809
LOCUS       AR438809                 15 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6664105.
ACCESSION   AR438809
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VERSION     AR438809.1  GI:42663812
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in genetically modified cells
  JOURNAL   Patent: US 6664105-A 5 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 246
AR439678
LOCUS       AR439678                 15 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6664388.
ACCESSION   AR439678
VERSION     AR439678.1  GI:42665611
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Nelson,J.S.
  TITLE     Reagents for oligonucleotide cleavage and deprotection
  JOURNAL   Patent: US 6664388-A 2 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 247
AR452072
LOCUS       AR452072                 15 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6677137.
ACCESSION   AR452072
VERSION     AR452072.1  GI:42683499
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Goldshmidt,O., Pecker,I., Vlodavsky,I., Michal,I. and Zcharia,E.
  TITLE     Avian and reptile derived polynucleotide encoding a polypeptide
            having heparanase activity
  JOURNAL   Patent: US 6677137-A 5 13-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 248
AR489501
LOCUS       AR489501                 15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 17 from patent US 6710163.
ACCESSION   AR489501
VERSION     AR489501.1  GI:47256526
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acid synthons
  JOURNAL   Patent: US 6710163-A 17 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 249
AR489502/c
LOCUS       AR489502                 15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 18 from patent US 6710163.
ACCESSION   AR489502
VERSION     AR489502.1  GI:47256527
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acid synthons
  JOURNAL   Patent: US 6710163-A 18 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 250
AR491112
LOCUS       AR491112                 15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 17 from patent US 6713602.
ACCESSION   AR491112
VERSION     AR491112.1  GI:47258972
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Synthetic procedures for peptide nucleic acids
  JOURNAL   Patent: US 6713602-A 17 30-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 251
AR491113/c
LOCUS       AR491113                 15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 18 from patent US 6713602.
ACCESSION   AR491113
VERSION     AR491113.1  GI:47258973
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Synthetic procedures for peptide nucleic acids
  JOURNAL   Patent: US 6713602-A 18 30-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 252
AX004877
LOCUS       AX004877                 15 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 6 from Patent WO9910527.
ACCESSION   AX004877
VERSION     AX004877.1  GI:9928277
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 6 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl modified oligonucleotide"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 253
AX026066
LOCUS       AX026066                 15 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 4 from Patent WO0028046.
ACCESSION   AX026066
VERSION     AX026066.1  GI:10187502
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Marraccini,P. and Rogers,J.
  TITLE     Coffea arabica mannanase
  JOURNAL   Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHESE"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 254
AX048407
LOCUS       AX048407                 15 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 6 from Patent WO0071747.
ACCESSION   AX048407
VERSION     AX048407.1  GI:12225571
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 6 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 255
AX106973/c
LOCUS       AX106973                 15 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 26 from Patent WO0125442.
```

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ACCESSION   AX106973
VERSION     AX106973.1  GI:13922522
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
  JOURNAL   Patent: WO 0125442-A 26 12-APR-2001;
            CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligo dA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 256
AX127272
LOCUS       AX127272                 15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 3 from Patent EP1111068.
ACCESSION   AX127272
VERSION     AX127272.1  GI:14133346
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 3 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_structure  1
                     /note="(NH2-C6-ttt)2-branch-"
     misc_feature    15
                     /note="NH2
                     kunstliche"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 257
AX127273
LOCUS       AX127273                 15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 4 from Patent EP1111068.
ACCESSION   AX127273
VERSION     AX127273.1  GI:14133347
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 4 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_structure  1
                     /note="(dt-COOH)2-branch-"
     misc_feature    15
                     /note="NH2
                     kunstliche"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 258
AX180140
LOCUS       AX180140                 15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 3 from Patent WO0146464.
ACCESSION   AX180140
VERSION     AX180140.1  GI:15132181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 3 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified-Modification is (NH2-C6-TTT)2-branch-"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 259
AX180141
LOCUS       AX180141                 15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 4 from Patent WO0146464.
ACCESSION   AX180141
VERSION     AX180141.1  GI:15132182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
```

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  JOURNAL   Patent: WO 0146464-A 4 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (dT-COOH)2-branch-"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 260
AX429224
LOCUS       AX429224                 15 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 1 from Patent EP1201765.
ACCESSION   AX429224
VERSION     AX429224.1  GI:21540537
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
  TITLE     Cellular kinases involved in cytomegalovirus infection and their
            inhibition
  JOURNAL   Patent: EP 1201765-A 1 02-MAY-2002;
            Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="N/A"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 261
AX525141/c
LOCUS       AX525141                 15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 1 from Patent WO02066675.
ACCESSION   AX525141
VERSION     AX525141.1  GI:25170126
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 1 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Biotin"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 262
AX525143/c
LOCUS       AX525143                 15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 3 from Patent WO02066675.
ACCESSION   AX525143
VERSION     AX525143.1  GI:25170128
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 3 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Digoxigenin"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 263
AX633197
LOCUS       AX633197                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 336 from Patent EP1260586.
ACCESSION   AX633197
VERSION     AX633197.1  GI:28468811
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 336 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 264
AX633199
LOCUS       AX633199                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 338 from Patent EP1260586.
ACCESSION   AX633199
VERSION     AX633199.1  GI:28468813
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 338 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 265
AX696087
LOCUS       AX696087                  15 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 6 from Patent WO03008643.
ACCESSION   AX696087
VERSION     AX696087.1  GI:29419249
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hammonds,T.R.
  TITLE     Method and polynukleotides for assaying the activity of a dna
            modifying enzyme
  JOURNAL   Patent: WO 03008643-A 6 30-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide 6"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 266
AX711176/c
LOCUS       AX711176                  15 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 476 from Patent EP1288296.
ACCESSION   AX711176
VERSION     AX711176.1  GI:29787557
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 476 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Polyadenylation region"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 267
BD074424
LOCUS       BD074424                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell.
ACCESSION   BD074424
VERSION     BD074424.1  GI:22620027
KEYWORDS    JP 2001514855-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Elena,F.
  TITLE     Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell
  JOURNAL   Patent: JP 2001514855-A 5 18-SEP-2001;
            INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
            & DEVELOPMENT LTD
COMMENT     OS   Nucleic acid
            PN   JP 2001514855-A/5
            PD   18-SEP-2001
            PF   31-AUG-1998 JP 2000508806
            PR   02-SEP-1997 US    08/922170,02-JUL-1998 US    09/109386 PI
            IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
            PC   C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00, PC
              A61P37/00,
            PC   A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC
             A61K39/395,
            PC   A61K39/395,C12N15/00,A61K37/02,C12N5/00
            CC   Polynucleotide encoding polypeptide having
            heparanase activity
            CC           and
            CC   expression of the polypeptide in induced cell FH   Key
                Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Nucleic acid'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

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RESULT 268
BD084687
LOCUS       BD084687                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Releasable nonvolatile mass-label molecules.
ACCESSION   BD084687
VERSION     BD084687.1  GI:22630297
KEYWORDS    JP 2001524808-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass-label molecules
  JOURNAL   Patent: JP 2001524808-A 5 04-DEC-2001;
            GENETRACE SYSTEMS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001524808-A/5
            PD   04-DEC-2001
            PF   10-DEC-1997 JP 1998526924
            PR   10-DEC-1996 US    60/033037,16-MAY-1997 US    60/046719 PI
            JOSEPH A MONTFORTE,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
            THOMAS A SHALER
            PC   C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
              B01D59/44,
            PC   H01J49/00,C07H21/04,C07K15/26,C07K15/28
            CC   Description of Artificial Sequence: oligo dT15 primer FH   Key
                      Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .15
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

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RESULT 269
AR027678
LOCUS       AR027678                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5856435.
ACCESSION   AR027678
VERSION     AR027678.1  GI:5938498
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
  TITLE     Nucleic acid-containing composition, its preparation and use
  JOURNAL   Patent: US 5856435-A 15 05-JAN-1999;
FEATURES                Location/Qualifiers
     source             1. .16
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

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RESULT 270
AR037355
LOCUS       AR037355                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5801155.
ACCESSION   AR037355
VERSION     AR037355.1  GI:5955211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor grove binder conjugates
  JOURNAL   Patent: US 5801155-A 2 01-SEP-1998;
FEATURES                Location/Qualifiers
     source             1. .16
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

```
RESULT 271
AR104584/c
LOCUS       AR104584                  16 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 131 from patent US 6093809.
ACCESSION   AR104584
VERSION     AR104584.1  GI:12817292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 131 25-JUL-2000;
FEATURES                Location/Qualifiers
     source             1. .16
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2
```

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RESULT 272
AR175845/c
LOCUS       AR175845                  16 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 131 from patent US 6309867.
ACCESSION   AR175845
VERSION     AR175845.1  GI:17917144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Nakamura,T.
```

```
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 131 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 273
BD167413/c
LOCUS       BD167413                  16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION   BD167413
VERSION     BD167413.1  GI:27873225
KEYWORDS    JP 2002211954-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
  TITLE     Surface-roughened slide glass and method of analyzing biological
            substance using the same
  JOURNAL   Patent: JP 2002211954-A 1 31-JUL-2002;
            TOYO KOHAN CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002211954-A/1
            PD   31-JUL-2002
            PF   30-OCT-2001 JP 2001332778
            PI   HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            PI   KENICHI TAKAGI
            PC   C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing  CC
             biological substance
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 274
BD167414/c
LOCUS       BD167414                  16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION   BD167414
VERSION     BD167414.1  GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
  TITLE     Surface-roughened slide glass and method of analyzing biological
            substance using the same
  JOURNAL   Patent: JP 2002211954-A 2 31-JUL-2002;
            TOYO KOHAN CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002211954-A/2
            PD   31-JUL-2002
            PF   30-OCT-2001 JP 2001332778
            PI   HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            PI   KENICHI TAKAGI
            PC   C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing  CC
             biological substance
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 275
CQ800970
LOCUS       CQ800970                  16 bp    DNA     linear   PAT 05-MAY-2004
DEFINITION  Sequence 9 from Patent EP1413630.
ACCESSION   CQ800970
VERSION     CQ800970.1  GI:47057749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
  TITLE     Analyssis of biological targets using a biochip comprising a
            fluorescent marker
  JOURNAL   Patent: EP 1413630-A 9 28-APR-2004;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR); Universite Joseph Fourier
            de Grenoble (FR)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: synthetic"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 276
CQ827693/c
LOCUS       CQ827693                  16 bp    DNA     linear   PAT 29-JUN-2004
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DEFINITION  Sequence 130 from Patent WO2004050918.
ACCESSION   CQ827693
VERSION     CQ827693.1  GI:49456143
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ruan,Y. and Wei,C.
  TITLE     Method to generate or determine nucleic acid tags corresponding to
            the terminal ends of dna molecules using sequence analysis of gene
            expression (terminal sage)
  JOURNAL   Patent: WO 2004050918-A 130 17-JUN-2004;
            Agency for Science, Technology and Research (SG)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="tag"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 277
I38676
LOCUS       I38676                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 36 from patent US 5614617.
ACCESSION   I38676
VERSION     I38676.1  GI:2084730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 36 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 278
I38682
LOCUS       I38682                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 42 from patent US 5614617.
ACCESSION   I38682
VERSION     I38682.1  GI:2084736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 42 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 279
I38700
LOCUS       I38700                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 60 from patent US 5614617.
ACCESSION   I38700
VERSION     I38700.1  GI:2084754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 60 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 280
AR221692
LOCUS       AR221692                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from patent US 6426408.
ACCESSION   AR221692
VERSION     AR221692.1  GI:23328764
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 2 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 281
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AR221693
LOCUS       AR221693                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6426408.
ACCESSION   AR221693
VERSION     AR221693.1  GI:23328765
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 3 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 282
AR221694
LOCUS       AR221694                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 4 from patent US 6426408.
ACCESSION   AR221694
VERSION     AR221694.1  GI:23328766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 4 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 283
AR221695
LOCUS       AR221695                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from patent US 6426408.
ACCESSION   AR221695
VERSION     AR221695.1  GI:23328767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 5 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 284
AR221696
LOCUS       AR221696                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from patent US 6426408.
ACCESSION   AR221696
VERSION     AR221696.1  GI:23328768
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 6 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 285
AR221697
LOCUS       AR221697                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 7 from patent US 6426408.
ACCESSION   AR221697
VERSION     AR221697.1  GI:23328769
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 7 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 286
AR221698
LOCUS       AR221698                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 8 from patent US 6426408.
ACCESSION   AR221698
VERSION     AR221698.1  GI:23328770
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 8 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 287
AR222462/c
LOCUS       AR222462                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 22 from patent US 6429300.
ACCESSION   AR222462
VERSION     AR222462.1  GI:23329993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 22 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 288
AR257437
LOCUS       AR257437                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6486308.
ACCESSION   AR257437
VERSION     AR257437.1  GI:27307448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 2 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 289
AR257438
LOCUS       AR257438                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6486308.
ACCESSION   AR257438
VERSION     AR257438.1  GI:27307449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 290
AR257439
LOCUS       AR257439                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 4 from patent US 6486308.
ACCESSION   AR257439
VERSION     AR257439.1  GI:27307450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 4 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 291
AR257440
LOCUS       AR257440                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6486308.
ACCESSION   AR257440
VERSION     AR257440.1  GI:27307451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
```

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  JOURNAL   Patent: US 6486308-A 5 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 292
AR257441
LOCUS       AR257441                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6486308.
ACCESSION   AR257441
VERSION     AR257441.1  GI:27307452
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 6 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 293
AR257442
LOCUS       AR257442                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6486308.
ACCESSION   AR257442
VERSION     AR257442.1  GI:27307453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 7 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 294
AR257443
LOCUS       AR257443                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6486308.
ACCESSION   AR257443
VERSION     AR257443.1  GI:27307454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 8 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 295
AR561628/c
LOCUS       AR561628                  16 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 1 from patent US 6756492.
ACCESSION   AR561628
VERSION     AR561628.1  GI:53974736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Beier,M. and Honeisel,J.
  TITLE     Nucleoside derivatives with photo-unstable protective groups
  JOURNAL   Patent: US 6756492-A 1 29-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 296
AR561693
LOCUS       AR561693                  16 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 9 from patent US 6759039.
ACCESSION   AR561693
VERSION     AR561693.1  GI:53974843
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Tsang,W.-G., Zheng,T. and Huang,C.J.
  TITLE     Culturing pancreatic stem cells having a specified, intermediate
            stage of development
  JOURNAL   Patent: US 6759039-A 9 06-JUL-2004;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 297
AX039049/c
LOCUS       AX039049                 16 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 2 from Patent WO0061594.
ACCESSION   AX039049
VERSION     AX039049.1  GI:11228345
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Beier,M. and Hoheisel,J.
  TITLE     Nucleoside derivatives with photo-unstable protective groups
  JOURNAL   Patent: WO 0061594-A 2 19-OCT-2000;
            DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG
            (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 298
AX235176
LOCUS       AX235176                 16 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 9 from Patent WO0163282.
ACCESSION   AX235176
VERSION     AX235176.1  GI:15593767
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
  TITLE     Analysis of biological targets using a biochip comprising a
            fluorescent marker
  JOURNAL   Patent: WO 0163282-A 9 30-AUG-2001;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence synthetique"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 299
A28997
LOCUS       A28997                   17 bp    DNA     linear   PAT 30-JUN-1995
DEFINITION  primer sequence 4 from patent EP0522880.
ACCESSION   A28997
VERSION     A28997.1  GI:1248848
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: EP 0522880-A 16 13-JAN-1993;
            INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 300
AR104585
LOCUS       AR104585                 17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 132 from patent US 6093809.
ACCESSION   AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 132 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 301
AR141074
LOCUS       AR141074                 17 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 5 from patent US 6207819.
ACCESSION   AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
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          backbone oligomeric compounds
  JOURNAL   Patent: US 6207819-A 5 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 302
AR172076
LOCUS       AR172076                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6297425.
ACCESSION   AR172076
VERSION     AR172076.1  GI:17911026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6297425-A 30 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 303
AR173367
LOCUS       AR173367                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6303846.
ACCESSION   AR173367
VERSION     AR173367.1  GI:17912858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6303846-A 30 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 304
AR175846
LOCUS       AR175846                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 132 from patent US 6309867.
ACCESSION   AR175846
VERSION     AR175846.1  GI:17917145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 132 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 305
BD233654
LOCUS       BD233654                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Two-color differential display as a method for detecting regulated
            genes.
ACCESSION   BD233654
VERSION     BD233654.1  GI:33043424
KEYWORDS    JP 2002524088-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
  JOURNAL   Patent: JP 2002524088-A 2 06-AUG-2002;
            AVENTIS PHARMA DEUTSCHLAND GMBH
COMMENT     OS   Unidentified
            PN   JP 2002524088-A/2
            PD   06-AUG-2002
            PF   26-AUG-1999 JP 2000569015
            PR   07-SEP-1998 DE 198 40 731.9
            PI   DETLEF KOZIAN,BIRGIT REUNER
            PC   C12Q1/68,G01N33/58//A61K45/00,C12N15/09,C12N15/09,C12N15/00,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /note= 'M = A, C, G; N = A, C, G, T'
            FH   Key             Location/Qualifiers
            FT   exon            1. .17.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 306
AR187062
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LOCUS       AR187062                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2550 from patent US 6346398.
ACCESSION   AR187062
VERSION     AR187062.1  GI:20233027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 307
AR187063
LOCUS       AR187063                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2551 from patent US 6346398.
ACCESSION   AR187063
VERSION     AR187063.1  GI:20233028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 308
AR187064
LOCUS       AR187064                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2552 from patent US 6346398.
ACCESSION   AR187064
VERSION     AR187064.1  GI:20233029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 309
AR190154/c
LOCUS       AR190154                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 5642 from patent US 6346398.
ACCESSION   AR190154
VERSION     AR190154.1  GI:20236119
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 5642 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
             |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 310
AR222463/c
LOCUS       AR222463                 17 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 23 from patent US 6429300.
ACCESSION   AR222463
VERSION     AR222463.1  GI:23329994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 23 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         17 TTTTTTTTTTTTTTT 3


RESULT 311
AR236087
LOCUS       AR236087                 17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6462184.
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ACCESSION   AR236087
VERSION     AR236087.1  GI:27279786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6462184-A 5 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 312
AR241830
LOCUS       AR241830                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 118 from patent US 6472154.
ACCESSION   AR241830
VERSION     AR241830.1  GI:27287642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 118 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 313
AR266625
LOCUS       AR266625                  17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 63 from patent US 6495319.
ACCESSION   AR266625
VERSION     AR266625.1  GI:29695689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 63 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 314
AR323672
LOCUS       AR323672                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1074 from patent US 6566127.
ACCESSION   AR323672
VERSION     AR323672.1  GI:33709480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 315
AR323673
LOCUS       AR323673                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1075 from patent US 6566127.
ACCESSION   AR323673
VERSION     AR323673.1  GI:33709481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 316
AR323674
LOCUS       AR323674                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1076 from patent US 6566127.
ACCESSION   AR323674
VERSION     AR323674.1  GI:33709482
KEYWORDS    .
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 317
AR325130/c
LOCUS       AR325130                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2532 from patent US 6566127.
ACCESSION   AR325130
VERSION     AR325130.1  GI:33710938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 2532 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 318
AX361606
LOCUS       AX361606                  17 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 24 from Patent WO0208461.
ACCESSION   AX361606
VERSION     AX361606.1  GI:18694225
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 24 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Double-stranded product DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 319
AX423361/c
LOCUS       AX423361                  17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1697 from Patent WO0188124.
ACCESSION   AX423361
VERSION     AX423361.1  GI:21526743
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1697 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4481 GAATGTATTTGATTT 4495
              |||||||||||||||
Db         16 GAATGTATTTGATTT 2


RESULT 320
AX692524
LOCUS       AX692524                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5256 from Patent EP1281758.
ACCESSION   AX692524
VERSION     AX692524.1  GI:29415482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5256 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          3 TTTTTTTTTTTTTTT 17
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RESULT 321
AX692525
LOCUS       AX692525                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5257 from Patent EP1281758.
ACCESSION   AX692525
VERSION     AX692525.1  GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 322
AX814938
LOCUS       AX814938                 17 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 24 from Patent WO03064691.
ACCESSION   AX814938
VERSION     AX814938.1  GI:39104076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 24 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 323
AR034896
LOCUS       AR034896                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5869643.
ACCESSION   AR034896
VERSION     AR034896.1  GI:5950501
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 12 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 324
AR034899/c
LOCUS       AR034899                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 18 from patent US 5869643.
ACCESSION   AR034899
VERSION     AR034899.1  GI:5950504
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 18 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 325
AR058305/c
LOCUS       AR058305                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5837820.
ACCESSION   AR058305
VERSION     AR058305.1  GI:5983882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
  TITLE     Seed specific biotinylated protein, SBP65, from leguminous plants
  JOURNAL   Patent: US 5837820-A 3 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 326
AR097579
LOCUS       AR097579                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6071745.
ACCESSION   AR097579
VERSION     AR097579.1  GI:12806309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6071745-A 9 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 327
AR106506/c
LOCUS       AR106506                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 30 from patent US 6107060.
ACCESSION   AR106506
VERSION     AR106506.1  GI:12821036
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Keeling,P. and Guan,H.
  TITLE     Starch encapsulation
  JOURNAL   Patent: US 6107060-A 30 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 328
BD190553/c
LOCUS       BD190553                  18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secretory proteins and polynucleotides encoding the same.
ACCESSION   BD190553
VERSION     BD190553.1  GI:33000292
KEYWORDS    JP 2002515753-A/12.
SOURCE      Rattus
  ORGANISM  Rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secretory proteins and polynucleotides encoding the same
  JOURNAL   Patent: JP 2002515753-A 12 28-MAY-2002;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2002515753-A/12
            PD   28-MAY-2002
            PF   31-OCT-1997 JP 1998521609
            PR   01-NOV-1996 US    08/724973
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Rattus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10114"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 329
BD222596
LOCUS       BD222596                  18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222596
VERSION     BD222596.1  GI:33032366
KEYWORDS    JP 2002522447-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom
  JOURNAL   Patent: JP 2002522447-A 14 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522447-A/14
            PD   23-JUL-2002
            PF   09-AUG-1999 JP 2000563675
            PR   07-AUG-1998 US    09/130973
            PI   MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            PI   KAWASAKI
            PC   C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence: antisense sequence FH
            Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 330
E28535/c
LOCUS       E28535                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28535
VERSION     E28535.1  GI:13025387
KEYWORDS    JP 1999075880-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 2 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/2
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4

RESULT 331
E28536
LOCUS       E28536                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28536
VERSION     E28536.1  GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 3 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/3
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 332
I79509
LOCUS       I79509                    18 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 16 from patent US 5707807.
ACCESSION   I79509
VERSION     I79509.1  GI:3207799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 16 13-JAN-1998;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 333
AR208427
LOCUS       AR208427                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 7 from patent US 6383754.
ACCESSION   AR208427
VERSION     AR208427.1  GI:21509578
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 7 07-MAY-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 334
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AR215435
LOCUS       AR215435                  18 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 9 from patent US 6410321.
ACCESSION   AR215435
VERSION     AR215435.1  GI:23313691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6410321-A 9 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 335
AR222464/c
LOCUS       AR222464                  18 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 24 from patent US 6429300.
ACCESSION   AR222464
VERSION     AR222464.1  GI:23329995
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 24 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 336
AR412363
LOCUS       AR412363                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14 from patent US 6639062.
ACCESSION   AR412363
VERSION     AR412363.1  GI:40167473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleosidic compounds and oligomeric compounds
            prepared therefrom
  JOURNAL   Patent: US 6639062-A 14 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 337
AR473365
LOCUS       AR473365                  18 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9 from patent US 6686460.
ACCESSION   AR473365
VERSION     AR473365.1  GI:42708816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6686460-A 9 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 338
AR487019/c
LOCUS       AR487019                  18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 6 from patent US 6706476.
ACCESSION   AR487019
VERSION     AR487019.1  GI:47251966
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Thirstrup,K., Warthoe,P. and Pettersson,N.B.
  TITLE     Process for amplifying and labeling single stranded cDNA by 5'
            ligated adaptor mediated amplification
  JOURNAL   Patent: US 6706476-A 6 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 339
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AR487020
LOCUS       AR487020                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 7 from patent US 6706476.
ACCESSION   AR487020
VERSION     AR487020.1  GI:47251967
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Thirstrup,K., Warthoe,P. and Pettersson,N.B.
  TITLE     Process for amplifying and labeling single stranded cDNA by 5'
            ligated adaptor mediated amplification
  JOURNAL   Patent: US 6706476-A 7 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 340
AX004875
LOCUS       AX004875                 18 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 4 from Patent WO9910527.
ACCESSION   AX004875
VERSION     AX004875.1  GI:9928275
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 4 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl oligonucleotide"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 341
AX004879
LOCUS       AX004879                 18 bp    RNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 8 from Patent WO9910527.
ACCESSION   AX004879
VERSION     AX004879.1  GI:9928279
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 8 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="2' methyl-modified oligonucleotide"
     modified_base   1. .18
                     /mod_base=um

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 342
AX008117/c
LOCUS       AX008117                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 2 from Patent WO9967378.
ACCESSION   AX008117
VERSION     AX008117.1  GI:9995742
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 2 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 343
AX008118
LOCUS       AX008118                 18 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 3 from Patent WO9967378.
ACCESSION   AX008118
VERSION     AX008118.1  GI:9995743
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 3 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
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           (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
           BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 344
AX008122
LOCUS       AX008122                  18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 7 from Patent WO9967378.
ACCESSION   AX008122
VERSION     AX008122.1  GI:9995747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 7 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 345
AX008123/c
LOCUS       AX008123                  18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 8 from Patent WO9967378.
ACCESSION   AX008123
VERSION     AX008123.1  GI:9995748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 8 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 346
AX028843
LOCUS       AX028843                  18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 27 from Patent WO9732023.
ACCESSION   AX028843
VERSION     AX028843.1  GI:10189946
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 27 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 347
AX028844
LOCUS       AX028844                  18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 28 from Patent WO9732023.
ACCESSION   AX028844
VERSION     AX028844.1  GI:10189947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 28 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
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```
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 348
AX047271/c
LOCUS       AX047271                 18 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 21 from Patent WO0068422.
ACCESSION   AX047271
VERSION     AX047271.1  GI:11876551
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
  TITLE     High density labeling of dna with modified or chromophore carrying
            nucleotides and dna polymerases used
  JOURNAL   Patent: WO 0068422-A 21 16-NOV-2000;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="second fragment of SEQ ID NO: 6"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 349
AX047273
LOCUS       AX047273                 18 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 23 from Patent WO0068422.
ACCESSION   AX047273
VERSION     AX047273.1  GI:11876553
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
  TITLE     High density labeling of dna with modified or chromophore carrying
            nucleotides and dna polymerases used
  JOURNAL   Patent: WO 0068422-A 23 16-NOV-2000;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="second fragment of SEQ ID NO: 6"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 350
AX085253
LOCUS       AX085253                 18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 7 from Patent WO0112855.
ACCESSION   AX085253
VERSION     AX085253.1  GI:13275311
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 7 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 351
AX104721
LOCUS       AX104721                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 913 from Patent WO0122972.
ACCESSION   AX104721
VERSION     AX104721.1  GI:13920918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 913 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 352
AX104747
LOCUS       AX104747                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 939 from Patent WO0122972.
ACCESSION   AX104747
VERSION     AX104747.1  GI:13920944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
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```
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 939 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 353
AX105651
LOCUS       AX105651                  18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123564.
ACCESSION   AX105651
VERSION     AX105651.1  GI:13921674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0123564-A 10 05-APR-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 354
AX108642
LOCUS       AX108642                  18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123419.
ACCESSION   AX108642
VERSION     AX108642.1  GI:13923875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Differentially expressed genes
  JOURNAL   Patent: WO 0123419-A 10 05-APR-2001;
            SCIOS INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 355
AX268883
LOCUS       AX268883                  18 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 84 from Patent WO0174901.
ACCESSION   AX268883
VERSION     AX268883.1  GI:16541910
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and White,R.T.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0174901-A 84 11-OCT-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligos corresponding to polylinker sequence."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 356
AX355809
LOCUS       AX355809                  18 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 837 from Patent WO0197843.
ACCESSION   AX355809
VERSION     AX355809.1  GI:18620477
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 837 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

```
RESULT 357
AX547774
LOCUS       AX547774                  18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 913 from Patent WO02053141.
ACCESSION   AX547774
VERSION     AX547774.1  GI:25812918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 913 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 358
AX547800
LOCUS       AX547800                  18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 939 from Patent WO02053141.
ACCESSION   AX547800
VERSION     AX547800.1  GI:25812944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 939 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 359
AX814716
LOCUS       AX814716                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 1 from Patent WO03064441.
ACCESSION   AX814716
VERSION     AX814716.1  GI:39103916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 1 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 360
AX814723
LOCUS       AX814723                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 8 from Patent WO03064441.
ACCESSION   AX814723
VERSION     AX814723.1  GI:39103922
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 8 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .17
                     /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                     2'-O-methyl-D-uridi ne"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 361
AX814724
LOCUS       AX814724                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 9 from Patent WO03064441.
ACCESSION   AX814724
VERSION     AX814724.1  GI:39103923
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 9 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
```

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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .15
                     /note="Residues 1-3, 7-9, and 13-15 are
                     2'-O-methyl-D-uridine"

  Query Match              0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 362
AX814725
LOCUS       AX814725                18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 10 from Patent WO03064441.
ACCESSION   AX814725
VERSION     AX814725.1  GI:39103924
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 10 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .18
                     /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

  Query Match              0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 363
AX814736/c
LOCUS       AX814736                18 bp    RNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 21 from Patent WO03064441.
ACCESSION   AX814736
VERSION     AX814736.1  GI:39103935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 21 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Target RNA oligonucleotide"

  Query Match              0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 364
BD085545
LOCUS       BD085545                18 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085545
VERSION     BD085545.1  GI:22631155
KEYWORDS    JP 2001333800-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shimada,K.
  TITLE     Method of comparison and detection of RNA amount and DNA amount
  JOURNAL   Patent: JP 2001333800-A 2 04-DEC-2001;
            UNITECH CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001333800-A/2
            PD   04-DEC-2001
            PF   30-MAY-2000 JP 2000160324
            PI   KAORI SHIMADA
            PC   C12Q1/68,C12N15/09,G01N33/50,C12N15/00
            CC   Method of comparison and detection of RNA amount and DNA  CC
                 amount
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match              0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 365
AR063243
LOCUS       AR063243                18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5844110.
ACCESSION   AR063243
VERSION     AR063243.1  GI:5990934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gold,B.I.
  TITLE     Synthetic triple helix-forming compound precursors
  JOURNAL   Patent: US 5844110-A 4 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTTT 2144
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              ||||| ||||||||||
Db          1 TCTTTCTTTTTTTTCTTT 18


RESULT 366
AR152179
LOCUS       AR152179                  18 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 13 from patent US 6232456.
ACCESSION   AR152179
VERSION     AR152179.1  GI:15118229
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Klass,M.R.,
            Russell,J.C., Stewart,K.D. and Stroupe,S.D.
  TITLE     Serine protease reagents and methods useful for detecting and
            treating diseases of the prostate
  JOURNAL   Patent: US 6232456-A 13 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1960 TCAAGCCCCACCACATAG 1977
              ||||||||| | ||||||
Db          1 TCAAGCCCCGCTACATAG 18


RESULT 367
AR178167/c
LOCUS       AR178167                  18 bp    DNA     linear   PAT 18-DEC-2001
DEFINITION  Sequence 3 from patent US 6316186.
ACCESSION   AR178167
VERSION     AR178167.1  GI:17921060
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ekins,R.Philip.
  TITLE     Binding assay using binding agents with tail groups
  JOURNAL   Patent: US 6316186-A 3 13-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTC 3199
              |||||||| ||| |||||
Db         18 TCTCTCTCTCTCTCTCTC 1


RESULT 368
AR178168
LOCUS       AR178168                  18 bp    DNA     linear   PAT 18-DEC-2001
DEFINITION  Sequence 4 from patent US 6316186.
ACCESSION   AR178168
VERSION     AR178168.1  GI:17921061
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ekins,R.Philip.
  TITLE     Binding assay using binding agents with tail groups
  JOURNAL   Patent: US 6316186-A 4 13-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              ||||||||| ||| ||||
Db          1 CTCTCTCTCTCTCTCTCT 18


RESULT 369
CQ807858
LOCUS       CQ807858                  18 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 1308 from Patent WO2004035803.
ACCESSION   CQ807858
VERSION     CQ807858.1  GI:47113252
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2004035803-A 1308 29-APR-2004;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PTEN"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              |||| ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 370
CQ808096/c
LOCUS       CQ808096                  18 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 1546 from Patent WO2004035803.
ACCESSION   CQ808096
VERSION     CQ808096.1  GI:47113490
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2004035803-A 1546 29-APR-2004;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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```
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for EGFR"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2336 TTCCAAACATCCAAAAAA 2353
              | ||||||||||||||| |
Db         18 TACCAAACATCCAAAATA 1


RESULT 371
AX599310
LOCUS       AX599310                  18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 650 from Patent WO02077272.
ACCESSION   AX599310
VERSION     AX599310.1  GI:28399452
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 650 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTTGTTTTTGGG 18


RESULT 372
AX599486
LOCUS       AX599486                  18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 826 from Patent WO02077272.
ACCESSION   AX599486
VERSION     AX599486.1  GI:28399630
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 826 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PTEN"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 373
AX599902
LOCUS       AX599902                  18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1242 from Patent WO02077272.
ACCESSION   AX599902
VERSION     AX599902.1  GI:28400052
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1242 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTTGTTTTTGGG 18


RESULT 374
AX601145
LOCUS       AX601145                  18 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 240 from Patent WO02092851.
ACCESSION   AX601145
VERSION     AX601145.1  GI:28401218
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Binns,M.M. and Swinburne,J.E.
  TITLE     Genetic typing
  JOURNAL   Patent: WO 02092851-A 240 21-NOV-2002;
            ANIMAL HEALTH TRUST (GB) ; The British Horseracing Board (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4693 ACTTGCTGTGTGACCCTG 4710
              |||||||||| ||| |||
Db          1 ACTTGCTGTGCGACTCTG 18
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RESULT 375
AX767726
LOCUS       AX767726                  18 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 374 from Patent WO03044226.
ACCESSION   AX767726
VERSION     AX767726.1  GI:32436331
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 374 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTGTTTTGGG 18


RESULT 376
AX767836
LOCUS       AX767836                  18 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 484 from Patent WO03044226.
ACCESSION   AX767836
VERSION     AX767836.1  GI:32436522
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 484 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PTEN"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 377
AX796164
LOCUS       AX796164                  18 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 507 from Patent WO03052135.
ACCESSION   AX796164
VERSION     AX796164.1  GI:37516830
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 507 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTGTTTTGGG 18


RESULT 378
AX796386
LOCUS       AX796386                  18 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 729 from Patent WO03052135.
ACCESSION   AX796386
VERSION     AX796386.1  GI:37517052
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 729 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PTEN"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 379
AX823056
LOCUS       AX823056                  18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 948 from Patent EP1340818.
ACCESSION   AX823056
VERSION     AX823056.1  GI:39749692
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
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            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
  JOURNAL   Patent: EP 1340818-A 948 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PTEN"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 380
AX826696
LOCUS       AX826696                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 948 from Patent WO03072821.
ACCESSION   AX826696
VERSION     AX826696.1  GI:39752210
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferactive disorder
  JOURNAL   Patent: WO 03072821-A 948 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PTEN"

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 381
S61969
LOCUS       S61969                   23 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  (A3 beta C)=beta-globin {5'region} [human, Genomic Mutant, 23 nt].
ACCESSION   S61969
VERSION     S61969.1  GI:236199
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Trabuchet,G., Elion,J., Dunda,O., Lapoumeroulie,C., Ducrocq,R.,
            Nadifi,S., Zohoun,I., Chaventre,A., Carnevale,P., Nagel,R.L. et,al.
  TITLE     Nucleotide sequence evidence of the unicentric origin of the beta C
            mutation in Africa
  JOURNAL   Hum. Genet. 87 (5), 597-601 (1991)
  MEDLINE   92009838
   PUBMED   1680789
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 61969] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1. .23
                     /gene="beta-globin"
                     /allele="A3 beta C"

  Query Match             0.3%;  Score 14.6;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 4.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTTT 4512
              || ||||  | ||||||||||
Db          2 ATATATATATATTTTTTTTT 22


RESULT 382
A42632/c
LOCUS       A42632                   16 bp    DNA     linear   PAT 06-MAR-1997
DEFINITION  Sequence 150 from Patent WO9502051.
ACCESSION   A42632
VERSION     A42632.1  GI:2298081
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
            Brysch,W.
  TITLE     A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
            PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
            CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
  JOURNAL   Patent: WO 9502051-A 150 19-JAN-1995;
            BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT     Other publication AU 7345694 950206.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2314 AGTAATAAGATGGCTG 2329
              || |||||||||||||
Db         16 AGGAATAAGATGGCTG 1


RESULT 383
A88821/c
LOCUS       A88821                   16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 969 from Patent WO9833904.
ACCESSION   A88821
VERSION     A88821.1  GI:6737391
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 969 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
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                  /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2314 AGTAATAAGATGGCTG 2329
              || |||||||||||||
Db         16 AGGAATAAGATGGCTG 1


RESULT 384
AR002257
LOCUS       AR002257                  16 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION     AR002257.1  GI:3963811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | |||||||||||||
Db          1 ACTTTTTTTTTTTTT 16


RESULT 385
AR045207
LOCUS       AR045207                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5817795.
ACCESSION   AR045207
VERSION     AR045207.1  GI:5966672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | |||||||||||||
Db          1 ACTTTTTTTTTTTTT 16


RESULT 386
AR051238
LOCUS       AR051238                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5830658.
ACCESSION   AR051238
VERSION     AR051238.1  GI:5974602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | |||||||||||||
Db          1 ACTTTTTTTTTTTTT 16


RESULT 387
I16032
LOCUS       I16032                    16 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION     I16032.1  GI:1250940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | |||||||||||||
Db          1 ACTTTTTTTTTTTTT 16


RESULT 388
I28367
LOCUS       I28367                    16 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION     I28367.1  GI:1819143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
```

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  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTT 16


RESULT 389
I38642
LOCUS       I38642                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 2 from patent US 5614617.
ACCESSION   I38642
VERSION     I38642.1  GI:2084696
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 2 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATAT 2409
              ||||||||| ||||||
Db          1 ATATATATATATATAT 16


RESULT 390
I38642/c
LOCUS       I38642                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 2 from patent US 5614617.
ACCESSION   I38642
VERSION     I38642.1  GI:2084696
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 2 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATAT 2409
              ||||||||| ||||||
Db         16 ATATATATATATATAT 1


RESULT 391
AR328421/c
LOCUS       AR328421                  16 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5823 from patent US 6566127.
ACCESSION   AR328421
VERSION     AR328421.1  GI:33714229
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 5823 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3653 TAGCTCAGTCATCAAA 3668
              |||||||||||||| |
Db         16 TAGCTCAGTCATCAGA 1


RESULT 392
AX359760/c
LOCUS       AX359760                  16 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 64 from Patent WO0200691.
ACCESSION   AX359760
VERSION     AX359760.1  GI:18675467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Tchernev,V., Putturajan,M., Malyankar,U.M., Gusev,V.,
            Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
            Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and Smithson,G.
  TITLE     Novel polynucleotides and polypeptides encoded thereby
  JOURNAL   Patent: WO 0200691-A 64 03-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              | ||||||||||||||
Db         16 GCTTTTTTTTTTTTT 1


RESULT 393
BD066334/c
LOCUS       BD066334                  16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD066334
VERSION     BD066334.1  GI:22611937
KEYWORDS    JP 2001511000-A/969.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 969 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/969
            PD   07-AUG-2001
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            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2314 AGTAATAAGATGGCTG 2329
                || ||||||||||||
Db         16 AGGAATAAGATGGCTG 1


RESULT 394
BD089822/c
LOCUS       BD089822                 16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089822
VERSION     BD089822.1  GI:22635432
KEYWORDS    JP 2001321190-A/2066.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2066 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2066
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                  Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4696 TGCTGTGTGACCCTGG 4711
                ||||||| |||||||
Db         16 TGCTGTGTCACCCTGG 1


RESULT 395
HSDNA2129
LOCUS       HSDNA2129                16 bp    DNA     linear   PRI 09-SEP-2004
DEFINITION  Homo sapiens Solid-phase minisequencing detection primer for PBGD
            gene in exon 10.
ACCESSION   AJ002129
VERSION     AJ002129.1  GI:2546968
KEYWORDS    PBGD gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Mustajoki,S., Kauppinen,R., Mustajoki,P., Suomalainen,A. and
            Peltonen,L.
  TITLE     Steady-state transcript levels of the porphobilinogen deaminase
            gene in patients with acute intermittent porphyria
  JOURNAL   Genome Res. 7 (11), 1054-1060 (1997)
  MEDLINE   98041951
   PUBMED   9371741
REFERENCE   2  (bases 1 to 16)
  AUTHORS   Mustajoki,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-OCT-1997) Mustajoki S., Department of Medicine,
            Division of Endocrinology, Helsinki University Central Hsopital,
            Meilahti Hospital, 1 st floor, room P0155, FIN-00290 Helsinki,
            FINLAND
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="q24"
     gene            1. .16
                     /gene="PBGD"
     misc_feature    1. .16
                     /gene="PBGD"
                     /note="Solid-phase minisequencing detection primer"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1626 GTCCAGCTTCCAAAGC 1641
                ||||||||||| ||||
Db          1 GTCCAGCTTCCGAAGC 16


RESULT 396
AB068105/c
LOCUS       AB068105                 16 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-D1S2870
            at 1p36.
ACCESSION   AB068105
VERSION     AB068105.1  GI:15128909
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 16)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .16
                     /note="reverse primer for human STS sts-D1S2870 at 1p36
                     sts-D1S2870 obtained from clones B71M19, B260I21, B222A18,
                     B29A21, Human BAC library RPCI-11"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4696 TGCTGTGTGACCCTGG 4711
              |||||||| |||||||
Db         16 TGCTGTGTCACCCTGG 1


RESULT 397
AR046267
LOCUS       AR046267                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1060 from patent US 5817796.
ACCESSION   AR046267
VERSION     AR046267.1  GI:5967732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 1060 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              |||| ||||||||||
Db          2 TATATATATATACATT 17


RESULT 398
AR047356/c
LOCUS       AR047356                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2149 from patent US 5817796.
ACCESSION   AR047356
VERSION     AR047356.1  GI:5968821
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2149 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3964 ATATAAACAATAAAAA 3979
              ||||||| ||||||||
Db         17 ATATAAAAAATAAAAA 2


RESULT 399
AR047362/c
LOCUS       AR047362                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2155 from patent US 5817796.
ACCESSION   AR047362
VERSION     AR047362.1  GI:5968827
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2155 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAA 3977
              ||||||||| ||||||
Db         16 ATATATAAAAAATAAA 1


RESULT 400
BD167562
LOCUS       BD167562                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of detecting norwalk-like virus (GII).
ACCESSION   BD167562
VERSION     BD167562.1  GI:27873374
KEYWORDS    WO 0229120-A/13.
SOURCE      Norwalk-like virus
  ORGANISM  Norwalk-like virus
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Caliciviridae; Norovirus.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kageyama,T., Kojima,S., Fukushi,S., Hoshino,F. and Katayama,K.
  TITLE     Method of detecting norwalk-like virus (GII)
  JOURNAL   Patent: WO 0229120-A 13 11-APR-2002;
            BML INC,TSUTOMU KAGEYAMA,SHIGEYUKI KOJIMA,SHUETSU FUKUSHI,FUMINORI
            HOSHINO, KAZUHIKO KATAYAMA
COMMENT     OS   Norwalk-like Virus (GII)
            PN   WO 0229120-A/13
            PD   11-APR-2002
            PF   28-MAR-2001 WO 2001JP002542
            PR   29-SEP-2000 JP 00P   300724
            PI   TSUTOMU KAGEYAMA,SHIGEYUKI KOJIMA,SHUETSU FUKUSHI,FUMINORI  PI
              HOSHINO,
            PI   KAZUHIKO KATAYAMA
            PC   C12Q1/70,C12N15/40,C12Q1/68
            CC   Method of detecting norwalk-like virus (GII)
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Norwalk-like Virus (GII)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Norwalk-like virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:95340"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1562 ATTGCTATCGCCCTCC 1577
              ||||| ||||||||||
Db          1 ATTGCGATCGCCCTCC 16


RESULT 401
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BD199224
LOCUS       BD199224                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD199224
VERSION     BD199224.1  GI:33008994
KEYWORDS    JP 2002509721-A/2250.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 2250 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/2250
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2121 GGGTTTTCTTTTCTTT 2136
              || |||||||||||||
Db          2 GGATTTTCTTTTCTTT 17


RESULT 402
BD199225
LOCUS       BD199225                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD199225
VERSION     BD199225.1  GI:33008995
KEYWORDS    JP 2002509721-A/2251.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 2251 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/2251
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2122 GGTTTTCTTTTCTTTT 2137
              | |||||||||||||
Db          1 GATTTTCTTTTCTTTT 16


RESULT 403
BD199226
LOCUS       BD199226                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD199226
VERSION     BD199226.1  GI:33008996
KEYWORDS    JP 2002509721-A/2252.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 2252 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/2252
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2124 TTTTCTTTTCTTTTTT 2139
              ||||||||||||||| |
Db          2 TTTTCTTTTCTTTTCT 17


RESULT 404
BD199227
LOCUS       BD199227                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD199227
VERSION     BD199227.1  GI:33008997
KEYWORDS    JP 2002509721-A/2253.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 2253 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/2253
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTT 2139
              ||||||||||||||| |
Db          1 TTTTCTTTTCTTTTCT 16


RESULT 405
BD202793
LOCUS       BD202793                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202793
VERSION     BD202793.1  GI:33012563
KEYWORDS    JP 2002509721-A/5819.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5819 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5819
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTT 2139
              ||||||||| |||||||
Db          2 TTTTCTTTCCTTTTTT 17


RESULT 406
BD202794
LOCUS       BD202794                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202794
VERSION     BD202794.1  GI:33012564
KEYWORDS    JP 2002509721-A/5820.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5820 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5820
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTT 2139
              ||||||||  |||||||
Db          1 TTTTCTTTCCTTTTTT 16


RESULT 407
BD202802
LOCUS       BD202802                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202802
VERSION     BD202802.1  GI:33012572
KEYWORDS    JP 2002509721-A/5828.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5828 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5828
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2129 TTTTCTTTTTTTCTTT 2144
              ||||||||  |||||||
Db          2 TTTTCTTTCTTTCTTT 17


RESULT 408
BD202803
LOCUS       BD202803                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202803
VERSION     BD202803.1  GI:33012573
KEYWORDS    JP 2002509721-A/5829.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5829 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5829
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2129 TTTTCTTTTTTTCTTT 2144
              ||||||||  |||||||
Db          1 TTTTCTTTCTTTCTTT 16


RESULT 409
I53319
LOCUS       I53319                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1060 from patent US 5646042.
ACCESSION   I53319
VERSION     I53319.1  GI:2474522
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1060 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||  ||||||||||
Db          2 TATATATATATACATT 17


RESULT 410
I54408/c
LOCUS       I54408                    17 bp    DNA     linear   PAT 07-OCT-1997
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DEFINITION  Sequence 2149 from patent US 5646042.
ACCESSION   I54408
VERSION     I54408.1  GI:2475611
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2149 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3964 ATATAAACAATAAAAA 3979
              ||||||| ||||||||
Db         17 ATATAAAAAATAAAAA 2


RESULT 411
I54414/c
LOCUS       I54414                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2155 from patent US 5646042.
ACCESSION   I54414
VERSION     I54414.1  GI:2475617
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2155 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAA 3977
              ||||||||| ||||||
Db         16 ATATATAAAAAATAAA 1


RESULT 412
AR187060
LOCUS       AR187060                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2548 from patent US 6346398.
ACCESSION   AR187060
VERSION     AR187060.1  GI:20233025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | |||||||||||||||
Db          2 ACTTTTTTTTTTTTT 17


RESULT 413
AR187065/c
LOCUS       AR187065                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2553 from patent US 6346398.
ACCESSION   AR187065
VERSION     AR187065.1  GI:20233030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2553 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         17 TGGAAAAAAAAAAAAA 2


RESULT 414
AR187066/c
LOCUS       AR187066                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2554 from patent US 6346398.
ACCESSION   AR187066
VERSION     AR187066.1  GI:20233031
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2554 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         16 TGGAAAAAAAAAAAAA 1


RESULT 415
AR190427/c
LOCUS       AR190427                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 5915 from patent US 6346398.
ACCESSION   AR190427
VERSION     AR190427.1  GI:20236392
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 5915 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCA 3486
              ||||| ||||||||||
Db         17 GTCAGCGTGAACTGCA 2


RESULT 416
AR323670
LOCUS       AR323670                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1072 from patent US 6566127.
ACCESSION   AR323670
VERSION     AR323670.1  GI:33709478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1072 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          2 ACTTTTTTTTTTTTTT 17


RESULT 417
AR323675/c
LOCUS       AR323675                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1077 from patent US 6566127.
ACCESSION   AR323675
VERSION     AR323675.1  GI:33709483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1077 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         17 TGGAAAAAAAAAAAAA 2


RESULT 418
AR323676/c
LOCUS       AR323676                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1078 from patent US 6566127.
ACCESSION   AR323676
VERSION     AR323676.1  GI:33709484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1078 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         16 TGGAAAAAAAAAAAAA 1


RESULT 419
AR325352/c
LOCUS       AR325352                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2754 from patent US 6566127.
ACCESSION   AR325352
VERSION     AR325352.1  GI:33711160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 2754 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCA 3486
              ||||| ||||||||||
Db         17 GTCAGCGTGAACTGCA 2


RESULT 420
AR327337/c
LOCUS       AR327337                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4739 from patent US 6566127.
ACCESSION   AR327337
VERSION     AR327337.1  GI:33713145
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 4739 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3651 TGTAGCTCAGTCATCA 3666
              | ||||||||||||||
Db         17 TTTAGCTCAGTCATCA 2

.

RESULT 421
AR434321
LOCUS       AR434321                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 744 from patent US 6656700.
ACCESSION   AR434321
VERSION     AR434321.1  GI:40197164
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 744 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3057 GCTAGCTGCCACTTTC 3072
              |||||||||| |||||
Db          2 GCTAGCTGCCTCTTTC 17


RESULT 422
AR434322
LOCUS       AR434322                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 745 from patent US 6656700.
ACCESSION   AR434322
VERSION     AR434322.1  GI:40197165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 745 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3057 GCTAGCTGCCACTTTC 3072
              |||||||||| |||||
Db          1 GCTAGCTGCCTCTTTC 16


RESULT 423
AX217422/c
LOCUS       AX217422                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2864 from Patent WO0159103.
ACCESSION   AX217422
VERSION     AX217422.1  GI:15527483
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2864 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5120 TTGGAATAATTTCTAT 5135
              |||||||||||||| ||
Db         16 TTGGAATAATTTCAAT 1


RESULT 424
AX423583
LOCUS       AX423583                  17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1919 from Patent WO0188124.
ACCESSION   AX423583
VERSION     AX423583.1  GI:21526965
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1919 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1061 TATGACAAGAACATTA 1076
              |||||||||||||| |
Db          1 TATGACAAGAACATCA 16


RESULT 425
AX578222/c
LOCUS       AX578222                  17 bp    RNA     linear   PAT 10-JAN-2003
```

```
DEFINITION  Sequence 60 from Patent WO0211674.
ACCESSION   AX578222
VERSION     AX578222.1  GI:27647424
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 60 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATAT 2409
              ||||||||||| ||||
Db         16 ATATATATACAGATAT 1


RESULT 426
AX673808/c
LOCUS       AX673808                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2253 from Patent WO03004526.
ACCESSION   AX673808
VERSION     AX673808.1  GI:29332156
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2253 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3682 TTTGCTCTATTAAGAT 3697
              ||||||||||| ||||
Db         17 TTTGCTCTATTTAGAT 2


RESULT 427
AX692529
LOCUS       AX692529                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5261 from Patent EP1281758.
ACCESSION   AX692529
VERSION     AX692529.1  GI:29415487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5261 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGGG 4518
              |||||||||||||| |
Db          1 TTTTTTTTTTTTTGAG 16


RESULT 428
AX724631/c
LOCUS       AX724631                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2318 from Patent WO03025176.
ACCESSION   AX724631
VERSION     AX724631.1  GI:30503974
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 2318 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATC 2556
              ||||| ||||||||||
Db         16 GCTGAAGGACAGGATC 1


RESULT 429
AX725632/c
LOCUS       AX725632                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3319 from Patent WO03025176.
ACCESSION   AX725632
VERSION     AX725632.1  GI:30504975
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3319 27-MAR-2003;
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            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2583 CACATAGGAAGGGATC 2598
              || |||||||||||||
Db         16 CATATAGGAAGGGATC 1


RESULT 430
AR241816
LOCUS       AR241816                 18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 104 from patent US 6472154.
ACCESSION   AR241816
VERSION     AR241816.1  GI:27287628
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 104 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              |||||||| |||||||
Db          2 TATATATATATATATA 17


RESULT 431
AR098809/c
LOCUS       AR098809                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 64 from patent US 6077672.
ACCESSION   AR098809
VERSION     AR098809.1  GI:12808575
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 64 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1348 ACCAGCCAGGCAGAGG 1363
              ||||||| ||||||||
Db         17 ACCAGCCTGGCAGAGG 2


RESULT 432
AR130254/c
LOCUS       AR130254                 18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 58 from patent US 6187757.
ACCESSION   AR130254
VERSION     AR130254.1  GI:14118151
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Clackson,T.P., Gilman,M.Z., Holt,D.A., Keenan,T.P., Rozamus,L. and
            Yang,W.
  TITLE     Regulation of biological events using novel compounds
  JOURNAL   Patent: US 6187757-A 58 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              |||||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 433
BD139558/c
LOCUS       BD139558                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Regulation of biological event using polymer chimeric protein.
ACCESSION   BD139558
VERSION     BD139558.1  GI:23234503
KEYWORDS    JP 2002508971-A/36.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Clackson,T.P., Gilman,M.Z., Holt,D.A., Keenan,T.P., Rozamus,L. and
            Yang,W.
  TITLE     Regulation of biological event using polymer chimeric protein
  JOURNAL   Patent: JP 2002508971-A 36 26-MAR-2002;
            ARIAD GENE THERAPEUTICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002508971-A/36
            PD   26-MAR-2002
            PF   15-JAN-1999 JP 2000540254
            PR   15-JAN-1998 US    60/071591,21-JAN-1998 US    60/072016 PR
            22-JAN-1998 US    60/072219,22-JAN-1998 US    09/012097 PI
            TIMOTHY P CLACKSON,MICHAEL Z GILMAN,DENNIS A HOLT,TERENCE P  PI
            KEENAN,
            PI   LEONARD ROZAMUS,WU YANG
            PC   C12N15/09,A61K31/436,A61K48/00,A61P37/06,C07D498/18,C07K14/00,
            PC   C07K19/00//
            PC   (C07D498/18,C07D273:00,C07D311:00,C07D221:00),C12N15/00 CC
            oligo5
            CC   oligo5
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              |||||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2
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RESULT 434
BD145035
LOCUS       BD145035                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145035
VERSION     BD145035.1  GI:27850793
KEYWORDS    JP 2002119291-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 16 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/16
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 435
BD145039
LOCUS       BD145039                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145039
VERSION     BD145039.1  GI:27850797
KEYWORDS    JP 2002119291-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 20 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/20
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 436
BD166035
LOCUS       BD166035                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166035
VERSION     BD166035.1  GI:27871847
KEYWORDS    JP 2002191372-A/15.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 15 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/15
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
```

```
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 437
BD166039
LOCUS       BD166039                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166039
VERSION     BD166039.1  GI:27871851
KEYWORDS    JP 2002191372-A/19.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 19 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/19
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                  labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 438
BD218015/c
LOCUS       BD218015                  18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of biological phenomenon based on rapamycin.
ACCESSION   BD218015
VERSION     BD218015.1  GI:33027785
KEYWORDS    JP 2002514893-A/79.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Clackson,T., Holt,D.A. and Gilman,M.Z.
  TITLE     Regulation of biological phenomenon based on rapamycin
  JOURNAL   Patent: JP 2002514893-A 79 21-MAY-2002;
            ARIAD GENE THERAPEUTICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002514893-A/79
            PD   21-MAY-2002
            PF   07-JUN-1996 JP 1997503244
            PR   07-JUN-1995 US    08/481941,09-FEB-1996 US    08/598776 PI
            TIMOTHY CLACKSON,DENNIS A HOLT,MICHAEL Z GILMAN PC
            C12N5/10,C12N9/90,C12N15/12,C12N15/10,C12N15/31,C12N15/62, PC
            C12N15/63,
            PC   C12N15/85,C12N15/86,C07K14/395,C07K14/47,C07K14/715,C12Q1/68,
            PC   A01K67/027
            CC   oligo sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              |||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 439
I73187
LOCUS       I73187                    18 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686242.
ACCESSION   I73187
VERSION     I73187.1  GI:3009326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bruice,T.W. and Lima,W.F.
  TITLE     Determination of oligonucleotides for therapeutics, diagnostics and
            research reagents
  JOURNAL   Patent: US 5686242-A 1 11-NOV-1997;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       4498 AAGTTTTTTTTTTTTT 4513
              | ||||||||||||||
Db          3 ATGTTTTTTTTTTTTT 18


RESULT 440
AR187532/c
LOCUS       AR187532                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 3020 from patent US 6346398.
ACCESSION   AR187532
VERSION     AR187532.1  GI:20233497
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 3020 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGC 3670
              |||||||||||| |||
Db         18 GCTCAGTCATCAGAGC 3


RESULT 441
AR264931
LOCUS       AR264931                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from patent US 6492121.
ACCESSION   AR264931
VERSION     AR264931.1  GI:29693318
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 15 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 442
AR264935
LOCUS       AR264935                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6492121.
ACCESSION   AR264935
VERSION     AR264935.1  GI:29693322
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 19 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 443
AR274241/c
LOCUS       AR274241                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 91 from patent US 6506379.
ACCESSION   AR274241
VERSION     AR274241.1  GI:29706483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Clackson,T.P., Gilman,M. and Holt,D.
  TITLE     Intramuscular delivery of recombinant AAV
  JOURNAL   Patent: US 6506379-A 91 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              |||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 444
AR292403
LOCUS       AR292403                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4138 from patent US 6537751.
ACCESSION   AR292403
VERSION     AR292403.1  GI:31679687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4138 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
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  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3998 ATTGTAATCGTGTGCC 4013
              ||||||||||| ||||
Db          2 ATTGTAATCGTATGCC 17


RESULT 445
AR302718/c
LOCUS       AR302718                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 17 from patent US 6541448.
ACCESSION   AR302718
VERSION     AR302718.1  GI:31691098
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Isaac,B., Krieger,E.K., Mettus,A.-M.L., Moshiri,F. and
            Sivasupramanian,S.
  TITLE     Polypeptide compositions toxic to anthonomus insects, and methods
            of use
  JOURNAL   Patent: US 6541448-A 17 01-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              ||||||||||||| |||
Db         17 TATTTCTAATTCAACA 2


RESULT 446
AR302719
LOCUS       AR302719                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 18 from patent US 6541448.
ACCESSION   AR302719
VERSION     AR302719.1  GI:31691099
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Isaac,B., Krieger,E.K., Mettus,A.-M.L., Moshiri,F. and
            Sivasupramanian,S.
  TITLE     Polypeptide compositions toxic to anthonomus insects, and methods
            of use
  JOURNAL   Patent: US 6541448-A 18 01-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              ||||||||||||| |||
Db          2 TATTTCTAATTCAACA 17


RESULT 447
AR324046/c
LOCUS       AR324046                  18 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1448 from patent US 6566127.
ACCESSION   AR324046
VERSION     AR324046.1  GI:33709854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1448 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGC 3670
              |||||||||||| |||
Db         18 GCTCAGTCATCAGAGC 3


RESULT 448
AR430883/c
LOCUS       AR430883                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 58 from patent US 6649595.
ACCESSION   AR430883
VERSION     AR430883.1  GI:40192003
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Clackson,T.P., Gilman,M.Z., Holt,D.A., Keenan,T.P., Rozamus,L. and
            Yang,W.
  TITLE     Regulation of biological events using novel compounds
  JOURNAL   Patent: US 6649595-A 58 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              |||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 449
AR442120/c
LOCUS       AR442120                  18 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 19 from patent US 6670124.
ACCESSION   AR442120
VERSION     AR442120.1  GI:42669377
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chow,R. and Tonai,R.
  TITLE     High throughput methods of HLA typing
  JOURNAL   Patent: US 6670124-A 19 30-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
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  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3492 TTGGCTGAGACCTGGG 3507
              ||||||| ||||||||
Db         18 TTGGCTGCGACCTGGG 3


RESULT 450
AR478212
LOCUS       AR478212                  18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 15 from patent US 6699661.
ACCESSION   AR478212
VERSION     AR478212.1  GI:47236860
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 15 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 451
AR478216
LOCUS       AR478216                  18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 19 from patent US 6699661.
ACCESSION   AR478216
VERSION     AR478216.1  GI:47236864
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 19 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 452
AX329281
LOCUS       AX329281                  18 bp    DNA     linear   PAT 08-JAN-2002
DEFINITION  Sequence 17 from Patent WO0194387.
ACCESSION   AX329281
VERSION     AX329281.1  GI:18102296
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kirchhoff,C. and Ivell,R.
  TITLE     Epididymis-specific proteins with fibronectin type II modules
  JOURNAL   Patent: WO 0194387-A 17 13-DEC-2001;
            IHF INSTITUT FUER HORMON- UND FORTPFLANZUNGSFORSCHUNG GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="CE12-Antisense-Primer"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4001 GTAATCGTGTGCCATG 4016
              |||||||| |||||||
Db          2 GTAATCGTCTGCCATG 17


RESULT 453
AX472780/c
LOCUS       AX472780                  18 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 17 from Patent WO0187940.
ACCESSION   AX472780
VERSION     AX472780.1  GI:22207634
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Isaac,B.C., Krieger,E.K., mettus Light,A.M., Sivasupramaniam,S. and
            Moshiri,F.
  TITLE     Polypeptide composionns toxic to anthonomus insects, and methods of
            use
  JOURNAL   Patent: WO 0187940-A 17 22-NOV-2001;
            Monsanto Technology LLC (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              |||||||||||| |||
Db         17 TATTTCTAATTCAACA 2


RESULT 454
AX472781
LOCUS       AX472781                  18 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 18 from Patent WO0187940.
ACCESSION   AX472781
VERSION     AX472781.1  GI:22207635
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Isaac,B.C., Krieger,E.K., mettus Light,A.M., Sivasupramaniam,S. and
            Moshiri,F.
  TITLE     Polypeptide composionns toxic to anthonomus insects, and methods of
```

use
JOURNAL Patent: WO 0187940-A 18 22-NOV-2001;
Monsanto Technology LLC (US)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3923 TATTTCTAATTCCACA 3938
||||||||||||| |||
Db 2 TATTTCTAATTCAACA 17

RESULT 455
AX937388/c
LOCUS AX937388 18 bp DNA linear PAT 06-JAN-2004
DEFINITION Sequence 65 from Patent WO03091388.
ACCESSION AX937388
VERSION AX937388.1 GI:40713464
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lancet,D., Menashe,I., Man,O. and Gilad,Y.
TITLE Polymorphic olfactory receptor genes and arrays, kits and methodsutilizing them
JOURNAL Patent: WO 03091388-A 65 06-NOV-2003;
YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthtic DNA oligonucleotide"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 906 TGATGTGCTTCATCCT 921
|| |||||||||||||
Db 18 TGGTGTGCTTCATCCT 3

RESULT 456
BD072876
LOCUS BD072876 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD072876
VERSION BD072876.1 GI:22618479
KEYWORDS JP 2001286300-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 14 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/14
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2386 AAAATAAAATATATAT 2401
|||| ||||||||||||
Db 3 AAAAAAAAATATATAT 18

RESULT 457
BD072880
LOCUS BD072880 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD072880
VERSION BD072880.1 GI:22618483
KEYWORDS JP 2001286300-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 18 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/18
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18

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          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 458
BD107503
LOCUS       BD107503                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107503
VERSION     BD107503.1  GI:23202321
KEYWORDS    JP 2002000275-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 12 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/12
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 459
BD107507
LOCUS       BD107507                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107507
VERSION     BD107507.1  GI:23202325
KEYWORDS    JP 2002000275-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 16 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/16
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 460
E52143
LOCUS       E52143                   16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  TSA7005 gene.
ACCESSION   E52143
VERSION     E52143.1  GI:18629626
KEYWORDS    JP 2001025389-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ogawara,T., Suzuki,M. and Ozaki,K.
  TITLE     TSA7005 gene
  JOURNAL   Patent: JP 2001025389-A 3 30-JAN-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unknown
            PN   JP 2001025389-A/3
            PD   30-JAN-2001
            PF   15-JUL-1999 JP 1999201279
            PR
            PI   TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
            PC   C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10//A61K31/00,
            PC   A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unknown'.
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FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTH 15


RESULT 461
E53842
LOCUS       E53842                    16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION   E53842
VERSION     E53842.1  GI:18633612
KEYWORDS    JP 2001078772-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
  TITLE     LUNX gene and method for detecting micrometastasis of cancer
  JOURNAL   Patent: JP 2001078772-A 3 27-MAR-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 2001078772-A/3
            PD   27-MAR-2001
            PF   07-SEP-1999 JP 1999253186
            PR
            PI   MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI
            PC   C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
            A61K35/12,A61K35/76,
            PC   A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTV 15


RESULT 462
BD145051
LOCUS       BD145051                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145051
VERSION     BD145051.1  GI:27850809
KEYWORDS    JP 2002119291-A/32.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 32 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/32
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 463
BD145062/c
LOCUS       BD145062                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145062
VERSION     BD145062.1  GI:27850820
KEYWORDS    JP 2002119291-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 43 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/43
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
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          PC   G01N1/28,
          PC   G01N1/28
          CC   The base sequence was prepared synthetically on the aim of  CC
                  examining the
          CC   decrease in fluorescence emission of
          CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                  hybridization of
          CC   the probe with a target nucleic acid.
          FH   Key             Location/Qualifiers
          FT   source          1. .20
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         19 ATATATATATTTTTTTTT 1


RESULT 464
BD166051
LOCUS       BD166051                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166051
VERSION     BD166051.1  GI:27871863
KEYWORDS    JP 2002191372-A/31.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 31 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/31
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         2 ATATATATATTTTTTTTT 20


RESULT 465
BD166062/c
LOCUS       BD166062                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166062
VERSION     BD166062.1  GI:27871874
KEYWORDS    JP 2002191372-A/42.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 42 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/42
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         19 ATATATATATTTTTTTTT 1


RESULT 466
AR264947
LOCUS       AR264947                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 31 from patent US 6492121.
ACCESSION   AR264947
VERSION     AR264947.1  GI:29693334
KEYWORDS    .
SOURCE      Unknown.
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 31 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 467
AR478228
LOCUS       AR478228                 20 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 31 from patent US 6699661.
ACCESSION   AR478228
VERSION     AR478228.1  GI:47236876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 31 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 468
BD072892
LOCUS       BD072892                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072892
VERSION     BD072892.1  GI:22618495
KEYWORDS    JP 2001286300-A/30.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 30 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/30
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC          nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 469
BD072903/c
LOCUS       BD072903                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072903
VERSION     BD072903.1  GI:22618506
KEYWORDS    JP 2001286300-A/41.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 41 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/41
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
```

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            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         19 ATATATATATTTTTTTTTT 1


RESULT 470
BD107519
LOCUS       BD107519                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107519
VERSION     BD107519.1  GI:23202337
KEYWORDS    JP 2002000275-A/28.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 28 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/28
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 471
BD107530/c
LOCUS       BD107530                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107530
VERSION     BD107530.1  GI:23202348
KEYWORDS    JP 2002000275-A/39.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 39 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/39
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         19 ATATATATATTTTTTTTTT 1


RESULT 472
AX825150/c
LOCUS       AX825150                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 48 from Patent WO03072818.
ACCESSION   AX825150
VERSION     AX825150.1  GI:39750879
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 48 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Beschreibung der kuenstlichen
                      Sequenz:Capture-Oligonukleotid"
     misc_binding     1
                      /bound_moiety="Biotin"
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     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              |||||||| ||||| | ||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 473
AR029886/c
LOCUS       AR029886                  14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 75 from patent US 5861244.
ACCESSION   AR029886
VERSION     AR029886.1  GI:5943100
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 75 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 474
AR029887
LOCUS       AR029887                  14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 76 from patent US 5861244.
ACCESSION   AR029887
VERSION     AR029887.1  GI:5943101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 76 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 475
AR174022
LOCUS       AR174022                  14 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 12 from patent US 6306624.
ACCESSION   AR174022
VERSION     AR174022.1  GI:17914342
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
  TITLE     Retinoid metabolizing protein
  JOURNAL   Patent: US 6306624-A 12 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 476
BD132850
LOCUS       BD132850                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Methods of nucleic acid detection.
ACCESSION   BD132850
VERSION     BD132850.1  GI:23227795
KEYWORDS    JP 2002509443-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
  TITLE     Methods of nucleic acid detection
  JOURNAL   Patent: JP 2002509443-A 1 26-MAR-2002;
            GEN PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002509443-A/1
            PD   26-MAR-2002
            PF   30-OCT-1998 JP 1999526687
            PR   31-OCT-1997 US    60/063969
            PI   WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
            C12Q1/68
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 477
BD176795/c
LOCUS       BD176795                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176795
VERSION     BD176795.1  GI:29122507
KEYWORDS    WO 02074951-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 42 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/42
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 478
BD176796/c
LOCUS       BD176796                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176796
VERSION     BD176796.1  GI:29122508
KEYWORDS    WO 02074951-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 43 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/43
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTT 4513
              ||||||||||||||
Db         14 GTTTTTTTTTTTTT 1


RESULT 479
BD176803
LOCUS       BD176803                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176803
VERSION     BD176803.1  GI:29122515
KEYWORDS    WO 02074951-A/50.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 50 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/50
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTG 4516
              ||||||||||||||
Db          1 TTTTTTTTTTTTTG 14


RESULT 480
BD176804
LOCUS       BD176804                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176804
VERSION     BD176804.1  GI:29122516
KEYWORDS    WO 02074951-A/51.
SOURCE      synthetic construct
```

```
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 51 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/51
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 481
BD237464/c
LOCUS       BD237464                  14 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof.
ACCESSION   BD237464
VERSION     BD237464.1  GI:33047234
KEYWORDS    JP 2002534434-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Dale,R.M.K., Gatton,S.L. and Arrow,A.
  TITLE     Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof
  JOURNAL   Patent: JP 2002534434-A 2 15-OCT-2002;
            OLIGOS ETC INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002534434-A/2
            PD   15-OCT-2002
            PF   16-DEC-1999 JP 2000592300
            PR   30-DEC-1998 US    09/223498,19-JUL-1999 US    09/356069 PI
            RODERIC M K DALE,STEVEN L GATTON,AMY ARROW
            PC   C07H21/00,A61K9/127,A61K9/50,A61K31/7088,A61K47/44,A61K48/00,
            PC   A61P3/00,
            PC   A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
            PC   C12N5/10,
            PC   C12N15/09,C12N15/00,C12N5/00
            CC   Nucleic acid having blocked terminals modified with an acid-
            CC           stable
            CC   skeleton and therapeutic method thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 482
CQ827692/c
LOCUS       CQ827692                  14 bp    DNA     linear   PAT 29-JUN-2004
DEFINITION  Sequence 129 from Patent WO2004050918.
ACCESSION   CQ827692
VERSION     CQ827692.1  GI:49456142
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ruan,Y. and Wei,C.
  TITLE     Method to generate or determine nucleic acid tags corresponding to
            the terminal ends of dna molecules using sequence analysis of gene
            expression (terminal sage)
  JOURNAL   Patent: WO 2004050918-A 129 17-JUN-2004;
            Agency for Science, Technology and Research (SG)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="tag"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 483
AR222460/c
LOCUS       AR222460                  14 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 20 from patent US 6429300.
ACCESSION   AR222460
VERSION     AR222460.1  GI:23329991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 20 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 484
```

```
AR364948
LOCUS       AR364948                  14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 4 from patent US 5453496.
ACCESSION   AR364948
VERSION     AR364948.1  GI:34428168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 4 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 485
AR364949/c
LOCUS       AR364949                  14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 5 from patent US 5453496.
ACCESSION   AR364949
VERSION     AR364949.1  GI:34428169
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 5 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 486
AR491866
LOCUS       AR491866                  14 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 1 from patent US 6716585.
ACCESSION   AR491866
VERSION     AR491866.1  GI:47260087
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Al-Mahmood,S.
  TITLE     Method for identifying novel genes involved in the regulation of
            angiogenesis, study of said genes and use thereof for therapeutic
            purposes
  JOURNAL   Patent: US 6716585-A 1 06-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 487
AX016298
LOCUS       AX016298                  14 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9949046.
ACCESSION   AX016298
VERSION     AX016298.1  GI:10041861
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Roberts,J.A., Wyatt,P. and Whitelaw,C.
  TITLE     Signal transduction protein involved in plant dehiscence
  JOURNAL   Patent: WO 9949046-A 1 30-SEP-1999;
            ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAUL (GB);
            WHITELAW CATHERINE (GB)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligo dT anchor primer 7"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 488
AX048406
LOCUS       AX048406                  14 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 5 from Patent WO0071747.
ACCESSION   AX048406
VERSION     AX048406.1  GI:12225570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 5 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
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Db          1 TTTTTTTTTTTTTT 14


RESULT 489
AX642208
LOCUS       AX642208                  14 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 26 from Patent WO02061082.
ACCESSION   AX642208
VERSION     AX642208.1  GI:28474656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Day,R.
  TITLE     Zis-sr nucleic acid and amino acid sequences involved in the
            regulated secretory pathway and/or the regulation of the
            neuroendocrine phenotype (nep)
  JOURNAL   Patent: WO 02061082-A 26 08-AUG-2002;
            Universite de Sherbrooke (CA)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 490
AX659630
LOCUS       AX659630                  14 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 24 from Patent WO02103014.
ACCESSION   AX659630
VERSION     AX659630.1  GI:29161812
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Al-Mahmood,S.
  TITLE     Antisense oligonucleotides which can inhibit the formation of
            capillary tubes by endothelial cells
  JOURNAL   Patent: WO 02103014-A 24 27-DEC-2002;
            Al-Mahmood, Salman (FR)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide anti-sens"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 491
AX827014/c
LOCUS       AX827014                  14 bp    RNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 11 from Patent EP1344835.
ACCESSION   AX827014
VERSION     AX827014.1  GI:39837221
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
            Liu,D.
  TITLE     Real-time nucleic acid detection processes and compositions
  JOURNAL   Patent: EP 1344835-A 11 17-SEP-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 492
AX839906/c
LOCUS       AX839906                  14 bp    RNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 11 from Patent EP1348713.
ACCESSION   AX839906
VERSION     AX839906.1  GI:39978437
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stavrianopoulos,J.G. and Rabbani,E.
  TITLE     Labeling reagents and labeled tabeled targets, target labeling
            processes and other processes for using same in nucleic acid
            determinations and analyses
  JOURNAL   Patent: EP 1348713-A 11 01-OCT-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 493
BD073884
LOCUS       BD073884                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073884
VERSION     BD073884.1  GI:22619487
KEYWORDS    JP 2001512698-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
```

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  JOURNAL   Patent: JP 2001512698-A 9 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/9
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 494
BD084127/c
LOCUS       BD084127                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084127
VERSION     BD084127.1  GI:22629737
KEYWORDS    JP 2001525663-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 15 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/15
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 495
BD096963
LOCUS       BD096963                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096963
VERSION     BD096963.1  GI:22642551
KEYWORDS    JP 2001346579-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 2 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/2
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
            FT   modified_base   1.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 496
BD096965
LOCUS       BD096965                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096965
VERSION     BD096965.1  GI:22642553
KEYWORDS    JP 2001346579-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 4 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/4
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
            FT   modified_base   1.
FEATURES              Location/Qualifiers
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     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 497
AR056156
LOCUS       AR056156                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 360 from patent US 5837542.
ACCESSION   AR056156
VERSION     AR056156.1  GI:5981733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 360 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 498
AR056159
LOCUS       AR056159                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 363 from patent US 5837542.
ACCESSION   AR056159
VERSION     AR056159.1  GI:5981736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 363 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 499
AR084518/c
LOCUS       AR084518                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 7 from patent US 5981185.
ACCESSION   AR084518
VERSION     AR084518.1  GI:10011289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 7 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTG 4516
              ||||||||||||||
Db         15 TTTTTTTTTTTTTG 2


RESULT 500
AR113914
LOCUS       AR113914                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 360 from patent US 6132967.
ACCESSION   AR113914
VERSION     AR113914.1  GI:14094236
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 360 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 501
AR113917
LOCUS       AR113917                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 363 from patent US 6132967.
ACCESSION   AR113917
VERSION     AR113917.1  GI:14094239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 363 17-OCT-2000;
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FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 502
AR132214/c
LOCUS       AR132214                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 639 from patent US 6194150.
ACCESSION   AR132214
VERSION     AR132214.1  GI:14121119
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 639 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGA 1417
              ||||||||||||||
Db         14 GATGCTAAAGATGA 1


RESULT 503
AR132215/c
LOCUS       AR132215                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 640 from patent US 6194150.
ACCESSION   AR132215
VERSION     AR132215.1  GI:14121120
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 640 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGA 1417
              ||||||||||||||
Db         14 GATGCTAAAGATGA 1


RESULT 504
I29065/c
LOCUS       I29065                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5576427.
ACCESSION   I29065
VERSION     I29065.1  GI:1819856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 3 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              | ||||||||||||||
Db         15 TNTTTTTTTTTTTT 1


RESULT 505
I29066/c
LOCUS       I29066                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 4 from patent US 5576427.
ACCESSION   I29066
VERSION     I29066.1  GI:1819857
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 4 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              || ||||||||||||
Db         15 TTNTTTTTTTTTTT 1


RESULT 506
AR241870
LOCUS       AR241870                  15 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 158 from patent US 6472154.
ACCESSION   AR241870
VERSION     AR241870.1  GI:27287682
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 158 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              ||||||||||| |||
Db          1 TTTTTTTTTTNTTT 15


RESULT 507
AR560062
LOCUS       AR560062                  15 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 28 from patent US 6753154.
ACCESSION   AR560062
VERSION     AR560062.1  GI:53970361
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chen,H.-M. and Bissell,M.
  TITLE     Human AZU-1 gene, variants thereof and expressed gene products
  JOURNAL   Patent: US 6753154-A 28 22-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTT 4511
              ||||||||||||||
Db          1 AAGTTTTTTTTTTT 14


RESULT 508
AX009448
LOCUS       AX009448                  15 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 1 from Patent WO9961662.
ACCESSION   AX009448
VERSION     AX009448.1  GI:9996734
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Shchepinov,M.S. and Southern,E.M.
  TITLE     Polynucleotide multimers and their use in hybridisation assays
  JOURNAL   Patent: WO 9961662-A 1 02-DEC-1999;
            SHCHEPINOV MIKHAIL SERGEEVICH (GB); SOUTHERN EDWIN MELLOR (GB);
            ISIS INNOVATION (GB)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2904 TCTTTCTCTTCCCT 2917
              ||||||||||||||
Db          2 TCTTTCTCTTCCCT 15


RESULT 509
AX190915
LOCUS       AX190915                  15 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 266 from Patent WO0142493.
ACCESSION   AX190915
VERSION     AX190915.1  GI:15144199
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A. and Piepenbrock,C.
  TITLE     Method for the parallel detection of the degree of methylation of
            genomic dna
  JOURNAL   Patent: WO 0142493-A 266 14-JUN-2001;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemisch vorbehandelte Genom-DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTT 4512
              ||||||||||||||
Db          2 AGTTTTTTTTTTTT 15


RESULT 510
AX190916/c
LOCUS       AX190916                  15 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 267 from Patent WO0142493.
ACCESSION   AX190916
VERSION     AX190916.1  GI:15144200
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A. and Piepenbrock,C.
  TITLE     Method for the parallel detection of the degree of methylation of
            genomic dna
  JOURNAL   Patent: WO 0142493-A 267 14-JUN-2001;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemisch vorbehandelte Genom-DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTT 4512
              ||||||||||||||
Db         14 AGTTTTTTTTTTTT 1


RESULT 511
AX633195
LOCUS       AX633195                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 334 from Patent EP1260586.
ACCESSION   AX633195
VERSION     AX633195.1  GI:28468809
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
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          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
  TITLE   Method and reagent for inhibiting the expression of disease related
          genes
  JOURNAL Patent: EP 1260586-A 334 27-NOV-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="unidentified"
                    /mol_type="unassigned RNA"
                    /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 512
AX633201
LOCUS       AX633201                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 340 from Patent EP1260586.
ACCESSION   AX633201
VERSION     AX633201.1  GI:28468815
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 340 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="unidentified"
                    /mol_type="unassigned RNA"
                    /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 513
I47692/c
LOCUS       I47692                    16 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5639873.
ACCESSION   I47692
VERSION     I47692.1  GI:2471657
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Barascut,J.-L. and Imbach,J.-L.
  TITLE     Oligothionucleotides
  JOURNAL   Patent: US 5639873-A 4 17-JUN-1997;
FEATURES            Location/Qualifiers
     source         1. .16
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db         14 TTTTTTTTTTTTGG 1


RESULT 514
AR187065
LOCUS       AR187065                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2553 from patent US 6346398.
ACCESSION   AR187065
VERSION     AR187065.1  GI:20233030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2553 12-FEB-2002;
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 515
AR323675
LOCUS       AR323675                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1077 from patent US 6566127.
ACCESSION   AR323675
VERSION     AR323675.1  GI:33709483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1077 20-MAY-2003;
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unknown"
                    /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 516
BD197546
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LOCUS       BD197546                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD197546
VERSION     BD197546.1  GI:33007316
KEYWORDS    JP 2002509721-A/572.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 572 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/572
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2562 GCAGCTTCTAAGAG 2575
              ||||||||||||||
Db          3 GCAGCTTCTAAGAG 16


RESULT 517
BD197547
LOCUS       BD197547                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD197547
VERSION     BD197547.1  GI:33007317
KEYWORDS    JP 2002509721-A/573.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 573 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/573
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2562 GCAGCTTCTAAGAG 2575
              ||||||||||||||
Db          2 GCAGCTTCTAAGAG 15


RESULT 518
BD255102
LOCUS       BD255102                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255102
VERSION     BD255102.1  GI:33064872
KEYWORDS    JP 2002541795-A/2895.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2895 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2895
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1126 CCACAACTACCACC 1139
              ||||||||||||||
Db          1 CCACAACTACCACC 14
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RESULT 519
AX421959/c
LOCUS       AX421959                  17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 295 from Patent WO0188124.
ACCESSION   AX421959
VERSION     AX421959.1  GI:21525341
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 295 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4481 GAATGTATTTGATT 4494
              ||||||||||||||
Db         14 GAATGTATTTGATT 1


RESULT 520
AX422478
LOCUS       AX422478                  17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 814 from Patent WO0188124.
ACCESSION   AX422478
VERSION     AX422478.1  GI:21525860
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 814 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1061 TATGACAAGAACAT 1074
              ||||||||||||||
Db          3 TATGACAAGAACAT 16


RESULT 521
AX422678/c
LOCUS       AX422678                  17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1014 from Patent WO0188124.
ACCESSION   AX422678
VERSION     AX422678.1  GI:21526060
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1014 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4482 AATGTATTTGATTT 4495
              ||||||||||||||
Db         17 AATGTATTTGATTT 4


RESULT 522
AX580099/c
LOCUS       AX580099                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 1937 from Patent WO0211674.
ACCESSION   AX580099
VERSION     AX580099.1  GI:27649301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1937 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2731 CTTCTCTCCACAGT 2744
              ||||||||||||||
Db         17 CTTCTCTCCACAGT 4


RESULT 523
AX580100/c
LOCUS       AX580100                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 1938 from Patent WO0211674.
ACCESSION   AX580100
VERSION     AX580100.1  GI:27649302
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
```

```
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1938 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2731 CTTCTCTCCACAGT 2744
              ||||||||||||||
Db         16 CTTCTCTCCACAGT 3


RESULT 524
AX580101/c
LOCUS       AX580101                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 1939 from Patent WO0211674.
ACCESSION   AX580101
VERSION     AX580101.1  GI:27649303
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1939 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2731 CTTCTCTCCACAGT 2744
              ||||||||||||||
Db         14 CTTCTCTCCACAGT 1


RESULT 525
AX692523
LOCUS       AX692523                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5255 from Patent EP1281758.
ACCESSION   AX692523
VERSION     AX692523.1  GI:29415481
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5255 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          4 TTTTTTTTTTTTTT 17


RESULT 526
AX726054
LOCUS       AX726054                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3741 from Patent WO03025176.
ACCESSION   AX726054
VERSION     AX726054.1  GI:30505397
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3741 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1989 TCTCTCCTGGCTCG 2002
              ||||||||||||||
Db          3 TCTCTCCTGGCTCG 16


RESULT 527
AX727280/c
LOCUS       AX727280                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4967 from Patent WO03025176.
ACCESSION   AX727280
VERSION     AX727280.1  GI:30506623
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 4967 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1154 GACTACTCTGCCAG 1167
              ||||||||||||||
Db         17 GACTACTCTGCCAG 4


RESULT 528
AX729364/c
LOCUS       AX729364                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 998 from Patent WO03025175.
ACCESSION   AX729364
VERSION     AX729364.1  GI:30508707
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 998 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2892 TCTTTGACCAGATC 2905
              ||||||||||||||
Db         14 TCTTTGACCAGATC 1


RESULT 529
AX731686/c
LOCUS       AX731686                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3320 from Patent WO03025175.
ACCESSION   AX731686
VERSION     AX731686.1  GI:30511029
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 3320 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4822 AGCATTTTGGGATC 4835
              ||||||||||||||
Db         14 AGCATTTTGGGATC 1


RESULT 530
AX739654/c
LOCUS       AX739654                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5244 from Patent WO03025177.
ACCESSION   AX739654
VERSION     AX739654.1  GI:30518951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 5244 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTG 4516
              ||||||||||||||
Db         17 TTTTTTTTTTTTTG 4


RESULT 531
S61964
LOCUS       S61964                    23 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  (beta C)=beta-globin {5'region} [human, Genomic Mutant, 23 nt].
ACCESSION   S61964
VERSION     S61964.1  GI:236198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Trabuchet,G., Elion,J., Dunda,O., Lapoumeroulie,C., Ducrocq,R.,
            Nadifi,S., Zohoun,I., Chaventre,A., Carnevale,P., Nagel,R.L. et,al.
  TITLE     Nucleotide sequence evidence of the unicentric origin of the beta C
            mutation in Africa
  JOURNAL   Hum. Genet. 87 (5), 597-601 (1991)
  MEDLINE   92009838
   PUBMED   1680789
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 61964] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1. .23
                     /gene="beta-globin"
                     /allele="beta C"

  Query Match             0.3%;  Score 14;  DB 1;  Length 23;
  Best Local Similarity   77.3%;  Pred. No. 5.2e+02;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACATTGCTT 2418
              |||||| |||||||  ||  ||
Db          1 TATATATATATATATTTTTTT 22


RESULT 532
AR187064/c
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LOCUS       AR187064                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2552 from patent US 6346398.
ACCESSION   AR187064
VERSION     AR187064.1  GI:20233029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
             ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 533
AR241830/c
LOCUS       AR241830                 17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 118 from patent US 6472154.
ACCESSION   AR241830
VERSION     AR241830.1  GI:27287642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 118 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
             ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 534
AR323674/c
LOCUS       AR323674                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1076 from patent US 6566127.
ACCESSION   AR323674
VERSION     AR323674.1  GI:33709482
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
             ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 535
AX692524/c
LOCUS       AX692524                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5256 from Patent EP1281758.
ACCESSION   AX692524
VERSION     AX692524.1  GI:29415482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5256 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
             ||||||| ||||| |||
Db         17 AAAAAAAAAAAAAAAGA 1


RESULT 536
AX692523/c
LOCUS       AX692523                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5255 from Patent EP1281758.
ACCESSION   AX692523
VERSION     AX692523.1  GI:29415481
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5255 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
             |||||| ||||| ||||
Db         17 AAAAAAAAAAAAAAGAA 1
```

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RESULT 537
A88312
LOCUS       A88312                    17 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 460 from Patent WO9833904.
ACCESSION   A88312
VERSION     A88312.1  GI:6736882
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 460 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3599 GTCTGGAAAAAAACAAA 3615
              ||||  ||||||||||
Db          1 GTCTTTAAAAAAACAAA 17


RESULT 538
A90279
LOCUS       A90279                    17 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 460 from Patent EP0856579.
ACCESSION   A90279
VERSION     A90279.1  GI:6738793
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 460 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3599 GTCTGGAAAAAAACAAA 3615
              ||||  ||||||||||
Db          1 GTCTTTAAAAAAACAAA 17


RESULT 539
AR029813
LOCUS       AR029813                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5861244.
ACCESSION   AR029813
VERSION     AR029813.1  GI:5943027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 2 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1509 TTTCTTCTCTTATCCTC 1525
              |||||||||  | |||||
Db          1 TTTCTTCTCCTCTCCTC 17


RESULT 540
AR039423
LOCUS       AR039423                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 271 from patent US 5807743.
ACCESSION   AR039423
VERSION     AR039423.1  GI:5958786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 271 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2946 AGCCTCCTTTGTGTGTA 2962
              |||||  || ||||||||
Db          1 AGCCTTCTCTGTGTGTA 17


RESULT 541
AR040167
LOCUS       AR040167                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1015 from patent US 5807743.
ACCESSION   AR040167
VERSION     AR040167.1  GI:5959530
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 1015 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2102 AGTGGTCTCTGCTGGGG 2118
              ||  |||||||||||||
Db          1 AGCTGTCTCTGCTGGGG 17
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RESULT 542
AR045379/c
LOCUS       AR045379                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 172 from patent US 5817796.
ACCESSION   AR045379
VERSION     AR045379.1  GI:5966844
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 172 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3387 AGTAGGAGGAAACAGTT 3403
              || |||||||||||| |
Db         17 AGGAGGAGGAAACAGGT 1


RESULT 543
AR045381/c
LOCUS       AR045381                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 174 from patent US 5817796.
ACCESSION   AR045381
VERSION     AR045381.1  GI:5966846
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 174 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACA 3400
              || || ||||||||||||
Db         17 AGGAGGAGGAGGAAACA 1


RESULT 544
AR046269/c
LOCUS       AR046269                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1062 from patent US 5817796.
ACCESSION   AR046269
VERSION     AR046269.1  GI:5967734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 1062 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATAT 2407
              ||||| |||||| ||||
Db         17 AAAATGTATATATATAT 1


RESULT 545
AR074706/c
LOCUS       AR074706                  17 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 3 from patent US 5955276.
ACCESSION   AR074706
VERSION     AR074706.1  GI:10001459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Morgante,M. and Vogel,J.Marie.
  TITLE     Compound microsatellite primers for the detection of genetic
            polymorphisms
  JOURNAL   Patent: US 5955276-A 3 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCT 3198
              |||||||| ||| ||||
Db         17 TCTCTCTCTCTCTCTCT 1


RESULT 546
AR074707/c
LOCUS       AR074707                  17 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 4 from patent US 5955276.
ACCESSION   AR074707
VERSION     AR074707.1  GI:10001460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Morgante,M. and Vogel,J.Marie.
  TITLE     Compound microsatellite primers for the detection of genetic
            polymorphisms
  JOURNAL   Patent: US 5955276-A 4 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3185 CTCTCCCTCCCTCTCTC 3201
              ||||| ||| |||||||
Db         17 CTCTCTCTCTCTCTCTC 1


RESULT 547
AR074708
LOCUS       AR074708                  17 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 5 from patent US 5955276.
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ACCESSION   AR074708
VERSION     AR074708.1  GI:10001461
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Morgante,M. and Vogel,J.Marie.
  TITLE     Compound microsatellite primers for the detection of genetic
            polymorphisms
  JOURNAL   Patent: US 5955276-A 5 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCT 3198
              ||||||| ||| ||||
Db          1 TCTCTCTCTCTCTCTCT 17


RESULT 548
AR074709
LOCUS       AR074709                 17 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 6 from patent US 5955276.
ACCESSION   AR074709
VERSION     AR074709.1  GI:10001462
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Morgante,M. and Vogel,J.Marie.
  TITLE     Compound microsatellite primers for the detection of genetic
            polymorphisms
  JOURNAL   Patent: US 5955276-A 6 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3185 CTCTCCCTCCCTCTCTC 3201
              ||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTC 17


RESULT 549
BD197617/c
LOCUS       BD197617                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD197617
VERSION     BD197617.1  GI:33007387
KEYWORDS    JP 2002509721-A/643.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 643 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/643
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5043 GATGCCTTTTCTGTGAT 5059
              ||||||||| || ||||
Db         17 GATGCCTTTACTCTGAT 1


RESULT 550
BD197742/c
LOCUS       BD197742                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD197742
VERSION     BD197742.1  GI:33007512
KEYWORDS    JP 2002509721-A/768.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 768 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/768
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"
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  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1889 GGATGAGGGAAGCGAAG 1905
              || ||||||||| ||||
Db         17 GGGTGAGGGAAGGGAAG 1

RESULT 551
BD202801
LOCUS       BD202801                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202801
VERSION     BD202801.1  GI:33012571
KEYWORDS    JP 2002509721-A/5827.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5827 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5827
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTT 2143
              | |||||||| ||||||
Db          1 TTTTTTCTTTCTTTCTT 17

RESULT 552
BD202896/c
LOCUS       BD202896                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202896
VERSION     BD202896.1  GI:33012666
KEYWORDS    JP 2002509721-A/5922.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5922 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5922
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3961 AATATATAAACAATAAA 3977
              |||| ||||| ||||||
Db         17 AATAAATAAATAATAAA 1

RESULT 553
BD203005/c
LOCUS       BD203005                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD203005
VERSION     BD203005.1  GI:33012775
KEYWORDS    JP 2002509721-A/6031.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 6031 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/6031
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
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          FT   source          1. .17
          FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||| ||||||||| |||
Db         17 AAACAAACAAAAAAAGA 1


RESULT 554
BD203051
LOCUS       BD203051                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD203051
VERSION     BD203051.1  GI:33012821
KEYWORDS    JP 2002509721-A/6077.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 6077 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/6077
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1261 CGCCATCTTGGCCAGGA 1277
              | |||| ||||||||||
Db          1 CCCCATGTTGGCCAGGA 17


RESULT 555
BD241222
LOCUS       BD241222                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and products related to genotyping and DNA analysis.
ACCESSION   BD241222
VERSION     BD241222.1  GI:33050992
KEYWORDS    JP 2002525127-A/169.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
  TITLE     Methods and products related to genotyping and DNA analysis
  JOURNAL   Patent: JP 2002525127-A 169 13-AUG-2002;
            MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002525127-A/169
            PD   13-AUG-2002
            PF   24-SEP-1999 JP 2000572407
            PR   25-SEP-1998 US    60/101757
            PI   JOHN E LANDERS,BARBARA JORDAN,DAVID E HOUSMAN,ALAIN CHAREST PC
              C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
            G01N37/00,
            PC   C12N15/00
            CC   Methods and products related to genotyping and DNA analysis FH
              Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGGTT 4520
              |||||| ||||||| ||
Db          1 TTTTTTATTTTTGGATT 17


RESULT 556
BD254535/c
LOCUS       BD254535                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254535
VERSION     BD254535.1  GI:33064305
KEYWORDS    JP 2002541795-A/2328.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2328 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2328
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
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            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4749 CTGTTAAAATGGGGATA 4765
              ||||||||  |||||||
Db         17 CTGTTAAATAGGGGATA 1


RESULT 557
BD256600/c
LOCUS       BD256600                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD256600
VERSION     BD256600.1  GI:33066370
KEYWORDS    JP 2002541795-A/4393.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 4393 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/4393
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2205 ATTGGTAAAAACAGCAG 2221
              ||||  ||| ||||||||
Db         17 ATTGATAAGAACAGCAG 1


RESULT 558
BD256796
LOCUS       BD256796                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD256796
VERSION     BD256796.1  GI:33066566
KEYWORDS    JP 2002541795-A/4589.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 4589 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/4589
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1766 TCCCCTGTTGATTATCT 1782
              || ||| ||||||||||
Db          1 TCACCTCTTGATTATCT 17


RESULT 559
BD257048/c
LOCUS       BD257048                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD257048
VERSION     BD257048.1  GI:33066818
KEYWORDS    JP 2002541795-A/4841.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 4841 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/4841
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2205 ATTGGTAAAAACAGCAG 2221
              |||| ||| ||||||||
Db         17 ATTGATAAGAACAGCAG 1


RESULT 560
BD257747
LOCUS       BD257747                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD257747
VERSION     BD257747.1  GI:33067517
KEYWORDS    JP 2002541795-A/5540.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 5540 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/5540
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAA 5203
              | ||||| |||||||||
Db          1 ATTAAAATTGAAGTGAA 17


RESULT 561
BD258509
LOCUS       BD258509                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258509
VERSION     BD258509.1  GI:33068279
KEYWORDS    JP 2002541795-A/6302.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6302 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6302
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
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  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| |||||| ||||||
Db          1 AAGCTTTTTTATTTTTT 17


RESULT 562
BD258513/c
LOCUS       BD258513                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258513
VERSION     BD258513.1  GI:33068283
KEYWORDS    JP 2002541795-A/6306.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6306 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6306
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
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  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAAA 3979
              | |||||| ||||||||
Db         17 TGTATAAAAAATAAAAA 1


RESULT 563
CQ615333/c
LOCUS       CQ615333                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 73 from Patent WO0192524.
ACCESSION   CQ615333
VERSION     CQ615333.1  GI:41665551
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 73 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2521 GCTGGACATGAGATGGA 2537
              || | ||||||||||||
Db         17 GCAGCACATGAGATGGA 1


RESULT 564
CQ616034
LOCUS       CQ616034                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 774 from Patent WO0192524.
ACCESSION   CQ616034
VERSION     CQ616034.1  GI:41666252
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 774 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1588 TGCCTCCCAGGCAAGCA 1604
              || |||||||| ||||
Db          1 TGGCTCCCAGGCCAGCA 17


RESULT 565
CQ616269/c
LOCUS       CQ616269                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 1009 from Patent WO0192524.
ACCESSION   CQ616269
VERSION     CQ616269.1  GI:41666487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 1009 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2923 TTTTCTTCTTTCCCTGG 2939
              || ||| ||||||||||
Db         17 TTCTCTGCTTTCCCTGG 1


RESULT 566
CQ623194/c
LOCUS       CQ623194                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 7934 from Patent WO0192524.
ACCESSION   CQ623194
VERSION     CQ623194.1  GI:41673412
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 7934 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1627 TCCAGCTTCCAAAGCCT 1643
              |||| |||||| |||||
Db         17 TCCAACTTCCAGAGCCT 1


RESULT 567
E03610
LOCUS       E03610                    17 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA primer for cloning of GABA-A receptor alpha subunit.
ACCESSION   E03610
VERSION     E03610.1  GI:2171825
KEYWORDS    JP 1992144683-A/5.
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Watabe,W., Matsumoto,R., Shibui,T. and Nagahari,K.
  TITLE     PRODUCTION OF N-TERMINAL EXTRACELLULAR SITE PROTEIN OF ION CHANNEL
            DIRECTLY BINDING TYPE RECEPTOR
  JOURNAL   Patent: JP 1992144683-A 5 19-MAY-1992;
            MITSUBISHI KASEI CORP
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1992144683-A/5
            PD   19-MAY-1992
            PF   05-OCT-1990 JP 1990267743
            PI   WATABE WAKAKO, MATSUMOTO RIEKO, SHIBUI TATSURO, NAGAHARI KENJI
            PC   C12N15/12,C12N15/70,C12P21/02,(C12P21/02,C12R1:19); CC
            strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   misc_feature    1. .17
            FT                   /note='primer for cloning of GABA-A receptor
            FT                   alpha subunit'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3185 CTCTCCCTCCCTCTCTC 3201
              ||||  ||||||||||||
Db          1 CTCTGGCTCCCTCTCTC 17


RESULT 568
E12897
LOCUS       E12897                    17 bp    RNA     linear   PAT 27-APR-1998
DEFINITION  Modified antisense oligonucleotide.
ACCESSION   E12897
VERSION     E12897.1  GI:5708629
KEYWORDS    JP 1997095495-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsuda,A. and Ono,A.
  TITLE     ANTISENSE OLIGONUCLEOTIDE, NUCLEOSIDE AND INTERMEDIATE FOR
            PRODUCING THE SAME, ITS SYNTHESIS, OLIGONUCLEOTIDE SYNTHESIZING
            UNIT AND ITS
  JOURNAL   Patent: JP 1997095495-A 1 08-APR-1997;
            KANSAI SHIN GIJUTSU KENKYUSHO:KK, MATSUDA AKIRA
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997095495-A/1
            PD   08-APR-1997
            PF   29-SEP-1995 JP 1995277168
            PI   MATSUDA AKIRA, ONO AKIRA
            PC   C07H21/04//A61K31/70,A61K31/70,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .17
            FT                   /organism='Artificial sequences' FT
            misc_feature    1
            FT
            FT
            /note='5-(N,N-dimethylaminohexyl)carbamoyl-2'-deoxyuridine' FT
            misc_feature    2
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    4
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    6
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    7
            FT
            FT
            /note='5-(N,N-dimethylaminohexyl)carbamoyl-2'-deoxyuridine' FT
            misc_feature    8
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    10
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    11
            FT
            FT
            /note='5-(N,N-dimethylaminohexyl)carbamoyl-2'-deoxyuridine' FT
            misc_feature    12
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    14
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    16
            FT                   /note='5-methyl-2'-deoxycytidine' FT
            misc_feature    17
            FT                   /note='5-aminohexylcarbamoyl-2'-deoxyuridine'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCT 3198
              |||||||| ||| ||||
Db          1 TCTCTCTCTCTCTCTCT 17


RESULT 569
I28581/c
LOCUS       I28581                    17 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 34 from patent US 5571937.
ACCESSION   I28581
VERSION     I28581.1  GI:1819357
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Watanabe,K.A., Ren,W.-Y. and Weil,R.
  TITLE     Complementary DNA and toxins
  JOURNAL   Patent: US 5571937-A 34 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTT 2143
              ||||| ||||| |||||
Db         17 TCTTTGCTTTTCTTCTT 1


RESULT 570
I32318/c
LOCUS       I32318                    17 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 10 from patent US 5587300.
```

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ACCESSION   I32318
VERSION     I32318.1  GI:1823109
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Malter,J.S.
  TITLE     Method to increase regulatory molecule production
  JOURNAL   Patent: US 5587300-A 10 24-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACAT 2413
              || ||||||| ||||||
Db         17 TACATACATACATACAT 1


RESULT 571
I32319
LOCUS       I32319                    17 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 11 from patent US 5587300.
ACCESSION   I32319
VERSION     I32319.1  GI:1823110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Malter,J.S.
  TITLE     Method to increase regulatory molecule production
  JOURNAL   Patent: US 5587300-A 11 24-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACAT 2413
              || ||||||| ||||||
Db          1 TACATACATACATACAT 17


RESULT 572
I37483
LOCUS       I37483                    17 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 496 from patent US 5612215.
ACCESSION   I37483
VERSION     I37483.1  GI:2085443
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
            Stinchcomb,D.T.
  TITLE     Stromelysin targeted ribozymes
  JOURNAL   Patent: US 5612215-A 496 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        899 TTGCTGCTGATGTGCTT 915
              ||||||| ||| ||||
Db          1 TTGCTGCTCATGAGCTT 17


RESULT 573
I52431/c
LOCUS       I52431                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 172 from patent US 5646042.
ACCESSION   I52431
VERSION     I52431.1  GI:2473632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 172 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3387 AGTAGGAGGAAACAGTT 3403
              || ||||||||||| |
Db         17 AGGAGGAGGAAACAGGT 1


RESULT 574
I52433/c
LOCUS       I52433                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 174 from patent US 5646042.
ACCESSION   I52433
VERSION     I52433.1  GI:2473634
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 174 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACA 3400
              || || ||||||||||
Db         17 AGGAGGAGGAGGAAACA 1


RESULT 575
I53321/c
LOCUS       I53321                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1062 from patent US 5646042.
ACCESSION   I53321
VERSION     I53321.1  GI:2474524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1062 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATAT 2407
              ||||| |||||| ||||
Db         17 AAAATGTATATATATAT 1


RESULT 576
I58743/c
LOCUS       I58743                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 34 from patent US 5652350.
ACCESSION   I58743
VERSION     I58743.1  GI:2477981
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Watanabe,K.A., Ren,W.-Y. and Weil,R.
  TITLE     Complementary DNA and toxins
  JOURNAL   Patent: US 5652350-A 34 29-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTT 2143
              ||||| ||||| |||||
Db         17 TCTTTGCTTTTCTTCTT 1


RESULT 577
I94333
LOCUS       I94333                    17 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 496 from patent US 5731295.
ACCESSION   I94333
VERSION     I94333.1  GI:3938803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
            Stinchcomb,D.T.
  TITLE     Method of reducing stromelysin RNA via ribozymes
  JOURNAL   Patent: US 5731295-A 496 24-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        899 TTGCTGCTGATGTGCTT 915
              |||||||| ||| ||||
Db          1 TTGCTGCTCATGAGCTT 17


RESULT 578
AR186534
LOCUS       AR186534                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2022 from patent US 6346398.
ACCESSION   AR186534
VERSION     AR186534.1  GI:20232499
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2022 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4545 TGGAAAATTTTCTCCTT 4561
              ||| |||| ||||||||
Db          1 TGGGAAATCTTCTCCTT 17


RESULT 579
AR187067/c
LOCUS       AR187067                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2555 from patent US 6346398.
ACCESSION   AR187067
VERSION     AR187067.1  GI:20233032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2555 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAA 3616
              | |||||||||| ||||
Db         17 TTTGGAAAAAAAAAAAA 1


RESULT 580
AR188493
LOCUS       AR188493                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 3981 from patent US 6346398.
ACCESSION   AR188493
VERSION     AR188493.1  GI:20234458
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
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  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 3981 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAA 5203
              ||||||| |||||| ||
Db          1 AATAAAATTGAAGTTAA 17


RESULT 581
AR190587
LOCUS       AR190587                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6075 from patent US 6346398.
ACCESSION   AR190587
VERSION     AR190587.1  GI:20236552
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 6075 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4854 CAAGACCTGAGTATTTT 4870
              |||| ||| ||||||||
Db          1 CAAGTCCTCAGTATTTT 17


RESULT 582
AR196417/c
LOCUS       AR196417                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 882 from patent US 6350934.
ACCESSION   AR196417
VERSION     AR196417.1  GI:20245854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 882 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAA 3982
              ||| | ||||||||||
Db         17 ATACAAAATAAAAACAA 1


RESULT 583
AR286352
LOCUS       AR286352                17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 724 from patent US 6528640.
ACCESSION   AR286352
VERSION     AR286352.1  GI:29723948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 724 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2016 CTGCGGTGTTTGGCAAT 2032
              |||||||| |||||| |
Db          1 CTGCGGTGGTTGGCATT 17


RESULT 584
AR323165
LOCUS       AR323165                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 567 from patent US 6566127.
ACCESSION   AR323165
VERSION     AR323165.1  GI:33708973
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 567 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4545 TGGAAAATTTTCTCCTT 4561
              ||| |||| ||||||||
Db          1 TGGGAAATCTTCTCCTT 17


RESULT 585
AR323677/c
LOCUS       AR323677                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1079 from patent US 6566127.
ACCESSION   AR323677
VERSION     AR323677.1  GI:33709485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
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          related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1079 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAA 3616
              | ||||||||||| ||||
Db         17 TTTGGAAAAAAAAAAAA 1


RESULT 586
AR324346
LOCUS       AR324346                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1748 from patent US 6566127.
ACCESSION   AR324346
VERSION     AR324346.1  GI:33710154
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1748 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAA 5203
              ||||||| |||||| ||
Db          1 AATAAAATTGAAGTTAA 17


RESULT 587
AR325510
LOCUS       AR325510                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2912 from patent US 6566127.
ACCESSION   AR325510
VERSION     AR325510.1  GI:33711318
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 2912 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4854 CAAGACCTGAGTATTTT 4870
              |||| ||| ||||||||
Db          1 CAAGTCCTCAGTATTTT 17


RESULT 588
AR398342
LOCUS       AR398342                  17 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 723 from patent US 6617438.
ACCESSION   AR398342
VERSION     AR398342.1  GI:40136077
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 723 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2016 CTGCGGTGTTTGGCAAT 2032
              |||||||| |||||| |
Db          1 CTGCGGTGGTTGGCATT 17


RESULT 589
AR402473
LOCUS       AR402473                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 813 from patent US 6623962.
ACCESSION   AR402473
VERSION     AR402473.1  GI:40149923
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and McSwiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: US 6623962-A 813 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4481 GAATGTATTTGATTTAT 4497
              ||| |||||||||||| |
Db          1 GAAAGTATTTGATTTTT 17


RESULT 590
AR433770/c
LOCUS       AR433770                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 193 from patent US 6656700.
ACCESSION   AR433770
VERSION     AR433770.1  GI:40196613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 193 02-DEC-2003;
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1448 TTTAAAATTCAAAAGTA 1464
              ||||||||  ||||| ||
Db         17 TTTAAAATGCAAAAATA 1


RESULT 591
AR433771/c
LOCUS       AR433771                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 194 from patent US 6656700.
ACCESSION   AR433771
VERSION     AR433771.1  GI:40196614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 194 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1447 TTTTAAAATTCAAAAGT 1463
              |||||||||  ||||| |
Db         17 TTTTAAAATGCAAAAAT 1


RESULT 592
AR433773/c
LOCUS       AR433773                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 196 from patent US 6656700.
ACCESSION   AR433773
VERSION     AR433773.1  GI:40196616
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 196 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1445 TCTTTTAAAATTCAAAA 1461
              | |||||||||  |||||
Db         17 TATTTTAAAATGCAAAA 1


RESULT 593
AR433774/c
LOCUS       AR433774                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 197 from patent US 6656700.
ACCESSION   AR433774
VERSION     AR433774.1  GI:40196617
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 197 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1444 TTCTTTTAAAATTCAAA 1460
              || |||||||||  ||||
Db         17 TTATTTTAAAATGCAAA 1


RESULT 594
AR434323
LOCUS       AR434323                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 746 from patent US 6656700.
ACCESSION   AR434323
VERSION     AR434323.1  GI:40197166
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 746 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3058 CTAGCTGCCACTTTCAC 3074
              |||||||||  |||||  |
Db          1 CTAGCTGCCTCTTTCTC 17


RESULT 595
AR434324
LOCUS       AR434324                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 747 from patent US 6656700.
ACCESSION   AR434324
VERSION     AR434324.1  GI:40197167
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 747 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.3%;  Score 13.8;  DB 1;  Length 17;
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  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3059 TAGCTGCCACTTTCACG 3075
              ||||||||  |||||  ||
Db          1 TAGCTGCCTCTTTCTCG 17


RESULT 596
AR434325
LOCUS       AR434325                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 748 from patent US 6656700.
ACCESSION   AR434325
VERSION     AR434325.1  GI:40197168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 748 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3060 AGCTGCCACTTTCACGT 3076
              |||||||  |||||  |||
Db          1 AGCTGCCTCTTTCTCGT 17


RESULT 597
AR434330
LOCUS       AR434330                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 753 from patent US 6656700.
ACCESSION   AR434330
VERSION     AR434330.1  GI:40197173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 753 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2268 CCTCTTTCTGCTCTGCC 2284
              |||||||||  ||||||
Db          1 CCTCTTTCTCGTCTGCC 17


RESULT 598
AR456396/c
LOCUS       AR456396                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 73 from patent US 6686188.
ACCESSION   AR456396
VERSION     AR456396.1  GI:42691453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 73 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2521 GCTGGACATGAGATGGA 2537
              || | ||||||||||||
Db         17 GCAGCACATGAGATGGA 1


RESULT 599
AR457097
LOCUS       AR457097                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 774 from patent US 6686188.
ACCESSION   AR457097
VERSION     AR457097.1  GI:42692154
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 774 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1588 TGCCTCCCAGGCAAGCA 1604
              ||  |||||||||  ||||
Db          1 TGGCTCCCAGGCCAGCA 17


RESULT 600
AR457332/c
LOCUS       AR457332                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1009 from patent US 6686188.
ACCESSION   AR457332
VERSION     AR457332.1  GI:42692389
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 1009 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
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  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2923 TTTTCTTCTTTCCCTGG 2939
              || ||| ||||||||||
Db         17 TTCTCTGCTTTCCCTGG 1


RESULT 601
AR464257/c
LOCUS       AR464257                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 7934 from patent US 6686188.
ACCESSION   AR464257
VERSION     AR464257.1  GI:42699314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 7934 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1627 TCCAGCTTCCAAAGCCT 1643
              |||| |||||| |||||
Db         17 TCCAACTTCCAGAGCCT 1


RESULT 602
AR482723
LOCUS       AR482723                  17 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 169 from patent US 6703228.
ACCESSION   AR482723
VERSION     AR482723.1  GI:47245246
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Landers,J., Jordan,B., Housman,D.E. and Charest,A.
  TITLE     Methods and products related to genotyping and DNA analysis
  JOURNAL   Patent: US 6703228-A 169 09-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGGTT 4520
              |||||| ||||||| ||
Db          1 TTTTTTATTTTTGGATT 17


RESULT 603
AX060746
LOCUS       AX060746                  17 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 34 from Patent WO0078972.
ACCESSION   AX060746
VERSION     AX060746.1  GI:12406133
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lawn,R.M., Wade,D. and Garvin,M.
  TITLE     Regulation with binding cassette transporter protein abc1
  JOURNAL   Patent: WO 0078972-A 34 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="ABC1 sequencing primer"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1623 AGTGTCCAGCTTCCAAA 1639
              ||||||||| || |||
Db          1 AGTGTCCAGCATCTAAA 17


RESULT 604
AX060925
LOCUS       AX060925                  17 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 34 from Patent WO0078971.
ACCESSION   AX060925
VERSION     AX060925.1  GI:12406300
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1                                 .
  AUTHORS   Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
  TITLE     Atp binding cassette transporter protein abc1 polypeptides
  JOURNAL   Patent: WO 0078971-A 34 28-DEC-2000;
            CV THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="ABC1 sequencing primer"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1623 AGTGTCCAGCTTCCAAA 1639
              ||||||||| || |||
Db          1 AGTGTCCAGCATCTAAA 17


RESULT 605
AX146685
LOCUS       AX146685                  17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 27 from Patent WO0134834.
ACCESSION   AX146685
VERSION     AX146685.1  GI:14285078
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 27 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| |||||||||||  |
Db          1 AAGCTTTTTTTTTTCT 17


RESULT 606
AX214618
LOCUS       AX214618                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 60 from Patent WO0159103.
ACCESSION   AX214618
VERSION     AX214618.1  GI:15524661
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 60 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4276 TGTTGCATATGAGCCTG 4292
              || ||||| ||||||||
Db          1 TGCTGCATCTGAGCCTG 17


RESULT 607
AX214795/c
LOCUS       AX214795                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 237 from Patent WO0159103.
ACCESSION   AX214795
VERSION     AX214795.1  GI:15524838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 237 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTT 2140
              ||||||| | |||||||
Db         17 TTTTCTTCTATTTTTTT 1


RESULT 608
AX215330/c
LOCUS       AX215330                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 772 from Patent WO0159103.
ACCESSION   AX215330
VERSION     AX215330.1  GI:15525373
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 772 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4462 TGGAGGGTGGAAATAAT 4478
              ||||||||||| || ||
Db         17 TGGAGGGTGGAGATGAT 1


RESULT 609
AX217114/c
LOCUS       AX217114                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2556 from Patent WO0159103.
ACCESSION   AX217114
VERSION     AX217114.1  GI:15527175
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2556 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2133 CTTTTTTTCTTTAATAA 2149
              |||| |||||||||| |
Db         17 CTTTGTTTCTTTAATTA 1


RESULT 610
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AX217452
LOCUS       AX217452                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2894 from Patent WO0159103.
ACCESSION   AX217452
VERSION     AX217452.1  GI:15527513
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2894 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1332 GTTTCCTTTTTCAAAAA 1348
              ||||||||||| ||| |
Db          1 GTTTCCTTTTTTAAACA 17


RESULT 611
AX217625/c
LOCUS       AX217625                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 3067 from Patent WO0159103.
ACCESSION   AX217625
VERSION     AX217625.1  GI:15527686
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3067 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1249 AGTCTCCAAGGCCGCCA 1265
              |||||||||||| | |
Db         17 AGTCTCCAAGGCCTCAA 1


RESULT 612
AX217981/c
LOCUS       AX217981                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 3423 from Patent WO0159103.
ACCESSION   AX217981
VERSION     AX217981.1  GI:15528042
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3423 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4473 AATAATTTGAATGTATT 4489
              |||||||| ||||| ||
Db         17 AATAATTTCAATGTCTT 1


RESULT 613
AX218200/c
LOCUS       AX218200                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 3642 from Patent WO0159103.
ACCESSION   AX218200
VERSION     AX218200.1  GI:15528261
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3642 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||| || |||||||||
Db         17 AGTTGTTATTTTTTTTT 1


RESULT 614
AX226806/c
LOCUS       AX226806                  17 bp    RNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 178 from Patent WO0157206.
ACCESSION   AX226806
VERSION     AX226806.1  GI:15555947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 178 09-AUG-2001;
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          RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4075 CAATGTATGTGTGGCTG 4091
              ||||||||| | |||||
Db         17 CAATGTATGAGGGGCTG 1


RESULT 615
AX227120
LOCUS       AX227120                  17 bp    RNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 492 from Patent WO0157206.
ACCESSION   AX227120
VERSION     AX227120.1  GI:15556261
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 492 09-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2336 TTCCAAACATCCAAAAA 2352
              ||||| ||||| |||||
Db          1 TTCCAGACATCAAAAAA 17


RESULT 616
AX262940/c
LOCUS       AX262940                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 331 from Patent WO0173002.
ACCESSION   AX262940
VERSION     AX262940.1  GI:16511739
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 331 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2930 CTTTCCCTGGACAGGCA 2946
              || |||| |||||||||
Db         17 CTCTCCCAGGACAGGCA 1


RESULT 617
AX262941
LOCUS       AX262941                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 332 from Patent WO0173002.
ACCESSION   AX262941
VERSION     AX262941.1  GI:16511740
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 332 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2930 CTTTCCCTGGACAGGCA 2946
              || |||| |||||||||
Db          1 CTCTCCCAGGACAGGCA 17


RESULT 618
AX272510
LOCUS       AX272510                  17 bp    RNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 79 from Patent WO0162911.
ACCESSION   AX272510
VERSION     AX272510.1  GI:16545247
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 79 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2726 GAAGGCTTCTCTCCACA 2742
              |||||| |||||| |||
Db          1 GAAGGCCTCTCTCGACA 17


RESULT 619
AX422191
LOCUS       AX422191                  17 bp    RNA     linear   PAT 18-JUN-2002
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DEFINITION  Sequence 527 from Patent WO0188124.
ACCESSION   AX422191
VERSION     AX422191.1  GI:21525573
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 527 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3411 GGAAGAAGCAAGGGCAA 3427
              || |||| |||||||||
Db          1 GGCAGAACCAAGGGCAA 17


RESULT 620
AX422333/c
LOCUS       AX422333                 17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 669 from Patent WO0188124.
ACCESSION   AX422333
VERSION     AX422333.1  GI:21525715
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 669 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1104 TTGGAGCTGTGGGTGAG 1120
              ||| ||||| |||||||
Db         17 TTGTAGCTGGGGGTGAG 1


RESULT 621
AX423696
LOCUS       AX423696                 17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 2032 from Patent WO0188124.
ACCESSION   AX423696
VERSION     AX423696.1  GI:21527078
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 2032 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3381 TGTAGAAGTAGGAGGAA 3397
              || ||||| ||||||||
Db          1 TGAAGAAGGAGGAGGAA 17


RESULT 622
AX475032/c
LOCUS       AX475032                 17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 253 from Patent WO0224750.
ACCESSION   AX475032
VERSION     AX475032.1  GI:22214317
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 253 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4595 GTGTAGCTCAAATAGGT 4611
              ||| |||||||||| ||
Db         17 GTGCAGCTCAAATACGT 1


RESULT 623
AX499406
LOCUS       AX499406                 17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 713 from Patent EP1229046.
ACCESSION   AX499406
VERSION     AX499406.1  GI:23381699
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 713 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2500 GATGCCAATTTCCTCTC 2516
              || ||||||||| ||||
Db          1 GAAGCCAATTTCGTCTC 17


RESULT 624
AX499603
LOCUS       AX499603                 17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 910 from Patent EP1229046.
ACCESSION   AX499603
VERSION     AX499603.1  GI:23381896
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 910 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1015 CACCTGGCTGGTGAACA 1031
              | ||||||| ||||||||
Db          1 CGCCTGGCAGGTGAACA 17


RESULT 625
AX500501/c
LOCUS       AX500501                 17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1808 from Patent EP1229046.
ACCESSION   AX500501
VERSION     AX500501.1  GI:23382794
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1808 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3286 TCTGGGTCAGAACCAGA 3302
              |||||| |||||||| |
Db         17 TCTGGGACAGAACCAAA 1


RESULT 626
AX527156
LOCUS       AX527156                 17 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 186 from Patent WO0226818.
ACCESSION   AX527156
VERSION     AX527156.1  GI:25171771
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Corrigan,A.
  TITLE     Human nedd-1
  JOURNAL   Patent: WO 0226818-A 186 04-APR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2292 GGATATTGGTTCTTCCC 2308
              || |||||| |||||||
Db          1 GGCTATTGGATCTTCCC 17


RESULT 627
AX531623/c
LOCUS       AX531623                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1132 from Patent EP1239051.
ACCESSION   AX531623
VERSION     AX531623.1  GI:25255035
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1132 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2989 CAGGCAGCTCCCTCCTG 3005
              |||||| || |||||||
Db         17 CAGGCACCTTCCTCCTG 1


RESULT 628
AX531624/c
LOCUS       AX531624                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1133 from Patent EP1239051.
ACCESSION   AX531624
VERSION     AX531624.1  GI:25255036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
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  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1133 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2988 CCAGGCAGCTCCCTCCT 3004
              ||||||| || ||||||
Db         17 CCAGGCACCTTCCTCCT 1


RESULT 629
AX531875
LOCUS       AX531875                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1384 from Patent EP1239051.
ACCESSION   AX531875
VERSION     AX531875.1  GI:25255523
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1384 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3152 CTCCCAGAAACATCTCT 3168
              ||||||| |||| ||||
Db          1 CTCCCAGCAACACCTCT 17


RESULT 630
AX615502/c
LOCUS       AX615502                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 309 from Patent EP1262488.
ACCESSION   AX615502
VERSION     AX615502.1  GI:28446548
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 309 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1974 ATAGCATGCTTCCTTTC 1990
              ||||| |||||| ||||
Db         17 ATAGCCTGCTTCTTTTC 1


RESULT 631
AX615503/c
LOCUS       AX615503                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 310 from Patent EP1262488.
ACCESSION   AX615503
VERSION     AX615503.1  GI:28446549
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 310 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 CATAGCATGCTTCCTTT 1989
              ||||||| ||||||| |||
Db         17 CATAGCCTGCTTCTTTT 1


RESULT 632
AX648698
LOCUS       AX648698                 17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 538 from Patent EP1273660.
ACCESSION   AX648698
VERSION     AX648698.1  GI:29151516
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 538 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2071 TAAAGAAAAGACATTTT 2087
              ||||||| ||||| |||
Db          1 TAAAGAAGAGACACTTT 17


RESULT 633
AX674470
LOCUS       AX674470                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2915 from Patent WO03004526.
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ACCESSION   AX674470
VERSION     AX674470.1  GI:29332818
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2915 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4022 GATCTGTACCATGACCC 4038
              ||||||||| || ||||
Db          1 GATCTGTACAATAACCC 17


RESULT 634
AX687430/c
LOCUS       AX687430                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 162 from Patent EP1281758.
ACCESSION   AX687430
VERSION     AX687430.1  GI:29410124
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 162 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              ||||||||| | |||||
Db         17 TGCTGCTGAGGAGCTTC 1


RESULT 635
AX687451
LOCUS       AX687451                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 183 from Patent EP1281758.
ACCESSION   AX687451
VERSION     AX687451.1  GI:29410145
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 183 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        939 GGTATTTCTGGGGTGAA 955
              |||||| ||| ||||||
Db          1 GGTATTCCTGTGGTGAA 17


RESULT 636
AX687452
LOCUS       AX687452                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 184 from Patent EP1281758.
ACCESSION   AX687452
VERSION     AX687452.1  GI:29410146
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 184 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        940 GTATTTCTGGGGTGAAA 956
              ||||| ||| |||||||
Db          1 GTATTCCTGTGGTGAAA 17


RESULT 637
AX687453
LOCUS       AX687453                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 185 from Patent EP1281758.
ACCESSION   AX687453
VERSION     AX687453.1  GI:29410147
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 185 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        941 TATTTCTGGGGTGAAAC 957
              |||| ||| ||||||||
Db          1 TATTCCTGTGGTGAAAC 17


RESULT 638
AX687454
LOCUS       AX687454                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 186 from Patent EP1281758.
ACCESSION   AX687454
VERSION     AX687454.1  GI:29410148
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 186 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        942 ATTTCTGGGGTGAAACT 958
              ||| ||| |||||||||
Db          1 ATTCCTGTGGTGAAACT 17


RESULT 639
AX688161
LOCUS       AX688161                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 893 from Patent EP1281758.
ACCESSION   AX688161
VERSION     AX688161.1  GI:29410861
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 893 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4216 CTGCTTTGGGGGGTGTG 4232
              |||||||||||  || ||
Db          1 CTGCTTTGGGGAGTATG 17


RESULT 640
AX690617
LOCUS       AX690617                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3349 from Patent EP1281758.
ACCESSION   AX690617
VERSION     AX690617.1  GI:29413498
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3349 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3493 TGGCTGAGACCTGGGAT 3509
              |||||||||||  | |||
Db          1 TGGCTGAGACCAGAGAT 17


RESULT 641
AX691268
LOCUS       AX691268                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 4000 from Patent EP1281758.
ACCESSION   AX691268
VERSION     AX691268.1  GI:29414204
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 4000 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3402 TTCTCACTGGGAAGAAG 3418
              ||| ||||||| |||||
Db          1 TTCACACTGGGGAGAAG 17


RESULT 642
AX691269
LOCUS       AX691269                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 4001 from Patent EP1281758.
ACCESSION   AX691269
VERSION     AX691269.1  GI:29414205
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 4001 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3403 TCTCACTGGGAAGAAGC 3419
              || ||||||| ||||||
Db          1 TCACACTGGGGAGAAGC 17


RESULT 643
AX692030
LOCUS       AX692030                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 4762 from Patent EP1281758.
ACCESSION   AX692030
VERSION     AX692030.1  GI:29414974
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 4762 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1982 CTTCCTTTCTCTCCTGG 1998
              ||||||| ||||||||
Db          1 CTTCCTTCTTCTCCTGG 17


RESULT 644
AX692031
LOCUS       AX692031                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 4763 from Patent EP1281758.
ACCESSION   AX692031
VERSION     AX692031.1  GI:29414975
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 4763 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1983 TTCCTTTCTCTCCTGGC 1999
              ||||||  |||||||||
Db          1 TTCCTTCTTCTCCTGGC 17


RESULT 645
AX692522
LOCUS       AX692522                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5254 from Patent EP1281758.
ACCESSION   AX692522
VERSION     AX692522.1  GI:29415480
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5254 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4515
              | | ||||||||||||||
Db          1 ATTCTTTTTTTTTTTT 17


RESULT 646
AX692522/c
LOCUS       AX692522                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5254 from Patent EP1281758.
ACCESSION   AX692522
VERSION     AX692522.1  GI:29415480
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5254 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGAAT 3623
              ||||| ||||| |||||
Db         17 AAAAAAAAAAAAAGAAT 1


RESULT 647
AX701168/c
LOCUS       AX701168                  17 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 4 from Patent WO03012097.
ACCESSION   AX701168
VERSION     AX701168.1  GI:29536938
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Price,G.B. and Zannis-Hadjopoulos,M.
  TITLE     Methods of inhibiting dna replication
  JOURNAL   Patent: WO 03012097-A 4 13-FEB-2003;
            Price, Gerald B. (CA) ; Zannis-Hadjopoulos, Maria (CA)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Mammalian cruciform oligonucleotide"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1373 CTGTTTATTAACTACTG 1389
              | ||| ||||||||||||
Db         17 CAGTTGATTAACTACTG 1


RESULT 648
AX727049/c
LOCUS       AX727049                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4736 from Patent WO03025176.
ACCESSION   AX727049
VERSION     AX727049.1  GI:30506392
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 4736 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3840 CTCAGTAGAAAAGGATC 3856
              || |||||||||| ||||
Db         17 CTTAGTAGAAAATGATC 1


RESULT 649
AX727491/c
LOCUS       AX727491                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5178 from Patent WO03025176.
ACCESSION   AX727491
VERSION     AX727491.1  GI:30506834
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5178 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3852 GGATCTAAGGGAAGATC 3868
              ||| | ||||||||||||
Db         17 GGAGCGAAGGGAAGATC 1


RESULT 650
AX728214
LOCUS       AX728214                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5901 from Patent WO03025176.
ACCESSION   AX728214
VERSION     AX728214.1  GI:30507557
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5901 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGCA 3671
              | |||||||||||||| |
Db         1 GATCAGTCATCAAAGAA 17


RESULT 651
AX728587
LOCUS       AX728587                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 221 from Patent WO03025175.
ACCESSION   AX728587
VERSION     AX728587.1  GI:30507930
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 221 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5067 GATTTTTTCCCTTTTTA 5083
              ||| | ||||||||||||
Db          1 GATCTCTTCCCTTTTTA 17


RESULT 652
AX729740/c
LOCUS       AX729740                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1374 from Patent WO03025175.
ACCESSION   AX729740
VERSION     AX729740.1  GI:30509083
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1374 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3929 TAATTCCACAGGTCATC 3945
              | ||||||||||| |||
Db         17 TCATTCCACAGGTGATC 1


RESULT 653
AX731343
LOCUS       AX731343                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2977 from Patent WO03025175.
ACCESSION   AX731343
VERSION     AX731343.1  GI:30510686
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 2977 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGGA 4848
              ||||||| ||| |||||
Db          1 GATCCTTGAGCCCAGGA 17


RESULT 654
AX732838/c
LOCUS       AX732838                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4472 from Patent WO03025175.
ACCESSION   AX732838
VERSION     AX732838.1  GI:30512181
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4472 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3802 CCTGGACTAAAGGCATC 3818
              |||||||| |||| |||
Db         17 CCTGGACTCAAGGGATC 1


RESULT 655
AX734075
LOCUS       AX734075                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5709 from Patent WO03025175.
ACCESSION   AX734075
VERSION     AX734075.1  GI:30513418
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5709 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4600 GCTCAAATAGGTCATCA 4616
              | |||||||| ||||||
Db          1 GATCAAATAGTTCATCA 17


RESULT 656
AX734450
LOCUS       AX734450                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 40 from Patent WO03025177.
ACCESSION   AX734450
VERSION     AX734450.1  GI:30513727
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 40 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4017 GATCTGATCTGTACCAT 4033
              |||||||| | ||||||
Db          1 GATCTGATTTATACCAT 17


RESULT 657
AX735055/c
LOCUS       AX735055                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 645 from Patent WO03025177.
ACCESSION   AX735055
VERSION     AX735055.1  GI:30514332
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 645 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2982 TGCTGTCCAGGCAGCTC 2998
              |||||||||||| | ||
Db          1 TGCTGTCCAGGCTGATC 17


RESULT 658
AX735079
LOCUS       AX735079                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 669 from Patent WO03025177.
ACCESSION   AX735079
VERSION     AX735079.1  GI:30514356
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 669 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4704 GACCCTGGGCAAGTCAC 4720
              || | |||||||||||||
Db          1 GATCATGGGCAAGTCAC 17


RESULT 659
AX735164
LOCUS       AX735164                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 754 from Patent WO03025177.
ACCESSION   AX735164
VERSION     AX735164.1  GI:30514441
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 754 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGGA 4848
              ||||||| ||| |||||
Db          1 GATCCTTGAGCCCAGGA 17


RESULT 660
AX737844
LOCUS       AX737844                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3434 from Patent WO03025177.
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ACCESSION   AX737844
VERSION     AX737844.1  GI:30517132
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3434 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3734 GAGCCCCAGTGCTGGAA 3750
              || |||||||||||| |
Db          1 GATCCCCAGTGCTGGCA 17


RESULT 661
AX738005
LOCUS       AX738005                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3595 from Patent WO03025177.
ACCESSION   AX738005
VERSION     AX738005.1  GI:30517293
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3595 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2381 GGTCAAAAATAAAATAT 2397
              | |||||||||||||| |
Db          1 GATCAAAAATAAAATGT 17


RESULT 662
AX757155/c
LOCUS       AX757155                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 476 from Patent WO03040369.
ACCESSION   AX757155
VERSION     AX757155.1  GI:32251771
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 476 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1985 CCTTTCTCTCCTGGCTC 2001
              |||| ||||||||| ||
Db         17 CCTTCCTCTCCTGGATC 1


RESULT 663
AX757231/c
LOCUS       AX757231                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 552 from Patent WO03040369.
ACCESSION   AX757231
VERSION     AX757231.1  GI:32251847
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 552 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2889 TTTTCTTTGACCAGATC 2905
              |||| || |||||||||
Db         17 TTTTTTTGGACCAGATC 1


RESULT 664
AX757248
LOCUS       AX757248                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 569 from Patent WO03040369.
ACCESSION   AX757248
VERSION     AX757248.1  GI:32251864
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 569 15-MAY-2003;
            Molecular Engines Laboratories (FR)
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1742 GATAAAACAGAATCTTC 1758
              ||| ||| |||||||||
Db          1 GATCAAAAAGAATCTTC 17


RESULT 665
AX758931/c
LOCUS       AX758931                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 2252 from Patent WO03040369.
ACCESSION   AX758931
VERSION     AX758931.1  GI:32253547
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 2252 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4170 AATGATAAACTCAGATC 4186
              |||| |||| |||||||
Db         17 AATGTTAAAATCAGATC 1


RESULT 666
AX760266
LOCUS       AX760266                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 3587 from Patent WO03040369.
ACCESSION   AX760266
VERSION     AX760266.1  GI:32254882
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 3587 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4600 GCTCAAATAGGTCATCA 4616
              | |||||||| ||||||
Db          1 GATCAAATAGTTCATCA 17


RESULT 667
AX760827/c
LOCUS       AX760827                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 4148 from Patent WO03040369.
ACCESSION   AX760827
VERSION     AX760827.1  GI:32255443
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 4148 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3802 CCTGGACTAAAGGCATC 3818
              |||||||| |||| |||
Db         17 CCTGGACTCAAGGGATC 1


RESULT 668
AX760846
LOCUS       AX760846                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 4167 from Patent WO03040369.
ACCESSION   AX760846
VERSION     AX760846.1  GI:32255462
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 4167 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        993 GATATGCTGTGGTGCTT 1009
              ||| | ||||||||||
Db          1 GATCTTCTGTGGTGCTT 17
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RESULT 669
AX761467
LOCUS       AX761467                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 4788 from Patent WO03040369.
ACCESSION   AX761467
VERSION     AX761467.1  GI:32256083
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 4788 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3129 GCTCAAGACAAGGCTGG 3145
              | |||||||||| ||||
Db          1 GATCAAGACAAGCCTGG 17


RESULT 670
BD065825
LOCUS       BD065825                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065825
VERSION     BD065825.1  GI:22611428
KEYWORDS    JP 2001511000-A/460.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 460 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/460
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3599 GTCTGGAAAAAAACAAA 3615
              ||||  ||||||||||
Db          1 GTCTTTAAAAAAACAAA 17


RESULT 671
BD067973
LOCUS       BD067973                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067973
VERSION     BD067973.1  GI:22613576
KEYWORDS    JP 2001511003-A/813.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 813 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/813
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                  related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4481 GAATGTATTTGATTTAT 4497
              ||| |||||||||||  |
Db          1 GAAAGTATTTGATTTTT 17


RESULT 672
E32461/c
LOCUS       E32461                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32461
VERSION     E32461.1  GI:13018697
KEYWORDS    JP 2000037190-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 21 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/21
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
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            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         18 GGAAAAAAAAAAAAAAA 2


RESULT 673
BD145037/c
LOCUS       BD145037                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145037
VERSION     BD145037.1  GI:27850795
KEYWORDS    JP 2002119291-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 18 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/18
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 674
BD166037/c
LOCUS       BD166037                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166037
VERSION     BD166037.1  GI:27871849
KEYWORDS    JP 2002191372-A/17.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 17 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/17
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC          nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 675
AR264933/c
LOCUS       AR264933                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6492121.
ACCESSION   AR264933
VERSION     AR264933.1  GI:29693320
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
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          analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 17 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 676
AR478214/c
LOCUS       AR478214                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 17 from patent US 6699661.
ACCESSION   AR478214
VERSION     AR478214.1  GI:47236862
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 17 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 677
BD072878/c
LOCUS       BD072878                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072878
VERSION     BD072878.1  GI:22618481
KEYWORDS    JP 2001286300-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 16 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/16
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 678
BD107505/c
LOCUS       BD107505                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107505
VERSION     BD107505.1  GI:23202323
KEYWORDS    JP 2002000275-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 14 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/14
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
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  Best Local Similarity   88.2%;  Pred. No. 4.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 679
BD143136/c
LOCUS       BD143136                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel testis-specific gene.
ACCESSION   BD143136
VERSION     BD143136.1  GI:27848894
KEYWORDS    JP 2002112777-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Novel testis-specific gene
  JOURNAL   Patent: JP 2002112777-A 3 16-APR-2002;
            KACHIKU KAIRYO JIGYODAN,PRESIDENT OF GUNMA UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002112777-A/3
            PD   16-APR-2002
            PF   03-OCT-2000 JP 2000303994
            PI   AKIRA AIZAWA,AKIKO KAWAKAMI,TOSHIHIKO KONDO
            PC   C12N15/09,C07K14/47,C12N15/00
            CC   Novel testis-specific gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 5.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAG 3620
              |||||||| ||||| ||
Db         20 GAAAAAAAAAAAAAAAG 4


RESULT 680
AR309844/c
LOCUS       AR309844                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4 from patent US 6555670.
ACCESSION   AR309844
VERSION     AR309844.1  GI:31701953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: US 6555670-A 4 29-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 5.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAG 3620
              |||||||| ||||| ||
Db         20 GAAAAAAAAAAAAAAAG 4


RESULT 681
AX404077/c
LOCUS       AX404077                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 4 from Patent EP1195382.
ACCESSION   AX404077
VERSION     AX404077.1  GI:21437393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: EP 1195382-A 4 10-APR-2002;
            Livestock Improvement Association of Japan, Inc. (JP) ; President
            of Gunma University (JP)
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 5.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAG 3620
              |||||||| ||||| ||
Db         20 GAAAAAAAAAAAAAAAG 4


RESULT 682
AR373540
LOCUS       AR373540                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 110 from patent US 6602713.
ACCESSION   AR373540
VERSION     AR373540.1  GI:40075669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 110 05-AUG-2003;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 5.6e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATACATT 2414
              |||||||  |||||||  ||
Db          1 TATATATGTATATATATTTT 20


RESULT 683
AR142677
LOCUS       AR142677                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6203988.
ACCESSION   AR142677
VERSION     AR142677.1  GI:15103963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 7 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 5.6e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAACA 3619
              |||  ||||||| ||||| |
Db          1 TCTCCAAAAAAAAAAAAAAA 20


RESULT 684
E28096
LOCUS       E28096                   20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28096
VERSION     E28096.1  GI:13018321
KEYWORDS    JP 1999196874-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 7 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/7
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 5.6e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAACA 3619
              |||  ||||||| ||||| |
Db          1 TCTCCAAAAAAAAAAAAAAA 20


RESULT 685
AX067205/c
LOCUS       AX067205                 20 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 57 from Patent WO0100669.
ACCESSION   AX067205
VERSION     AX067205.1  GI:12544870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Barry,C., Bougueleret,L., Chumakov,I. and Cohen-Akenine,A.
  TITLE     A bap28 gene and protein
  JOURNAL   Patent: WO 0100669-A 57 04-JAN-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide BAP28polyTcourt"

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 5.6e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAAACAA 3982
              |||| ||| || ||||| ||
Db         20 TATACAAAAAAAAAAAAAAA 1


RESULT 686
AR046269
LOCUS       AR046269                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1062 from patent US 5817796.
ACCESSION   AR046269
VERSION     AR046269.1  GI:5967734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 1062 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 5.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2400 ATACATATATACATT 2414
              ||| ||||||||||
Db          1 ATATATATATACATT 15


RESULT 687
I53321
LOCUS       I53321                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1062 from patent US 5646042.
ACCESSION   I53321
VERSION     I53321.1  GI:2474524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1062 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 5.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2400 ATACATATATACATT 2414
              ||| ||||||||||
Db          1 ATATATATATACATT 15
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RESULT 688
I73187/c
LOCUS       I73187                  18 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686242.
ACCESSION   I73187
VERSION     I73187.1  GI:3009326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bruice,T.W. and Lima,W.F.
  TITLE     Determination of oligonucleotides for therapeutics, diagnostics and
            research reagents
  JOURNAL   Patent: US 5686242-A 1 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         18 AAAAAAAAAAAAACA 4


RESULT 689
AR528447/c
LOCUS       AR528447                19 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 85 from patent US 6723897.
ACCESSION   AR528447
VERSION     AR528447.1  GI:53916512
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Brown,S.M., Elich,T.D., Heck,G.R., Kishore,G.M., Logusch,E.W.,
            Logusch,S.J., Piller,K.J., Rao,S., Ream,J.E. and Baerson,S.R.
  TITLE     Methods for controlling gibberellin levels
  JOURNAL   Patent: US 6723897-A 85 20-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 690
E32450/c
LOCUS       E32450                  18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32450
VERSION     E32450.1  GI:13018686
KEYWORDS    JP 2000037190-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 10 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/10
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAAC 3618
              ||  ||||||| ||||||
Db         18 CTAAAAAAAAAAAAAAAC 1


RESULT 691
E32453/c
LOCUS       E32453                  18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32453
VERSION     E32453.1  GI:13018689
KEYWORDS    JP 2000037190-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 13 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/13
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAAC 3983
              ||||| || ||||| |||
Db         18 ATAAAAAAAAAAAAAAAC 1
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RESULT 692
AR034896/c
LOCUS       AR034896                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5869643.
ACCESSION   AR034896
VERSION     AR034896.1  GI:5950501
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 12 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 693
AR034899
LOCUS       AR034899                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 18 from patent US 5869643.
ACCESSION   AR034899
VERSION     AR034899.1  GI:5950504
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 18 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 694
AR058305
LOCUS       AR058305                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5837820.
ACCESSION   AR058305
VERSION     AR058305.1  GI:5983882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
  TITLE     Seed specific biotinylated protein, SBP65, from leguminous plants
  JOURNAL   Patent: US 5837820-A 3 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 695
AR097579/c
LOCUS       AR097579                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6071745.
ACCESSION   AR097579
VERSION     AR097579.1  GI:12806309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6071745-A 9 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 696
AR106506
LOCUS       AR106506                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 30 from patent US 6107060.
ACCESSION   AR106506
VERSION     AR106506.1  GI:12821036
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Keeling,P. and Guan,H.
  TITLE     Starch encapsulation
  JOURNAL   Patent: US 6107060-A 30 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 697
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BD190553
LOCUS       BD190553                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secretory proteins and polynucleotides encoding the same.
ACCESSION   BD190553
VERSION     BD190553.1  GI:33000292
KEYWORDS    JP 2002515753-A/12.
SOURCE      Rattus
  ORGANISM  Rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secretory proteins and polynucleotides encoding the same
  JOURNAL   Patent: JP 2002515753-A 12 28-MAY-2002;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2002515753-A/12
            PD   28-MAY-2002
            PF   31-OCT-1997 JP 1998521609
            PR   01-NOV-1996 US    08/724973
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Rattus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10114"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db          1 GAAAAAAAAAAAAAAAAA 18


RESULT 698
BD222596/c
LOCUS       BD222596                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222596
VERSION     BD222596.1  GI:33032366
KEYWORDS    JP 2002522447-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom
  JOURNAL   Patent: JP 2002522447-A 14 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522447-A/14
            PD   23-JUL-2002
            PF   09-AUG-1999 JP 2000563675
            PR   07-AUG-1998 US    09/130973
            PI   MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            PI   KAWASAKI
            PC   C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence: antisense sequence FH
            Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 699
E28535
LOCUS       E28535                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28535
VERSION     E28535.1  GI:13025387
KEYWORDS    JP 1999075880-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 2 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/2
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 700
E28536/c
LOCUS       E28536                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28536
VERSION     E28536.1  GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 3 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/3
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            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            PT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 701
I79509/c
LOCUS       I79509                  18 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 16 from patent US 5707807.
ACCESSION   I79509
VERSION     I79509.1  GI:3207799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 16 13-JAN-1998;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 702
AR208427/c
LOCUS       AR208427                18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 7 from patent US 6383754.
ACCESSION   AR208427
VERSION     AR208427.1  GI:21509578
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 7 07-MAY-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
              || ||||||| ||||| |
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 703
AR215435/c
LOCUS       AR215435                18 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 9 from patent US 6410321.
ACCESSION   AR215435
VERSION     AR215435.1  GI:23313691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6410321-A 9 25-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 704
AR222464
LOCUS       AR222464                18 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 24 from patent US 6429300.
ACCESSION   AR222464
VERSION     AR222464.1  GI:23329995
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 24 06-AUG-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 705
AR412363/c
LOCUS       AR412363                18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14 from patent US 6639062.
ACCESSION   AR412363
VERSION     AR412363.1  GI:40167473
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleosidic compounds and oligomeric compounds
            prepared therefrom
  JOURNAL   Patent: US 6639062-A 14 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 706
AR473365/c
LOCUS       AR473365                 18 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9 from patent US 6686460.
ACCESSION   AR473365
VERSION     AR473365.1  GI:42708816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6686460-A 9 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 707
AR487019
LOCUS       AR487019                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 6 from patent US 6706476.
ACCESSION   AR487019
VERSION     AR487019.1  GI:47251966
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Thirstrup,K., Warthoe,P. and Pettersson,N.B.
  TITLE     Process for amplifying and labeling single stranded cDNA by 5'
            ligated adaptor mediated amplification
  JOURNAL   Patent: US 6706476-A 6 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 708
AR487020/c
LOCUS       AR487020                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 7 from patent US 6706476.
ACCESSION   AR487020
VERSION     AR487020.1  GI:47251967
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Thirstrup,K., Warthoe,P. and Pettersson,N.B.
  TITLE     Process for amplifying and labeling single stranded cDNA by 5'
            ligated adaptor mediated amplification
  JOURNAL   Patent: US 6706476-A 7 16-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 709
AX004875/c
LOCUS       AX004875                 18 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 4 from Patent WO9910527.
ACCESSION   AX004875
VERSION     AX004875.1  GI:9928275
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 4 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl oligonucleotide"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 710
AX004879/c
LOCUS       AX004879                 18 bp    RNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 8 from Patent WO9910527.
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ACCESSION   AX004879
VERSION     AX004879.1  GI:9928279
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 8 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="2' methyl-modified oligonucleotide"
     modified_base   1. .18
                     /mod_base=um

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 711
AX008117
LOCUS       AX008117                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 2 from Patent WO9967378.
ACCESSION   AX008117
VERSION     AX008117.1  GI:9995742
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 2 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 712
AX008118/c
LOCUS       AX008118                 18 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 3 from Patent WO9967378.
ACCESSION   AX008118
VERSION     AX008118.1  GI:9995743
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 3 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 713
AX008122/c
LOCUS       AX008122                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 7 from Patent WO9967378.
ACCESSION   AX008122
VERSION     AX008122.1  GI:9995747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 7 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 714
AX008123
LOCUS       AX008123                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 8 from Patent WO9967378.
ACCESSION   AX008123
VERSION     AX008123.1  GI:9995748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
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AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 8 29-DEC-1999; DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)

FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 715
AX028844/c
LOCUS AX028844 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 28 from Patent WO9732023.
ACCESSION AX028844
VERSION AX028844.1 GI:10189947
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: WO 9732023-A 28 04-SEP-1997; FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGA 3621
|||||||| ||||| | |
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 716
AX047271
LOCUS AX047271 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M., Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000; Roche Diagnostics GmbH (DE)

FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 717
AX047273/c
LOCUS AX047273 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M., Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000; Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 718
AX085253/c
LOCUS AX085253 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 7 from Patent WO0112855.
ACCESSION AX085253
VERSION AX085253.1 GI:13275311
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001; YALE UNIVERSITY (US)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.3%; Score 13.2; DB 1; Length 18;

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  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
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Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 719
AX104721/c
LOCUS       AX104721                  18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 913 from Patent WO0122972.
ACCESSION   AX104721
VERSION     AX104721.1  GI:13920918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 913 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 720
AX104747/c
LOCUS       AX104747                  18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 939 from Patent WO0122972.
ACCESSION   AX104747
VERSION     AX104747.1  GI:13920944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 939 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 721
AX105651/c
LOCUS       AX105651                  18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123564.
ACCESSION   AX105651
VERSION     AX105651.1  GI:13921674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0123564-A 10 05-APR-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 722
AX108642/c
LOCUS       AX108642                  18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123419.
ACCESSION   AX108642
VERSION     AX108642.1  GI:13923875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Differentially expressed genes
  JOURNAL   Patent: WO 0123419-A 10 05-APR-2001;
            SCIOS INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 723
AX268883/c
LOCUS       AX268883                  18 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 84 from Patent WO0174901.
ACCESSION   AX268883
VERSION     AX268883.1  GI:16541910
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and White,R.T.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0174901-A 84 11-OCT-2001;
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            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligos corresponding to polylinker sequence."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 724
AX355809/c
LOCUS       AX355809                 18 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 837 from Patent WO0197843.
ACCESSION   AX355809
VERSION     AX355809.1  GI:18620477
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 837 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 725
AX547774/c
LOCUS       AX547774                 18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 913 from Patent WO02053141.
ACCESSION   AX547774
VERSION     AX547774.1  GI:25812918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 913 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 726
AX547800/c
LOCUS       AX547800                 18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 939 from Patent WO02053141.
ACCESSION   AX547800
VERSION     AX547800.1  GI:25812944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 939 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 727
AX814716/c
LOCUS       AX814716                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 1 from Patent WO03064441.
ACCESSION   AX814716
VERSION     AX814716.1  GI:39103916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 1 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 728
AX814723/c
LOCUS       AX814723                 18 bp    DNA     linear   PAT 05-DEC-2003
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DEFINITION  Sequence 8 from Patent WO03064441.
ACCESSION   AX814723
VERSION     AX814723.1  GI:39103922
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 8 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .17
                     /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                     2'-O-methyl-D-uridi ne"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 729
AX814724/c
LOCUS       AX814724                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 9 from Patent WO03064441.
ACCESSION   AX814724
VERSION     AX814724.1  GI:39103923
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 9 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .15
                     /note="Residues 1-3, 7-9, and 13-15 are
                     2'-O-methyl-D-uridine"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 730
AX814725/c
LOCUS       AX814725                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 10 from Patent WO03064441.
ACCESSION   AX814725
VERSION     AX814725.1  GI:39103924
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 10 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .18
                     /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 731
AX814736
LOCUS       AX814736                  18 bp    RNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 21 from Patent WO03064441.
ACCESSION   AX814736
VERSION     AX814736.1  GI:39103935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 21 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Target RNA oligonucleotide"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 732
BD085545/c
LOCUS       BD085545                  18 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085545
VERSION     BD085545.1  GI:22631155
KEYWORDS    JP 2001333800-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shimada,K.
  TITLE     Method of comparison and detection of RNA amount and DNA amount
  JOURNAL   Patent: JP 2001333800-A 2 04-DEC-2001;
            UNITECH CO LTD
COMMENT     OS   Homo sapiens (human)
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            PN   JP 2001333800-A/2
            PD   04-DEC-2001
            PF   30-MAY-2000 JP 2000160324
            PI   KAORI SHIMADA
            PC   C12Q1/68,C12N15/09,G01N33/50,C12N15/00
            CC   Method of comparison and detection of RNA amount and DNA  CC
                 amount
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 733
AX643396
LOCUS       AX643396                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 262 from Patent WO02099099.
ACCESSION   AX643396
VERSION     AX643396.1  GI:28551047
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 262 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 6.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATA 2408
              ||||| ||||||  ||||
Db          1 AAAATGTATATATGTATA 18


RESULT 734
AX643399/c
LOCUS       AX643399                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 265 from Patent WO02099099.
ACCESSION   AX643399
VERSION     AX643399.1  GI:28551051
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 265 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 6.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATA 2408
              ||||| ||||||  ||||
Db         19 AAAATGTATATATGTATA 2


RESULT 735
AR139960/c
LOCUS       AR139960                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207417.
ACCESSION   AR139960
VERSION     AR139960.1  GI:14482456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 736
AR140279/c
LOCUS       AR140279                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207454.
ACCESSION   AR140279
VERSION     AR140279.1  GI:14482775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 737
AR140557/c
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LOCUS       AR140557                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207802.
ACCESSION   AR140557
VERSION     AR140557.1  GI:14483053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 738
AR562156/c
LOCUS       AR562156                 20 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 32 from patent US 6759215.
ACCESSION   AR562156
VERSION     AR562156.1  GI:53976019
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method of preparing human stem cell factor polypeptide
  JOURNAL   Patent: US 6759215-A 32 06-JUL-2004;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 739
BD234126
LOCUS       BD234126                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION   BD234126
VERSION     BD234126.1  GI:33043896
KEYWORDS    JP 2002532072-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipovsek,D.
  TITLE     Protein skeleton of antibody mimetics and other binding proteins
  JOURNAL   Patent: JP 2002532072-A 14 02-OCT-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002532072-A/14
            PD   02-OCT-2002
            PF   09-DEC-1999 JP 2000587187
            PR   10-DEC-1998 US    60/111737
            PI   DASA LIPOVSEK
            PC   C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC
              C12P21/02,
            PC   C12N15/00
            CC   Puromycin linker oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 740
AX825124/c
LOCUS       AX825124                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 22 from Patent WO03072818.
ACCESSION   AX825124
VERSION     AX825124.1  GI:39750853
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 22 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
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Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 741
AX825126/c
LOCUS       AX825126                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 24 from Patent WO03072818.
ACCESSION   AX825126
VERSION     AX825126.1  GI:39750855
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 24 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
                ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 742
AX825123/c
LOCUS       AX825123                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 21 from Patent WO03072818.
ACCESSION   AX825123
VERSION     AX825123.1  GI:39750852
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 21 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
                ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 743
AX825125/c
LOCUS       AX825125                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 23 from Patent WO03072818.
ACCESSION   AX825125
VERSION     AX825125.1  GI:39750854
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 23 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 744
AX825156/c
LOCUS       AX825156                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 54 from Patent WO03072818.
ACCESSION   AX825156
VERSION     AX825156.1  GI:39750885
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 54 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 745
AX825134/c
LOCUS       AX825134                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 32 from Patent WO03072818.
ACCESSION   AX825134
VERSION     AX825134.1  GI:39750863
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 32 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 746
AR187066
LOCUS       AR187066                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2554 from patent US 6346398.
ACCESSION   AR187066
VERSION     AR187066.1  GI:20233031
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2554 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13
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RESULT 747
AR323676
LOCUS       AR323676                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1078 from patent US 6566127.
ACCESSION   AR323676
VERSION     AR323676.1  GI:33709484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1078 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 748
BD142809/c
LOCUS       BD142809                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142809
VERSION     BD142809.1  GI:23237754
KEYWORDS    WO 0224903-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 3 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/3
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 749
BD143835/c
LOCUS       BD143835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143835
VERSION     BD143835.1  GI:27849593
KEYWORDS    JP 2002095500-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 3 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/3
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 750
BD167836/c
LOCUS       BD167836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167836
VERSION     BD167836.1  GI:27873648
KEYWORDS    WO 0233122-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
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  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 3 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/3
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 751
BD167908/c
LOCUS       BD167908                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167908
VERSION     BD167908.1  GI:27873720
KEYWORDS    WO 0226962-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 7 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/7
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 752
BD168112/c
LOCUS       BD168112                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168112
VERSION     BD168112.1  GI:27873924
KEYWORDS    WO 0233069-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 19 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/19
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2
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RESULT 753
BD171178/c
LOCUS       BD171178                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171178
VERSION     BD171178.1  GI:27876990
KEYWORDS    WO 0250269-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 3 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/3
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15C', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 754
E34259/c
LOCUS       E34259                   17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34259
VERSION     E34259.1  GI:18624264
KEYWORDS    JP 2000106879-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 3 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/3
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 755
BD011731/c
LOCUS       BD011731                 17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011731
VERSION     BD011731.1  GI:22091920
KEYWORDS    WO 0065050-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 3 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/3
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2
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RESULT 756
BD091743/c
LOCUS       BD091743                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091743
VERSION     BD091743.1  GI:22637354
KEYWORDS    WO 0073435-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 757
BD091751/c
LOCUS       BD091751                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091751
VERSION     BD091751.1  GI:22637362
KEYWORDS    WO 0073439-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 758
BD091774/c
LOCUS       BD091774                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091774
VERSION     BD091774.1  GI:22637385
KEYWORDS    WO 0073440-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 759
BD097335/c
LOCUS       BD097335                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097335
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VERSION     BD097335.1  GI:22642909
KEYWORDS    WO 0165259-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 6 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/6
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 760
AR187061/c
LOCUS       AR187061                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2549 from patent US 6346398.
ACCESSION   AR187061
VERSION     AR187061.1  GI:20233026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         17 AAAAAAAAAAAAAAAG 2


RESULT 761
AR323671/c
LOCUS       AR323671                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1073 from patent US 6566127.
ACCESSION   AR323671
VERSION     AR323671.1  GI:33709479
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1073 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         17 AAAAAAAAAAAAAAAG 2


RESULT 762
AR187062/c
LOCUS       AR187062                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2550 from patent US 6346398.
ACCESSION   AR187062
VERSION     AR187062.1  GI:20233027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 763
AR187063/c
LOCUS       AR187063                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2551 from patent US 6346398.
ACCESSION   AR187063
VERSION     AR187063.1  GI:20233028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 764
AR323672/c
LOCUS       AR323672                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1074 from patent US 6566127.
ACCESSION   AR323672
VERSION     AR323672.1  GI:33709480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 765
AR323673/c
LOCUS       AR323673                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1075 from patent US 6566127.
ACCESSION   AR323673
VERSION     AR323673.1  GI:33709481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 766
AX361606/c
LOCUS       AX361606                  17 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 24 from Patent WO0208461.
ACCESSION   AX361606
VERSION     AX361606.1  GI:18694225
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 24 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Double-stranded product DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 767
AX692525/c
LOCUS       AX692525                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5257 from Patent EP1281758.
ACCESSION   AX692525
VERSION     AX692525.1  GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 768
AX814938/c
LOCUS       AX814938                  17 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 24 from Patent WO03064691.
ACCESSION   AX814938
VERSION     AX814938.1  GI:39104076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
```

```
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 24 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 769
AR046267/c
LOCUS       AR046267                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1060 from patent US 5817796.
ACCESSION   AR046267
VERSION     AR046267.1  GI:5967732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 1060 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATA 2408
              ||| |||||| |||||
Db         17 AATGTATATATATATA 2


RESULT 770
I53319/c
LOCUS       I53319                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1060 from patent US 5646042.
ACCESSION   I53319
VERSION     I53319.1  GI:2474522
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1060 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATA 2408
              ||| |||||| |||||
Db         17 AATGTATATATATATA 2


RESULT 771
AX687451/c
LOCUS       AX687451                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 183 from Patent EP1281758.
ACCESSION   AX687451
VERSION     AX687451.1  GI:29410145
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 183 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4837 TTCAGCACAGGAATTC 4852
              |||| |||||||||| |
Db         17 TTCACCACAGGAATAC 2


RESULT 772
AX687452/c
LOCUS       AX687452                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 184 from Patent EP1281758.
ACCESSION   AX687452
VERSION     AX687452.1  GI:29410146
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 184 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4837 TTCAGCACAGGAATTC 4852
              |||| |||||||||| |
Db         16 TTCACCACAGGAATAC 1


RESULT 773
BD145036/c
LOCUS       BD145036                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145036
```

```
VERSION     BD145036.1  GI:27850794
KEYWORDS    JP 2002119291-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 17 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/17
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTT 2


RESULT 774
BD166036/c
LOCUS       BD166036                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166036
VERSION     BD166036.1  GI:27871848
KEYWORDS    JP 2002191372-A/16.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 16 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/16
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC          nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTT 2


RESULT 775
E32452/c
LOCUS       E32452                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32452
VERSION     E32452.1  GI:13018688
KEYWORDS    JP 2000037190-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 12 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/12
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
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```
Db         17 GAAAAAAAAAAAAAA 2


RESULT 776
AR264932/c
LOCUS       AR264932                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 16 from patent US 6492121.
ACCESSION   AR264932
VERSION     AR264932.1  GI:29693319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 16 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 777
AR478213/c
LOCUS       AR478213                  18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 16 from patent US 6699661.
ACCESSION   AR478213
VERSION     AR478213.1  GI:47236861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 16 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 778
BD072877/c
LOCUS       BD072877                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072877
VERSION     BD072877.1  GI:22618480
KEYWORDS    JP 2001286300-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 15 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/15
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                 nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 779
BD107504/c
LOCUS       BD107504                  18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107504
VERSION     BD107504.1  GI:23202322
KEYWORDS    JP 2002000275-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 13 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/13
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
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```
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTT 4510
              |||| ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 780
E32455/c
LOCUS       E32455                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32455
VERSION     E32455.1  GI:13018691
KEYWORDS    JP 2000037190-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 15 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/15
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 781
E32458/c
LOCUS       E32458                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32458
VERSION     E32458.1  GI:13018694
KEYWORDS    JP 2000037190-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 18 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/18
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              || ||||||| |||||
Db         18 TGAAAAAAAAAAAAAA 3


RESULT 782
BD145040/c
LOCUS       BD145040                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145040
VERSION     BD145040.1  GI:27850798
KEYWORDS    JP 2002119291-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 21 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/21
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
```

examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .18
FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 7.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4495 TATAAGTTTTTTTTTT 4510
|||| ||||||||||
Db 17 TATATATTTTTTTTT 2

RESULT 783
BD166040/c
LOCUS BD166040 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.
ACCESSION BD166040
VERSION BD166040.1 GI:27871852
KEYWORDS JP 2002191372-A/20.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method
JOURNAL Patent: JP 2002191372-A 20 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/20
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18
FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
source 1. .18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 7.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4495 TATAAGTTTTTTTTTT 4510
|||| ||||||||||
Db 17 TATATATTTTTTTTT 2

RESULT 784
AR264936/c
LOCUS AR264936 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 20 from patent US 6492121.
ACCESSION AR264936
VERSION AR264936.1 GI:29693323
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 20 10-DEC-2002;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 7.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4495 TATAAGTTTTTTTTTT 4510
|||| ||||||||||
Db 17 TATATATTTTTTTTT 2

RESULT 785
AR478217/c
LOCUS AR478217 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 20 from patent US 6699661.
ACCESSION AR478217
VERSION AR478217.1 GI:47236865
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 20 02-MAR-2004;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 7.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4495 TATAAGTTTTTTTTTT 4510
|||| ||||||||||
Db 17 TATATATTTTTTTTT 2

RESULT 786
AX361600/c
LOCUS AX361600 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 18 from Patent WO0208461.
ACCESSION AX361600

```
VERSION     AX361600.1  GI:18694219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 18 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Double-stranded product DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 787
AX814932/c
LOCUS       AX814932                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 18 from Patent WO03064691.
ACCESSION   AX814932
VERSION     AX814932.1  GI:39104070
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 18 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 788
BD072881/c
LOCUS       BD072881                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072881
VERSION     BD072881.1  GI:22618484
KEYWORDS    JP 2001286300-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 19 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/19
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTT 2


RESULT 789
BD107508/c
LOCUS       BD107508                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107508
VERSION     BD107508.1  GI:23202326
KEYWORDS    JP 2002000275-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 17 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/17
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
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          CC              nucleic
          CC   acid.
          FH   Key             Location/Qualifiers
          FT   source          1. .18
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 7.2e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTT 2


RESULT 790
AX643397
LOCUS       AX643397                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 263 from Patent WO02099099.
ACCESSION   AX643397
VERSION     AX643397.1  GI:28551049
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 263 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="r=g or a"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 7.4e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATA 2408
              ||||| |||:||  ||||
Db          1 AAAATGTATRTATGTATA 18


RESULT 791
AX643400/c
LOCUS       AX643400                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 266 from Patent WO02099099.
ACCESSION   AX643400
VERSION     AX643400.1  GI:28551052
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 266 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="y=t or c"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 7.4e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATA 2408
              ||||| |||:||  ||||
Db          19 AAAATGTATRTATGTATA 2


RESULT 792
AX498247
LOCUS       AX498247                 21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from Patent WO0218951.
ACCESSION   AX498247
VERSION     AX498247.1  GI:23343166
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 3 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 7.6e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db          1 GAAAAAAAAAAAAAAA 16


RESULT 793
AR003340/c
LOCUS       AR003340                 39 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 62 from patent US 5744300.
ACCESSION   AR003340
VERSION     AR003340.1  GI:3964599
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 62 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 39;
  Best Local Similarity   70.8%;  Pred. No. 5.7e+02;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1804 TGGAATGGAAAAGCAACTTCATTT 1827
              ||||||||   | || | |||| |
Db         24 TGGAATGGGTTAACATCATCATCT 1


RESULT 794
BD176796
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LOCUS       BD176796                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176796
VERSION     BD176796.1  GI:29122508
KEYWORDS    WO 02074951-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 43 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/43
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 7.4e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db          1 AAAAAAAAAAAAAC 14


RESULT 795
AR056159/c
LOCUS       AR056159                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 363 from patent US 5837542.
ACCESSION   AR056159
VERSION     AR056159.1  GI:5981736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 363 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 7.7e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
              |||||||| |||||
Db         15 GAAAAAAAAAAAAA 2


RESULT 796
AR113917/c
LOCUS       AR113917                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 363 from patent US 6132967.
ACCESSION   AR113917
VERSION     AR113917.1  GI:14094239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 363 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 7.7e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
              |||||||| |||||
Db         15 GAAAAAAAAAAAAA 2


RESULT 797
I29065
LOCUS       I29065                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5576427.
ACCESSION   I29065
VERSION     I29065.1  GI:1819856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 3 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 7.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAANA 15


RESULT 798
AX633201/c
LOCUS       AX633201                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 340 from Patent EP1260586.
ACCESSION   AX633201
VERSION     AX633201.1  GI:28468815
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
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  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 340 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 7.7e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
              ||||||||  |||||
Db         15 GAAAAAAAAAAAAA 2


RESULT 799
BD142810/c
LOCUS       BD142810                  17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142810
VERSION     BD142810.1  GI:23237755
KEYWORDS    WO 0224903-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 4 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/4
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              |||||||  ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 800
BD143836/c
LOCUS       BD143836                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143836
VERSION     BD143836.1  GI:27849594
KEYWORDS    JP 2002095500-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 4 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/4
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              |||||||  ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 801
BD167837/c
LOCUS       BD167837                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167837
VERSION     BD167837.1  GI:27873649
KEYWORDS    WO 0233122-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 4 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/4
```

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            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
           TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 802
BD167909/c
LOCUS       BD167909                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167909
VERSION     BD167909.1  GI:27873721
KEYWORDS    WO 0226962-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 8 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/8
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
           TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 803
BD168113/c
LOCUS       BD168113                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168113
VERSION     BD168113.1  GI:27873925
KEYWORDS    WO 0233069-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 20 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/20
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
           TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
           A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 804
BD171179/c
LOCUS       BD171179                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171179
VERSION     BD171179.1  GI:27876991
KEYWORDS    WO 0250269-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 4 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO
COMMENT OS Artificial Sequence
PN WO 0250269-A/4
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
PC A61P37/08,
PC C12Q1/68,G01N33/50
CC Description of Artificial Sequence:'GT15G', an artificially
CC synthesized
CC primer sequence
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAAC 3618
||||||| ||||||
Db 14 AAAAAAAAAAAAAC 1

RESULT 805
E34260/c
LOCUS E34260 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34260
VERSION E34260.1 GI:18624265
KEYWORDS JP 2000106879-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 4 18-APR-2000;
GENOX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 2000106879-A/4
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAAC 3618
||||||| ||||||
Db 14 AAAAAAAAAAAAAC 1

RESULT 806
E59657/c
LOCUS E59657 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for preparing nucleic acid sample for analyzing minor gene, nucleic acid sample thus prepared and method for analyzing nucleic acid sample by using the same, and reagent kit and analysis service for using the same.
ACCESSION E59657
VERSION E59657.1 GI:13019451
KEYWORDS JP 2000037193-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
TITLE Method for preparing nucleic acid sample for analyzing minor gene, nucleic acid sample thus prepared and method for analyzing nucleic acid sample by using the same, and reagent kit and analysis service for using the same
JOURNAL Patent: JP 2000037193-A 3 08-FEB-2000;
HITACHI LTD
COMMENT OS Unidentified
PN JP 2000037193-A/3
PD 08-FEB-2000
PF 19-MAY-1999 JP 1999138051
PR
PI TAKAMICHI MATSUMURA,TSUYOSHI FUJITA,MASAHARU KIYAMA, PI TAKASHI IRIE,
PI KAZUNORI OKANO
PC C12N15/09,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAAC 3618
||||||| ||||||
Db 14 AAAAAAAAAAAAAC 1

RESULT 807
AR256849/c
LOCUS AR256849 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6485916.
ACCESSION AR256849
VERSION AR256849.1 GI:27306475
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

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            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
  TITLE     Preparation method of nucleic acid sample for rare expressed genes
            and analyzing method using the prepared nucleic acid samples
            thereby
  JOURNAL   Patent: US 6485916-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 808
AR266626/c
LOCUS       AR266626                  17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 64 from patent US 6495319.
ACCESSION   AR266626
VERSION     AR266626.1  GI:29695690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 64 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 809
BD011732/c
LOCUS       BD011732                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011732
VERSION     BD011732.1  GI:22091921
KEYWORDS    WO 0065050-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 4 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/4
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 810
BD091744/c
LOCUS       BD091744                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091744
VERSION     BD091744.1  GI:22637355
KEYWORDS    WO 0073435-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 811
BD091752/c
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LOCUS       BD091752                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091752
VERSION     BD091752.1  GI:22637363
KEYWORDS    WO 0073439-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
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            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 812
BD091775/c
LOCUS       BD091775                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091775
VERSION     BD091775.1  GI:22637386
KEYWORDS    WO 0073440-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 813
BD097336/c
LOCUS       BD097336                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097336
VERSION     BD097336.1  GI:22642910
KEYWORDS    WO 0165259-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 7 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/7
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
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FEATURES              Location/Qualifiers
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  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 814
BD142808/c
LOCUS       BD142808                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142808
VERSION     BD142808.1  GI:23237753
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KEYWORDS    WO 0224903-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 2 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/2
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
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FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 815
BD143834/c
LOCUS       BD143834                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143834
VERSION     BD143834.1  GI:27849592
KEYWORDS    JP 2002095500-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 2 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/2
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
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            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 816
BD167835/c
LOCUS       BD167835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167835
VERSION     BD167835.1  GI:27873647
KEYWORDS    WO 0233122-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 2 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/2
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAAC 3618
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Db         14 AAAAAAAAAAAAAC 1


RESULT 817
BD167907/c
LOCUS       BD167907                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167907
VERSION     BD167907.1  GI:27873719
KEYWORDS    WO 0226962-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 6 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/6
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
             ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 818
BD168111/c
LOCUS       BD168111                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168111
VERSION     BD168111.1  GI:27873923
KEYWORDS    WO 0233069-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 18 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/18
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
             ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 819
BD171177/c
LOCUS       BD171177                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171177
VERSION     BD171177.1  GI:27876989
KEYWORDS    WO 0250269-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 2 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/2
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15A', an artificially
            CC            synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
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           FT   source          1. .17
           FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 820
E34258/c
LOCUS       E34258                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34258
VERSION     E34258.1  GI:18624263
KEYWORDS    JP 2000106879-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 2 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/2
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 821
BD011730/c
LOCUS       BD011730                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011730
VERSION     BD011730.1  GI:22091919
KEYWORDS    WO 0065050-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 2 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/2
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 822
BD091742/c
LOCUS       BD091742                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091742
VERSION     BD091742.1  GI:22637353
KEYWORDS    WO 0073435-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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/db_xref="taxon:32630"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAAC 3618
||||||| ||||||
Db 14 AAAAAAAAAAAAAC 1

RESULT 823
BD091750/c
LOCUS BD091750 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION BD091750
VERSION BD091750.1 GI:22637361
KEYWORDS WO 0073439-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.
TITLE 465, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073439-A 2 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0073439-A/2
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PR 27-MAY-1999 JP 99P 148784
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC Description of Artificial Sequence:Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .17
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAAC 3618
||||||| ||||||
Db 14 AAAAAAAAAAAAAC 1

RESULT 824
BD091773/c
LOCUS BD091773 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091773
VERSION BD091773.1 GI:22637384
KEYWORDS WO 0073440-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 2 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0073440-A/2
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of Artificial Sequence:Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAAC 3618
||||||| ||||||
Db 14 AAAAAAAAAAAAAC 1

RESULT 825
BD097334/c
LOCUS BD097334 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097334
VERSION BD097334.1 GI:22642908
KEYWORDS WO 0165259-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 5 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0165259-A/5
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI HIROHISA SAITO
PC G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
PC A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;

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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 826
BD217905/c
LOCUS       BD217905                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same.
ACCESSION   BD217905
VERSION     BD217905.1  GI:33027675
KEYWORDS    JP 2002516564-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Umansky,S. and Melkonyan,H.
  TITLE     Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same
  JOURNAL   Patent: JP 2002516564-A 6 04-JUN-2002;
            TANOX INC
COMMENT     OS   Unidentified
            PN   JP 2002516564-A/6
            PD   04-JUN-2002
            PF   24-SEP-1997 JP 1998515877
            PR   24-SEP-1996 US    60/026603,11-OCT-1996 US    60/028363 PI
            SAMUIL UMANSKY,HOVSEP MELKONYAN
            PC   C12N15/12,C12N15/62,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
              G01N33/68,
            PC   A61K38/17
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Gene family encoding apoptosis-associated peptides, peptides
            CC            encoded
            CC   thereby and method of using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              : ||||||| ||||| |
Db         17 SNAAAAAAAAAAAAAAA 1


RESULT 827
BD233654/c
LOCUS       BD233654                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Two-color differential display as a method for detecting regulated
            genes.
ACCESSION   BD233654
VERSION     BD233654.1  GI:33043424
KEYWORDS    JP 2002524088-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
  JOURNAL   Patent: JP 2002524088-A 2 06-AUG-2002;
            AVENTIS PHARMA DEUTSCHLAND GMBH
COMMENT     OS   Unidentified
            PN   JP 2002524088-A/2
            PD   06-AUG-2002
            PF   26-AUG-1999 JP 2000569015
            PR   07-SEP-1998 DE 198 40 731.9
            PI   DETLEF KOZIAN,BIRGIT REUNER
            PC   C12Q1/68,G01N33/58//A61K45/00,C12N15/09,C12N15/09,C12N15/00,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /note= 'M = A, C, G; N = A, C, G, T'
            FH   Key             Location/Qualifiers
            FT   exon            1. .17.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :||||||| ||||| |
Db         16 KAAAAAAAAAAAAAAA 1


RESULT 828
AX687453/c
LOCUS       AX687453                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 185 from Patent EP1281758.
ACCESSION   AX687453
VERSION     AX687453.1  GI:29410147
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 185 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4837 TTCAGCACAGGAAT 4850
              |||| |||||||||
Db         15 TTCACCACAGGAAT 2


RESULT 829
AX687454/c
LOCUS       AX687454                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 186 from Patent EP1281758.
ACCESSION   AX687454
VERSION     AX687454.1  GI:29410148
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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            mdz12
  JOURNAL   Patent: EP 1281758-A 186 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES                Location/Qualifiers
     source             1. .17
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 8.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4837 TTCAGCACAGGAAT 4850
              |||| |||||||||
Db         14 TTCACCACAGGAAT 1


RESULT 830
E32451/c
LOCUS       E32451                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32451
VERSION     E32451.1  GI:13018687
KEYWORDS    JP 2000037190-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/11
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES                Location/Qualifiers
     source             1. .18
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 831
E32454/c
LOCUS       E32454                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32454
VERSION     E32454.1  GI:13018690
KEYWORDS    JP 2000037190-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 14 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/14
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES                Location/Qualifiers
     source             1. .18
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 832
E32457/c
LOCUS       E32457                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32457
VERSION     E32457.1  GI:13018693
KEYWORDS    JP 2000037190-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 17 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/17
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES                Location/Qualifiers
     source             1. .18
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
```

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                ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 833
E32460/c
LOCUS       E32460                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32460
VERSION     E32460.1  GI:13018696
KEYWORDS    JP 2000037190-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 20 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/20
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
                ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 834
E32456/c
LOCUS       E32456                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32456
VERSION     E32456.1  GI:13018692
KEYWORDS    JP 2000037190-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 16 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/16
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
                ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 835
E32459/c
LOCUS       E32459                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32459
VERSION     E32459.1  GI:13018695
KEYWORDS    JP 2000037190-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 19 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/19
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 8.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
                ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 836
CQ759632
LOCUS       CQ759632                  19 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 62 from Patent WO2003106672.
ACCESSION   CQ759632
VERSION     CQ759632.1  GI:44849582
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
```

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REFERENCE   1
  AUTHORS   Hayashizaki,Y., Carninci,P. and Harbers,M.T.
  TITLE     Method of utilizing the 5' end of transcribed nucleic acid regions
            for cloning and analysis
  JOURNAL   Patent: WO 2003106672-A 62 24-DEC-2003;
            Riken (JP) ; Kabushiki Kaisha Dnaform (JP)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="tag3"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 8.4e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db          5 AAAAAAAAAAAAAC 18


RESULT 837
AR163080
LOCUS       AR163080                  19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6270966.
ACCESSION   AR163080
VERSION     AR163080.1  GI:16233563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weinstein,J.N. and Buolamwini,J.
  TITLE     Restriction display (RD-PCR) of differentially expressed mRNAs
  JOURNAL   Patent: US 6270966-A 1 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 8.4e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              :||||||| ||||| | |
Db          2 BAAAAAAAAAAAAAAAAA 19


RESULT 838
E08331/c
LOCUS       E08331                    19 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08331
VERSION     E08331.1  GI:2176448
KEYWORDS    JP 1994303997-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 2 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/2
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .19
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 8.4e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              :||||||| ||||| | |
Db         18 BAAAAAAAAAAAAAAAAA 1


RESULT 839
AX498246
LOCUS       AX498246                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from Patent WO0218951.
ACCESSION   AX498246
VERSION     AX498246.1  GI:23343165
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 2 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 8.4e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db          3 AAAAAAAAAAAAAC 16


RESULT 840
AX692528/c
LOCUS       AX692528                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5260 from Patent EP1281758.
ACCESSION   AX692528
VERSION     AX692528.1  GI:29415486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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                  /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAA 3617
              ||  ||||||| |||||
Db         17 CTCAAAAAAAAAAAAAA 1


RESULT 841
A28997/c
LOCUS       A28997                    17 bp    DNA     linear   PAT 30-JUN-1995
DEFINITION  primer sequence 4 from patent EP0522880.
ACCESSION   A28997
VERSION     A28997.1  GI:1248848
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: EP 0522880-A 16 13-JAN-1993;
            INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 842
AR104585/c
LOCUS       AR104585                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 132 from patent US 6093809.
ACCESSION   AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 132 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 843
AR141074/c
LOCUS       AR141074                  17 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 5 from patent US 6207819.
ACCESSION   AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6207819-A 5 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 844
AR175846/c
LOCUS       AR175846                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 132 from patent US 6309867.
ACCESSION   AR175846
VERSION     AR175846.1  GI:17917145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 132 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 845
AR222463
LOCUS       AR222463                  17 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 23 from patent US 6429300.
ACCESSION   AR222463
VERSION     AR222463.1  GI:23329994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 23 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 846
AR236087/c
LOCUS       AR236087                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6462184.
ACCESSION   AR236087
VERSION     AR236087.1  GI:27279786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6462184-A 5 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 847
AR187060/c
LOCUS       AR187060                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2548 from patent US 6346398.
ACCESSION   AR187060
VERSION     AR187060.1  GI:20233025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| || |
Db         17 AAAAAAAAAAAAAAGTA 1


RESULT 848
AR323670/c
LOCUS       AR323670                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1072 from patent US 6566127.
ACCESSION   AR323670
VERSION     AR323670.1  GI:33709478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1072 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| || |
Db         17 AAAAAAAAAAAAAAGTA 1


RESULT 849
AX578222
LOCUS       AX578222                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 60 from Patent WO0211674.
ACCESSION   AX578222
VERSION     AX578222.1  GI:27647424
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 60 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              |||| | || |||||||
Db          1 ATATCTGTATATATATA 17


RESULT 850
AX692529/c
LOCUS       AX692529                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5261 from Patent EP1281758.
ACCESSION   AX692529
VERSION     AX692529.1  GI:29415487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5261 05-FEB-2003;
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           Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAA 3616
              |||  ||||||| ||||
Db         17 TCTCAAAAAAAAAAAAA 1


RESULT 851
I32318
LOCUS       I32318                    17 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 10 from patent US 5587300.
ACCESSION   I32318
VERSION     I32318.1  GI:1823109
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Malter,J.S.
  TITLE     Method to increase regulatory molecule production
  JOURNAL   Patent: US 5587300-A 10 24-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1875 ATGTATGAATGTAAGGA 1891
              ||||||| ||||| | |
Db          1 ATGTATGTATGTATGTA 17


RESULT 852
I32319/c
LOCUS       I32319                    17 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 11 from patent US 5587300.
ACCESSION   I32319
VERSION     I32319.1  GI:1823110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Malter,J.S.
  TITLE     Method to increase regulatory molecule production
  JOURNAL   Patent: US 5587300-A 11 24-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1875 ATGTATGAATGTAAGGA 1891
              ||||||| ||||| | |
Db         17 ATGTATGTATGTATGTA 1


RESULT 853
AX218200
LOCUS       AX218200                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 3642 from Patent WO0159103.
ACCESSION   AX218200
VERSION     AX218200.1  GI:15528261
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3642 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 8.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3968 AAACAATAAAAACAACT 3984
              ||| || || |||||||
Db          1 AAAAAAAAATAACAACT 17


RESULT 854
A14689
LOCUS       A14689                    18 bp    DNA     linear   PAT 28-MAR-1994
DEFINITION  Nucleotide sequence 9 from patent number WO8303623.
ACCESSION   A14689
VERSION     A14689.1  GI:513760
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE
            ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a
            HPV TYPE AND CORRESPONDING POLYPEPTIDES
  JOURNAL   Patent: WO 8303623-A 9 27-OCT-1983;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db          1 GCAAAAAAAAAAAAAAA 17


RESULT 855
AR208425/c
LOCUS       AR208425                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6383754.
ACCESSION   AR208425
VERSION     AR208425.1  GI:21509576
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 5 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         18 GCAAAAAAAAAAAAAAA 2


RESULT 856
AX028845/c
LOCUS       AX028845                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 29 from Patent WO9732023.
ACCESSION   AX028845
VERSION     AX028845.1  GI:10189948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 29 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 857
AX085251/c
LOCUS       AX085251                 18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 5 from Patent WO0112855.
ACCESSION   AX085251
VERSION     AX085251.1  GI:13275309
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 5 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         18 GCAAAAAAAAAAAAAAA 2


RESULT 858
AX028843/c
LOCUS       AX028843                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 27 from Patent WO9732023.
ACCESSION   AX028843
VERSION     AX028843.1  GI:10189946
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 27 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 859
BD145035/c
LOCUS       BD145035                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145035
VERSION     BD145035.1  GI:27850793
KEYWORDS    JP 2002119291-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 16 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/16
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
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            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTGT 1


RESULT 860
BD145039/c
LOCUS       BD145039                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145039
VERSION     BD145039.1  GI:27850797
KEYWORDS    JP 2002119291-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 20 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/20
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTGT 1


RESULT 861
BD166035/c
LOCUS       BD166035                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166035
VERSION     BD166035.1  GI:27871847
KEYWORDS    JP 2002191372-A/15.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 15 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/15
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC          nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTGT 1


RESULT 862
BD166039/c
LOCUS       BD166039                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166039
VERSION     BD166039.1  GI:27871851
KEYWORDS    JP 2002191372-A/19.
SOURCE      unidentified
  ORGANISM  unidentified
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            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 19 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/19
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTCT 1


RESULT 863
AR264931/c
LOCUS       AR264931                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from patent US 6492121.
ACCESSION   AR264931
VERSION     AR264931.1  GI:29693318
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 15 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTGT 1


RESULT 864
AR264935/c
LOCUS       AR264935                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6492121.
ACCESSION   AR264935
VERSION     AR264935.1  GI:29693322
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 19 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTCT 1


RESULT 865
AR478212/c
LOCUS       AR478212                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 15 from patent US 6699661.
ACCESSION   AR478212
VERSION     AR478212.1  GI:47236860
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 15 02-MAR-2004;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTGT 1


RESULT 866
AR478216/c
LOCUS       AR478216                 18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 19 from patent US 6699661.
ACCESSION   AR478216
VERSION     AR478216.1  GI:47236864
KEYWORDS    .
SOURCE      Unknown.
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6699661-A 19 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTCT 1


RESULT 867
BD072876/c
LOCUS       BD072876                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072876
VERSION     BD072876.1  GI:22618479
KEYWORDS    JP 2001286300-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 14 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/14
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTCT 1


RESULT 868
BD072880/c
LOCUS       BD072880                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072880
VERSION     BD072880.1  GI:22618483
KEYWORDS    JP 2001286300-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 18 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/18
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTCT 1


RESULT 869
BD107503/c
LOCUS       BD107503                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107503
VERSION     BD107503.1  GI:23202321
KEYWORDS    JP 2002000275-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
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  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 12 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/12
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  |||||||||  |
Db         17 TATATATTTTTTTTTGT 1


RESULT 870
BD107507/c
LOCUS       BD107507                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107507
VERSION     BD107507.1  GI:23202325
KEYWORDS    JP 2002000275-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 16 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/16
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 8.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  |||||||||  |
Db         17 TATATATTTTTTTTTCT 1


RESULT 871
E52143/c
LOCUS       E52143                   16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  TSA7005 gene.
ACCESSION   E52143
VERSION     E52143.1  GI:18629626
KEYWORDS    JP 2001025389-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ogawara,T., Suzuki,M. and Ozaki,K.
  TITLE     TSA7005 gene
  JOURNAL   Patent: JP 2001025389-A 3 30-JAN-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unknown
            PN   JP 2001025389-A/3
            PD   30-JAN-2001
            PF   15-JUL-1999 JP 1999201279
            PR
            PI   TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
            PC   C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10//A61K31/00,
            PC   A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unidentified"
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                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 9.1e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |: ||||||| |||||
Db         16 TDAAAAAAAAAAAAAA 1


RESULT 872
E53842/c
LOCUS       E53842                   16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION   E53842
VERSION     E53842.1  GI:18633612
KEYWORDS    JP 2001078772-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
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  TITLE     LUNX gene and method for detecting micrometastasis of cancer
  JOURNAL   Patent: JP 2001078772-A 3 27-MAR-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 2001078772-A/3
            PD   27-MAR-2001
            PF   07-SEP-1999 JP 1999253186
            PR
            PI   MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI
            PC   C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
            A61K35/12,A61K35/76,
            PC   A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 9.1e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |: ||||||| |||||
Db         16 TBAAAAAAAAAAAAAA 1


RESULT 873
AR183909/c
LOCUS       AR183909                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6342376.
ACCESSION   AR183909
VERSION     AR183909.1  GI:20227878
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6342376-A 2 29-JAN-2002;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 9.2e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :||||||| ||||| |
Db         16 BAAAAAAAAAAAAAAA 1


RESULT 874
AR429726/c
LOCUS       AR429726                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6645741.
ACCESSION   AR429726
VERSION     AR429726.1  GI:40190064
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6645741-A 2 11-NOV-2003;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 9.2e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :||||||| ||||| |
Db         16 BAAAAAAAAAAAAAAA 1


RESULT 875
AR187067
LOCUS       AR187067                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2555 from patent US 6346398.
ACCESSION   AR187067
VERSION     AR187067.1  GI:20233032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2555 12-FEB-2002;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTT 4512
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 876
AR323677
LOCUS       AR323677                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1079 from patent US 6566127.
ACCESSION   AR323677
VERSION     AR323677.1  GI:33709485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1079 20-MAY-2003;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned RNA"

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       4501 TTTTTTTTTTTT 4512
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 877
AR491869
LOCUS       AR491869                  19 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 4 from patent US 6716585.
ACCESSION   AR491869
VERSION     AR491869.1  GI:47260090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Al-Mahmood,S.
  TITLE     Method for identifying novel genes involved in the regulation of
            angiogenesis, study of said genes and use thereof for therapeutic
            purposes
  JOURNAL   Patent: US 6716585-A 4 06-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 12;  DB 1;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 9.3e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :|||||||  |||||  |
Db          2 VAAAAAAAAAAAAAAA 17


RESULT 878
E15159/c
LOCUS       E15159                    20 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Phosphorothioate antisence oligo DNA for human VEGF mRNA.
ACCESSION   E15159
VERSION     E15159.1  GI:5709842
KEYWORDS    JP 1998052285-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K.
  TITLE     PREPARATION OF ANTISENSE NUCLEIC ACID
  JOURNAL   Patent: JP 1998052285-A 4 24-FEB-1998;
            TOAGOSEI CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1998052285-A/4
            PD   24-FEB-1998
            PF   20-MAY-1997 JP 1997129767
            PR   23-MAY-1996 JP 96P   128192
            PI   UCHIDA KIYOSHI
            PC   C12N15/09,C07H21/02,C07H21/04;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 9.2e+02;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACAGTT 3403
              || || | ||||||| || |
Db         20 AGCAGAAAGAGGAAAGAGGT 1


RESULT 879
E22402
LOCUS       E22402                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Antisense nucleic acid compound.
ACCESSION   E22402
VERSION     E22402.1  GI:13024045
KEYWORDS    JP 1999042091-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kinya,K., Yoko,M. and Kiyoshi,U.
  TITLE     Antisense nucleic acid compound
  JOURNAL   Patent: JP 1999042091-A 4 16-FEB-1999;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999042091-A/4
            PD   16-FEB-1999
            PF   25-JUL-1997 JP 1997213838
            PR
            PI   KINYA KAMIYA,YOKO MATSUDA,KIYOSHI UCHIDA
            PC   C12N15/09,A61K31/70,A61K48/00,C12Q1/68,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 9.2e+02;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACAGTT 3403
              || || | ||||||| || |
Db          1 AGCAGAAAGAGGAAAGAGGT 20


RESULT 880
AR029402/c
LOCUS       AR029402                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5859233.
ACCESSION   AR029402
VERSION     AR029402.1  GI:5941375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 881
AR029403
LOCUS       AR029403                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5859233.
ACCESSION   AR029403
VERSION     AR029403.1  GI:5941376
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 4 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 882
AR034895/c
LOCUS       AR034895                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5869643.
ACCESSION   AR034895
VERSION     AR034895.1  GI:5950500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 10 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 883
AR034898
LOCUS       AR034898                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5869643.
ACCESSION   AR034898
VERSION     AR034898.1  GI:5950503
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 16 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 884
AR048768
LOCUS       AR048768                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5821354.
ACCESSION   AR048768
VERSION     AR048768.1  GI:5971111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Leclerc,G. and Martel,R.
  TITLE     Radiolabeled DNA oligonucleotide and method of preparation
  JOURNAL   Patent: US 5821354-A 2 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 885
AR049970/c
LOCUS       AR049970                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5824793.
ACCESSION   AR049970
VERSION     AR049970.1  GI:5971962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 3 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
```

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              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 886
AR049971
LOCUS       AR049971                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5824793.
ACCESSION   AR049971
VERSION     AR049971.1  GI:5971963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 4 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 887
AR056157/c
LOCUS       AR056157                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 361 from patent US 5837542.
ACCESSION   AR056157
VERSION     AR056157.1  GI:5981734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 361 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 888
AR056158/c
LOCUS       AR056158                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 362 from patent US 5837542.
ACCESSION   AR056158
VERSION     AR056158.1  GI:5981735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 362 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 889
AR080676/c
LOCUS       AR080676                  15 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 5 from patent US 5968822.
ACCESSION   AR080676
VERSION     AR080676.1  GI:10007406
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in transduced cells
  JOURNAL   Patent: US 5968822-A 5 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 890
AR084516
LOCUS       AR084516                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 5 from patent US 5981185.
ACCESSION   AR084516
VERSION     AR084516.1  GI:10011287
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 5 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15
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RESULT 891
AR084520/c
LOCUS       AR084520                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 9 from patent US 5981185.
ACCESSION   AR084520
VERSION     AR084520.1  GI:10011291
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 9 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 892
AR105981/c
LOCUS       AR105981                  15 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6103474.
ACCESSION   AR105981
VERSION     AR105981.1  GI:12820046
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 4 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 893
AR113915/c
LOCUS       AR113915                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 361 from patent US 6132967.
ACCESSION   AR113915
VERSION     AR113915.1  GI:14094237
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 361 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 894
AR113916/c
LOCUS       AR113916                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 362 from patent US 6132967.
ACCESSION   AR113916
VERSION     AR113916.1  GI:14094238
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 362 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 895
AR170375
LOCUS       AR170375                  15 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6291438.
ACCESSION   AR170375
VERSION     AR170375.1  GI:17908334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Wang,J.H.
  TITLE     Antiviral anticancer poly-substituted phenyl derivatized
            oligoribonucleotides and methods for their use
  JOURNAL   Patent: US 6291438-A 1 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15
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RESULT 896
BD184668/c
LOCUS       BD184668                  15 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Method and detector for identifying subtypes of human papiloma
            viruses.
ACCESSION   BD184668
VERSION     BD184668.1  GI:31876868
KEYWORDS    JP 2002360271-A/647.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
            Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
  TITLE     Method and detector for identifying subtypes of human papiloma
  JOURNAL   Patent: JP 2002360271-A 647 17-DEC-2002;
            KING CAR FOOD INDUSTRIAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002360271-A/647
            PD   17-DEC-2002
            PF   28-NOV-2001 JP 2001362595
            PR   04-MAY-2001 TW     90110785
            PI   CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
            PI   HAENG LEE,
            PI   SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
            PI   WEN SHI,
            PI   CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
            PC   C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
            ,C12Q1/70,G01N21/64,
            PC   G01N33/53,G01N33/574,G01N33/58,G01N37/00//(C12M1/34,C12R1:93),
            PC   (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
            CC   Added sequence for 3' end labeling of oligonucleic acid. FH
            Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 897
BD206432/c
LOCUS       BD206432                  15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD206432
VERSION     BD206432.1  GI:33016202
KEYWORDS    JP 2002512791-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 22 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/22
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 898
BD209488/c
LOCUS       BD209488                  15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD209488
VERSION     BD209488.1  GI:33019258
KEYWORDS    JP 2002512791-A/3078.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 3078 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/3078
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 899
CQ832330/c
LOCUS       CQ832330                  15 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 13 from Patent WO2004058794.
ACCESSION   CQ832330
VERSION     CQ832330.1  GI:50831954
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Arar,K.
  TITLE     Methods and compositions for the tandem synthesis of two or more
            oligonuleotides on the same solid support
  JOURNAL   Patent: WO 2004058794-A 13 15-JUL-2004;
            Proligo LLC (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Nucleic Acid Ligand"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 900
CQ840762/c
LOCUS       CQ840762                  15 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 5 from Patent EP1439193.
ACCESSION   CQ840762
VERSION     CQ840762.1  GI:50838367
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Antibody directed to polypeptide having heparanase activity
  JOURNAL   Patent: EP 1439193-A 5 21-JUL-2004;
            Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH
            SERVICES AND DEVELOPMENT LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 901
CQ840854/c
LOCUS       CQ840854                  15 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 5 from Patent EP1439226.
ACCESSION   CQ840854
VERSION     CQ840854.1  GI:50838429
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     A nucleic acid antisense sequence to a polynucleotide encoding a
            polypeptide having heparanese activity
  JOURNAL   Patent: EP 1439226-A 5 21-JUL-2004;
            Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH
            SERVICES AND DEVELOPMENT LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Single strand DNA oligonucleotide"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 902
E08522/c
LOCUS       E08522                    15 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
  TITLE     S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
  JOURNAL   Patent: JP 1994335389-A 7 06-DEC-1994;
            KAGOME CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993 JP 1993126286
            PI   TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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                  ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 903
E12591/c
LOCUS       E12591                    15 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  pRIMER.
ACCESSION   E12591
VERSION     E12591.1  GI:3251423
KEYWORDS    JP 1997028381-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Minami,K. and Takagi,M.
  TITLE     S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE
  JOURNAL   Patent: JP 1997028381-A 8 04-FEB-1997;
            TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997028381-A/8
            PD   04-FEB-1997
            PF   24-JUL-1995 JP 1995187557
            PI   TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 904
I29068
LOCUS       I29068                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5576427.
ACCESSION   I29068
VERSION     I29068.1  GI:1819859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 6 19-NOV-1996;
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 905
I38641/c
LOCUS       I38641                    15 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5614617.
ACCESSION   I38641
VERSION     I38641.1  GI:2084695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 1 25-MAR-1997;
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 906
AR200476/c
LOCUS       AR200476                  15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 19 from patent US 6357163.
ACCESSION   AR200476
VERSION     AR200476.1  GI:20251364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 19 19-MAR-2002;
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 907
AR200477
LOCUS       AR200477                  15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 20 from patent US 6357163.
ACCESSION   AR200477
VERSION     AR200477.1  GI:20251365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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          Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 20 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 908
AR222461
LOCUS       AR222461                 15 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 21 from patent US 6429300.
ACCESSION   AR222461
VERSION     AR222461.1  GI:23329992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 21 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 909
AR266630/c
LOCUS       AR266630                 15 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 68 from patent US 6495319.
ACCESSION   AR266630
VERSION     AR266630.1  GI:29695694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 68 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1

. . . .
RESULT 910
AR371280/c
LOCUS       AR371280                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 17 from patent US 6395474.
ACCESSION   AR371280
VERSION     AR371280.1  GI:34608212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 17 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 911
AR371281
LOCUS       AR371281                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 18 from patent US 6395474.
ACCESSION   AR371281
VERSION     AR371281.1  GI:34608213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 18 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 912
AR410213/c
LOCUS       AR410213                 15 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 9 from patent US 6635452.
ACCESSION   AR410213
VERSION     AR410213.1  GI:40161460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass label molecules
  JOURNAL   Patent: US 6635452-A 9 21-OCT-2003;
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FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 913
AR438809/c
LOCUS       AR438809                  15 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6664105.
ACCESSION   AR438809
VERSION     AR438809.1  GI:42663812
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in genetically modified cells
  JOURNAL   Patent: US 6664105-A 5 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 914
AR439678/c
LOCUS       AR439678                  15 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6664388.
ACCESSION   AR439678
VERSION     AR439678.1  GI:42665611
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Nelson,J.S.
  TITLE     Reagents for oligonucleotide cleavage and deprotection
  JOURNAL   Patent: US 6664388-A 2 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 915
AR452072/c
LOCUS       AR452072                  15 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6677137.
ACCESSION   AR452072
VERSION     AR452072.1  GI:42683499
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Goldshmidt,O., Pecker,I., Vlodavsky,I., Michal,I. and Zcharia,E.
  TITLE     Avian and reptile derived polynucleotide encoding a polypeptide
            having heparanase activity
  JOURNAL   Patent: US 6677137-A 5 13-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 916
AR489501/c
LOCUS       AR489501                  15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 17 from patent US 6710163.
ACCESSION   AR489501
VERSION     AR489501.1  GI:47256526
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acid synthons
  JOURNAL   Patent: US 6710163-A 17 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 917
AR489502
LOCUS       AR489502                  15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 18 from patent US 6710163.
ACCESSION   AR489502
VERSION     AR489502.1  GI:47256527
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acid synthons
  JOURNAL   Patent: US 6710163-A 18 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 918
AR491112/c
LOCUS       AR491112                  15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 17 from patent US 6713602.
ACCESSION   AR491112
VERSION     AR491112.1  GI:47258972
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Synthetic procedures for peptide nucleic acids
  JOURNAL   Patent: US 6713602-A 17 30-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 919
AR491113
LOCUS       AR491113                  15 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 18 from patent US 6713602.
ACCESSION   AR491113
VERSION     AR491113.1  GI:47258973
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Synthetic procedures for peptide nucleic acids
  JOURNAL   Patent: US 6713602-A 18 30-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 920
AX004877/c
LOCUS       AX004877                  15 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 6 from Patent WO9910527.
ACCESSION   AX004877
VERSION     AX004877.1  GI:9928277
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 6 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl modified oligonucleotide"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 921
AX026066/c
LOCUS       AX026066                  15 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 4 from Patent WO0028046.
ACCESSION   AX026066
VERSION     AX026066.1  GI:10187502
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Marraccini,P. and Rogers,J.
  TITLE     Coffea arabica mannanase
  JOURNAL   Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHESE"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 922
AX048407/c
LOCUS       AX048407                  15 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 6 from Patent WO0071747.
ACCESSION   AX048407
VERSION     AX048407.1  GI:12225571
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 6 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
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     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 923
AX106973
LOCUS       AX106973                  15 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 26 from Patent WO0125442.
ACCESSION   AX106973
VERSION     AX106973.1  GI:13922522
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
  JOURNAL   Patent: WO 0125442-A 26 12-APR-2001;
            CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligo dA"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 924
AX127272/c
LOCUS       AX127272                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 3 from Patent EP1111068.
ACCESSION   AX127272
VERSION     AX127272.1  GI:14133346
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 3 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_structure  1
                     /note="(NH2-C6-ttt)2-branch-"
     misc_feature    15
                     /note="NH2
                     kunstliche"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 925
AX127273/c
LOCUS       AX127273                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 4 from Patent EP1111068.
ACCESSION   AX127273
VERSION     AX127273.1  GI:14133347
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 4 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_structure  1
                     /note="(dt-COOH)2-branch-"
     misc_feature    15
                     /note="NH2
                     kunstliche"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 926
AX180140/c
LOCUS       AX180140                  15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 3 from Patent WO0146464.
ACCESSION   AX180140
VERSION     AX180140.1  GI:15132181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 3 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (NH2-C6-TTT)2-branch-"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 927
AX180141/c
LOCUS       AX180141                  15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 4 from Patent WO0146464.
ACCESSION   AX180141
VERSION     AX180141.1  GI:15132182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 4 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (dT-COOH)2-branch-"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 928
AX429224/c
LOCUS       AX429224                  15 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 1 from Patent EP1201765.
ACCESSION   AX429224
VERSION     AX429224.1  GI:21540537
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
  TITLE     Cellular kinases involved in cytomegalovirus infection and their
            inhibition
  JOURNAL   Patent: EP 1201765-A 1 02-MAY-2002;
            Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="N/A"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 929
AX525141
LOCUS       AX525141                  15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 1 from Patent WO02066675.
ACCESSION   AX525141
VERSION     AX525141.1  GI:25170126
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 1 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Biotin"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         1 AAAAAAAAAAAAAAA 15


RESULT 930
AX525143
LOCUS       AX525143                  15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 3 from Patent WO02066675.
ACCESSION   AX525143
VERSION     AX525143.1  GI:25170128
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 3 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Digoxigenin"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         1 AAAAAAAAAAAAAAA 15


RESULT 931
AX633197/c
LOCUS       AX633197                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 336 from Patent EP1260586.
ACCESSION   AX633197
VERSION     AX633197.1  GI:28468811
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
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          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
  TITLE   Method and reagent for inhibiting the expression of disease related
          genes
  JOURNAL Patent: EP 1260586-A 336 27-NOV-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 932
AX633199/c
LOCUS       AX633199                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 338 from Patent EP1260586.
ACCESSION   AX633199
VERSION     AX633199.1  GI:28468813
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 338 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 933
AX696087/c
LOCUS       AX696087                 15 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 6 from Patent WO03008643.
ACCESSION   AX696087
VERSION     AX696087.1  GI:29419249
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hammonds,T.R.
  TITLE     Method and polynukleotides for assaying the activity of a dna
            modifying enzyme
  JOURNAL   Patent: WO 03008643-A 6 30-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide 6"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 934
AX711176
LOCUS       AX711176                 15 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 476 from Patent EP1288296.
ACCESSION   AX711176
VERSION     AX711176.1  GI:29787557
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 476 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Polyadenylation region"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 935
BD074424/c
LOCUS       BD074424                 15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell.
ACCESSION   BD074424
VERSION     BD074424.1  GI:22620027
KEYWORDS    JP 2001514855-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Elena,F.
  TITLE     Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell
  JOURNAL   Patent: JP 2001514855-A 5 18-SEP-2001;
            INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
            & DEVELOPMENT LTD
COMMENT     OS   Nucleic acid
            PN   JP 2001514855-A/5
            PD   18-SEP-2001
            PF   31-AUG-1998 JP 2000508806
            PR   02-SEP-1997 US    08/922170,02-JUL-1998 US    09/109386 PI
            IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
            PC   C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00, PC
              A61P37/00,
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            PC   A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC
             A61K39/395,
            PC   A61K39/395,C12N15/00,A61K37/02,C12N5/00
            CC   Polynucleotide encoding polypeptide having
            heparanase activity
            CC            and
            CC   expression of the polypeptide in induced cell FH   Key
                 Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Nucleic acid'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 936
BD084687/c
LOCUS       BD084687                 15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Releasable nonvolatile mass-label molecules.
ACCESSION   BD084687
VERSION     BD084687.1  GI:22630297
KEYWORDS    JP 2001524808-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass-label molecules
  JOURNAL   Patent: JP 2001524808-A 5 04-DEC-2001;
            GENETRACE SYSTEMS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001524808-A/5
            PD   04-DEC-2001
            PF   10-DEC-1997 JP 1998526924
            PR   10-DEC-1996 US    60/033037,16-MAY-1997 US    60/046719 PI
            JOSEPH A MONTFORTE,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
            THOMAS A SHALER
            PC   C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
              B01D59/44,
            PC   H01J49/00,C07H21/04,C07K15/26,C07K15/28
            CC   Description of Artificial Sequence: oligo dT15 primer FH   Key
                      Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 937
AR027678/c
LOCUS       AR027678                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5856435.
ACCESSION   AR027678
VERSION     AR027678.1  GI:5938498
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
  TITLE     Nucleic acid-containing composition, its preparation and use
  JOURNAL   Patent: US 5856435-A 15 05-JAN-1999;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 938
AR037355/c
LOCUS       AR037355                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5801155.
ACCESSION   AR037355
VERSION     AR037355.1  GI:5955211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor grove binder conjugates
  JOURNAL   Patent: US 5801155-A 2 01-SEP-1998;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 939
AR104584
LOCUS       AR104584                 16 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 131 from patent US 6093809.
ACCESSION   AR104584
VERSION     AR104584.1  GI:12817292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 131 25-JUL-2000;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 940
AR175845
LOCUS       AR175845                 16 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 131 from patent US 6309867.
ACCESSION   AR175845
VERSION     AR175845.1  GI:17917144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 131 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 941
BD167413
LOCUS       BD167413                 16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION   BD167413
VERSION     BD167413.1  GI:27873225
KEYWORDS    JP 2002211954-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
  TITLE     Surface-roughened slide glass and method of analyzing biological
            substance using the same
  JOURNAL   Patent: JP 2002211954-A 1 31-JUL-2002;
            TOYO KOHAN CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002211954-A/1
            PD   31-JUL-2002
            PF   30-OCT-2001 JP 2001332778
            PI   HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            PI   KENICHI TAKAGI
            PC   C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing  CC
             biological substance
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 942
BD167414
LOCUS       BD167414                 16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION   BD167414
VERSION     BD167414.1  GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
  TITLE     Surface-roughened slide glass and method of analyzing biological
            substance using the same
  JOURNAL   Patent: JP 2002211954-A 2 31-JUL-2002;
            TOYO KOHAN CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002211954-A/2
            PD   31-JUL-2002
            PF   30-OCT-2001 JP 2001332778
            PI   HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            PI   KENICHI TAKAGI
            PC   C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing  CC
             biological substance
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 943
CQ800970/c
LOCUS       CQ800970                 16 bp    DNA     linear   PAT 05-MAY-2004
DEFINITION  Sequence 9 from Patent EP1413630.
ACCESSION   CQ800970
VERSION     CQ800970.1  GI:47057749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
  TITLE     Analyssis of biological targets using a biochip comprising a
            fluorescent marker
  JOURNAL   Patent: EP 1413630-A 9 28-APR-2004;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR); Universite Joseph Fourier
            de Grenoble (FR)
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FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: synthetic"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 944
CQ827693
LOCUS       CQ827693                  16 bp    DNA     linear   PAT 29-JUN-2004
DEFINITION  Sequence 130 from Patent WO2004050918.
ACCESSION   CQ827693
VERSION     CQ827693.1  GI:49456143
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ruan,Y. and Wei,C.
  TITLE     Method to generate or determine nucleic acid tags corresponding to
            the terminal ends of dna molecules using sequence analysis of gene
            expression (terminal sage)
  JOURNAL   Patent: WO 2004050918-A 130 17-JUN-2004;
            Agency for Science, Technology and Research (SG)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="tag"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 945
I38676/c
LOCUS       I38676                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 36 from patent US 5614617.
ACCESSION   I38676
VERSION     I38676.1  GI:2084730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 36 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 946
I38682/c
LOCUS       I38682                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 42 from patent US 5614617.
ACCESSION   I38682
VERSION     I38682.1  GI:2084736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 42 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 947
I38700/c
LOCUS       I38700                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 60 from patent US 5614617.
ACCESSION   I38700
VERSION     I38700.1  GI:2084754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 60 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 948
AR221692/c
LOCUS       AR221692                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from patent US 6426408.
ACCESSION   AR221692
VERSION     AR221692.1  GI:23328764
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 2 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 949
AR221693/c
LOCUS       AR221693                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6426408.
ACCESSION   AR221693
VERSION     AR221693.1  GI:23328765
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 3 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 950
AR221694/c
LOCUS       AR221694                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 4 from patent US 6426408.
ACCESSION   AR221694
VERSION     AR221694.1  GI:23328766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 4 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 951
AR221695/c
LOCUS       AR221695                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from patent US 6426408.
ACCESSION   AR221695
VERSION     AR221695.1  GI:23328767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 5 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 952
AR221696/c
LOCUS       AR221696                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from patent US 6426408.
ACCESSION   AR221696
VERSION     AR221696.1  GI:23328768
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 6 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 953
AR221697/c
LOCUS       AR221697                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 7 from patent US 6426408.
ACCESSION   AR221697
VERSION     AR221697.1  GI:23328769
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 7 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
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                  /organism="unknown"
                  /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 954
AR221698/c
LOCUS       AR221698                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 8 from patent US 6426408.
ACCESSION   AR221698
VERSION     AR221698.1  GI:23328770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 8 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 955
AR222462
LOCUS       AR222462                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 22 from patent US 6429300.
ACCESSION   AR222462
VERSION     AR222462.1  GI:23329993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 22 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 956
AR257437/c
LOCUS       AR257437                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6486308.
ACCESSION   AR257437
VERSION     AR257437.1  GI:27307448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 2 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 957
AR257438/c
LOCUS       AR257438                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6486308.
ACCESSION   AR257438
VERSION     AR257438.1  GI:27307449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 958
AR257439/c
LOCUS       AR257439                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 4 from patent US 6486308.
ACCESSION   AR257439
VERSION     AR257439.1  GI:27307450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 4 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 959
AR257440/c
LOCUS       AR257440                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6486308.
ACCESSION   AR257440
VERSION     AR257440.1  GI:27307451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 5 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 960
AR257441/c
LOCUS       AR257441                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6486308.
ACCESSION   AR257441
VERSION     AR257441.1  GI:27307452
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 6 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 961
AR257442/c
LOCUS       AR257442                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6486308.
ACCESSION   AR257442
VERSION     AR257442.1  GI:27307453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 7 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 962
AR257443/c
LOCUS       AR257443                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6486308.
ACCESSION   AR257443
VERSION     AR257443.1  GI:27307454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 8 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 963
AR561628
LOCUS       AR561628                  16 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 1 from patent US 6756492.
ACCESSION   AR561628
VERSION     AR561628.1  GI:53974736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Beier,M. and Honeisel,J.
  TITLE     Nucleoside derivatives with photo-unstable protective groups
  JOURNAL   Patent: US 6756492-A 1 29-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15
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RESULT 964
AR561693/c
LOCUS       AR561693                  16 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 9 from patent US 6759039.
ACCESSION   AR561693
VERSION     AR561693.1  GI:53974843
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Tsang,W.-G., Zheng,T. and Huang,C.J.
  TITLE     Culturing pancreatic stem cells having a specified, intermediate
            stage of development
  JOURNAL   Patent: US 6759039-A 9 06-JUL-2004;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 965
AX039049
LOCUS       AX039049                  16 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 2 from Patent WO0061594.
ACCESSION   AX039049
VERSION     AX039049.1  GI:11228345
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Beier,M. and Hoheisel,J.
  TITLE     Nucleoside derivatives with photo-unstable protective groups
  JOURNAL   Patent: WO 0061594-A 2 19-OCT-2000;
            DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG
            (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 966
AX235176/c
LOCUS       AX235176                  16 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 9 from Patent WO0163282.
ACCESSION   AX235176
VERSION     AX235176.1  GI:15593767
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
  TITLE     Analysis of biological targets using a biochip comprising a
            fluorescent marker
  JOURNAL   Patent: WO 0163282-A 9 30-AUG-2001;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence synthetique"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 967
AR002257/c
LOCUS       AR002257                  16 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION     AR002257.1  GI:3963811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
             |||||| ||||| ||
Db         16 AAAAAAAAAAAAAAG 2


RESULT 968
AR045207/c
LOCUS       AR045207                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5817795.
ACCESSION   AR045207
VERSION     AR045207.1  GI:5966672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
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                ||||||  |||||  ||
Db          16 AAAAAAAAAAAAAAG 2


RESULT 969
AR051238/c
LOCUS       AR051238                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5830658.
ACCESSION   AR051238
VERSION     AR051238.1  GI:5974602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
                ||||||  |||||  ||
Db          16 AAAAAAAAAAAAAAG 2


RESULT 970
I16032/c
LOCUS       I16032                    16 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION     I16032.1  GI:1250940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
                ||||||  |||||  ||
Db          16 AAAAAAAAAAAAAAG 2


RESULT 971
I28367/c
LOCUS       I28367                    16 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION     I28367.1  GI:1819143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
                ||||||  |||||  ||
Db          16 AAAAAAAAAAAAAAG 2


RESULT 972
AX359760
LOCUS       AX359760                  16 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 64 from Patent WO0200691.
ACCESSION   AX359760
VERSION     AX359760.1  GI:18675467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Tchernev,V., Putturajan,M., Malyankar,U.M., Gusev,V.,
            Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
            Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and Smithson,G.
  TITLE     Novel polynucleotides and polypeptides encoded thereby
  JOURNAL   Patent: WO 0200691-A 64 03-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 9.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
                ||||||  |||||  ||
Db          1 AAAAAAAAAAAAAAG 15


RESULT 973
AX692526/c
LOCUS       AX692526                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5258 from Patent EP1281758.
ACCESSION   AX692526
VERSION     AX692526.1  GI:29415484
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5258 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 974
AX692527/c
LOCUS       AX692527                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5259 from Patent EP1281758.
ACCESSION   AX692527
VERSION     AX692527.1  GI:29415485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5259 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 975
AR172076/c
LOCUS       AR172076                 17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6297425.
ACCESSION   AR172076
VERSION     AR172076.1  GI:17911026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6297425-A 30 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 AAAAAAAAAAAAAAA 3


RESULT 976
AR173367/c
LOCUS       AR173367                 17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6303846.
ACCESSION   AR173367
VERSION     AR173367.1  GI:17912858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6303846-A 30 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 AAAAAAAAAAAAAAA 3


RESULT 977
AR266625/c
LOCUS       AR266625                 17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 63 from patent US 6495319.
ACCESSION   AR266625
VERSION     AR266625.1  GI:29695689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 63 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 978
AR047356
LOCUS       AR047356                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2149 from patent US 5817796.
ACCESSION   AR047356
VERSION     AR047356.1  GI:5968821
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2149 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||  |||||| |
Db          1 TTTTTTATTTTTTAT 15


RESULT 979
I54408
LOCUS       I54408                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2149 from patent US 5646042.
ACCESSION   I54408
VERSION     I54408.1  GI:2475611
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2149 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||  |||||| |
Db          1 TTTTTTATTTTTTAT 15


RESULT 980
BD203005
LOCUS       BD203005                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD203005
VERSION     BD203005.1  GI:33012775
KEYWORDS    JP 2002509721-A/6031.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 6031 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/6031
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||  ||| |||
Db          3 TTTTTTTGTTTGTTT 17


RESULT 981
AR208426/c
LOCUS       AR208426                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6383754.
ACCESSION   AR208426
VERSION     AR208426.1  GI:21509577
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 6 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              |||||||  |||||  |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 982
AX085252/c
LOCUS       AX085252                 18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 6 from Patent WO0112855.
ACCESSION   AX085252
VERSION     AX085252.1  GI:13275310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 6 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              |||||||  |||||  |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 983
```

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AX599310/c
LOCUS       AX599310                18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 650 from Patent WO02077272.
ACCESSION   AX599310
VERSION     AX599310.1  GI:28399452
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 650 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGA 3621
              ||||||||||| | |
Db         15 AAAAACAAAAATAAA 1


RESULT 984
AX599902/c
LOCUS       AX599902                18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1242 from Patent WO02077272.
ACCESSION   AX599902
VERSION     AX599902.1  GI:28400052
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1242 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGA 3621
              ||||||||||| | |
Db         15 AAAAACAAAAATAAA 1


RESULT 985
AX767726/c
LOCUS       AX767726                18 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 374 from Patent WO03044226.
ACCESSION   AX767726
VERSION     AX767726.1  GI:32436331
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 374 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGA 3621
              ||||||||||| | |
Db         15 AAAAACAAAAATAAA 1


RESULT 986
AX796164/c
LOCUS       AX796164                18 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 507 from Patent WO03052135.
ACCESSION   AX796164
VERSION     AX796164.1  GI:37516830
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 507 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ELK1"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 9.8e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGA 3621
              ||||||||||| | |
Db         15 AAAAACAAAAATAAA 1


RESULT 987
AR098809
LOCUS       AR098809                18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 64 from patent US 6077672.
ACCESSION   AR098809
VERSION     AR098809.1  GI:12808575
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
```

```
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 64 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3111 TCCCCTGCCACACTGATG 3128
              ||| ||||||  ||| ||
Db          1 TCCTCTGCCAGGCTGGTG 18


RESULT 988
AR072539
LOCUS       AR072539                 19 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 10 from patent US 5948622.
ACCESSION   AR072539
VERSION     AR072539.1  GI:9999303
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S., Goryshin,I.Yu., York,D.L. and Zhou,H.
  TITLE     System for in vitro transposition
  JOURNAL   Patent: US 5948622-A 10 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 989
AR121569
LOCUS       AR121569                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6159736.
ACCESSION   AR121569
VERSION     AR121569.1  GI:14105145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S. and Goryshin,I.Y.
  TITLE     Method for making insertional mutations using a Tn5 synaptic
            complex
  JOURNAL   Patent: US 6159736-A 2 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 990
BD251066
LOCUS       BD251066                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method for making insertional mutations.
ACCESSION   BD251066
VERSION     BD251066.1  GI:33060836
KEYWORDS    JP 2002531062-A/2.
SOURCE      Transposon Tn5
  ORGANISM  Transposon Tn5
            other sequences; transposons.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S. and Goryshin,I.Y.
  TITLE     Method for making insertional mutations
  JOURNAL   Patent: JP 2002531062-A 2 24-SEP-2002;
            WISCONSIN ALUMNI RESEARCH FOUNDATION
COMMENT     OS   Transposon Tn5
            PN   JP 2002531062-A/2
            PD   24-SEP-2002
            PF   21-SEP-1999 JP 2000574243
            PR   23-SEP-1998 US    09/159363
            PI   WILLIAM S REZNIKOFF,IGOR Y GORYSHIN
            PC   C12N15/09,C12N9/00,C12N15/01,C12Q1/02//G01N33/15,G01N33/50, PC
              G01N33/566,
            PC   C12N15/00,C12N15/00
            CC   Method for making insertional mutations
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Transposon Tn5'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Transposon Tn5"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:2411"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 991
AR214207
LOCUS       AR214207                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6406896.
ACCESSION   AR214207
VERSION     AR214207.1  GI:23311737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S. and Naumann,T.A.
  TITLE     Transposase enzyme and method for use
  JOURNAL   Patent: US 6406896-A 4 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 992
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AR360576/c
LOCUS       AR360576                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3 from patent US 6596509.
ACCESSION   AR360576
VERSION     AR360576.1  GI:33767641
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bauer,D.W., Beer,S.V., Bogdanove,A.J., Collmer,A. and Ham,J.H.
  TITLE     Recombinant constructs and systems for secretion of proteins via
            type III secretion systems
  JOURNAL   Patent: US 6596509-A 3 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db         19 CTGTCTCTTGATCAGATC 2


RESULT 993
AR363387
LOCUS       AR363387                  19 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 3 from patent US 5212080.
ACCESSION   AR363387
VERSION     AR363387.1  GI:34424883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Nag,D.K., Huang,H.V. and Berg,D.E.
  TITLE     Method of DNA sequencing using DNA transposon Tn5seql
  JOURNAL   Patent: US 5212080-A 3 18-MAY-1993;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 994
AX080722
LOCUS       AX080722                  19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 4 from Patent WO0109363.
ACCESSION   AX080722
VERSION     AX080722.1  GI:13169711
KEYWORDS    .
SOURCE      Transposon Tn5
  ORGANISM  Transposon Tn5
            other sequences; transposons.
REFERENCE   1
  AUTHORS   Reznikoff,W.S. and Naumann,T.A.
  TITLE     Mutant tn5 transposase enzymes and method for their use
  JOURNAL   Patent: WO 0109363-A 4 08-FEB-2001;
            WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Transposon Tn5"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:2411"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 995
BD064203
LOCUS       BD064203                  19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  System for in vitro transposition using modified TN5 transposase.
ACCESSION   BD064203
VERSION     BD064203.1  GI:22609806
KEYWORDS    JP 2001507565-A/6.
SOURCE      Conus quercinus
  ORGANISM  Conus quercinus
            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
            Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
            Neogastropoda; Conoidea; Conidae; Conus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Reznikoff,W.S., Goryshin,I.Y. and Zhou,H.
  TITLE     System for in vitro transposition using modified TN5 transposase
  JOURNAL   Patent: JP 2001507565-A 6 12-JUN-2001;
            WISCONSIN ALUMNI RESEARCH FOUNDATION
COMMENT     PN   JP 2001507565-A/6
            PD   12-JUN-2001
            PF   09-SEP-1997 JP 1998512997
            PR   09-SEP-1996 US    08/814877,02-MAY-1997 US    08/850880 PI
            WILLIAM S REZNIKOFF,IGOR YU GORYSHIN,HONG ZHOU PC
            C12N15/55,C12N9/22,C12N15/90,C12N15/85
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc= Tn5 wild inner end
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Conus quercinus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:101313"

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 996
AR029886
LOCUS       AR029886                  14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 75 from patent US 5861244.
ACCESSION   AR029886
VERSION     AR029886.1  GI:5943100
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 75 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 997
AR029887/c
LOCUS       AR029887                  14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 76 from patent US 5861244.
ACCESSION   AR029887
VERSION     AR029887.1  GI:5943101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 76 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 998
BD132850/c
LOCUS       BD132850                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Methods of nucleic acid detection.
ACCESSION   BD132850
VERSION     BD132850.1  GI:23227795
KEYWORDS    JP 2002509443-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
  TITLE     Methods of nucleic acid detection
  JOURNAL   Patent: JP 2002509443-A 1 26-MAR-2002;
            GEN PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002509443-A/1
            PD   26-MAR-2002
            PF   30-OCT-1998 JP 1999526687
            PR   31-OCT-1997 US    60/063969
            PI   WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
            C12Q1/68
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 999
BD176795
LOCUS       BD176795                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176795
VERSION     BD176795.1  GI:29122507
KEYWORDS    WO 02074951-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 42 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/42
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1000
BD176803/c
LOCUS       BD176803                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176803
VERSION     BD176803.1  GI:29122515
KEYWORDS    WO 02074951-A/50.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 50 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/50
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
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            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 1001
BD176804/c
LOCUS       BD176804                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176804
VERSION     BD176804.1  GI:29122516
KEYWORDS    WO 02074951-A/51.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 51 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/51
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 1002
BD237464
LOCUS       BD237464                  14 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof.
ACCESSION   BD237464
VERSION     BD237464.1  GI:33047234
KEYWORDS    JP 2002534434-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Dale,R.M.K., Gatton,S.L. and Arrow,A.
  TITLE     Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof
  JOURNAL   Patent: JP 2002534434-A 2 15-OCT-2002;
            OLIGOS ETC INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002534434-A/2
            PD   15-OCT-2002
            PF   16-DEC-1999 JP 2000592300
            PR   30-DEC-1998 US    09/223498,19-JUL-1999 US    09/356069 PI
            RODERIC M K DALE,STEVEN L GATTON,AMY ARROW
            PC   C07H21/00,A61K9/127,A61K9/50,A61K31/7088,A61K47/44,A61K48/00,
            PC   A61P3/00,
            PC   A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
            PC   C12N5/10,
            PC   C12N15/09,C12N15/00,C12N5/00
            CC   Nucleic acid having blocked terminals modified with an acid-
            CC          stable
            CC   skeleton and therapeutic method thereof
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1003
CQ827692
LOCUS       CQ827692                  14 bp    DNA     linear   PAT 29-JUN-2004
DEFINITION  Sequence 129 from Patent WO2004050918.
ACCESSION   CQ827692
VERSION     CQ827692.1  GI:49456142
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ruan,Y. and Wei,C.
  TITLE     Method to generate or determine nucleic acid tags corresponding to
            the terminal ends of dna molecules using sequence analysis of gene
            expression (terminal sage)
  JOURNAL   Patent: WO 2004050918-A 129 17-JUN-2004;
            Agency for Science, Technology and Research (SG)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1004
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LOCUS       AR222460                  14 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 20 from patent US 6429300.
ACCESSION   AR222460
VERSION     AR222460.1  GI:23329991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 20 06-AUG-2002;
FEATURES             Location/Qualifiers
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1005
AR364948/c
LOCUS       AR364948                  14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 4 from patent US 5453496.
ACCESSION   AR364948
VERSION     AR364948.1  GI:34428168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 4 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 1006
AR364949
LOCUS       AR364949                  14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 5 from patent US 5453496.
ACCESSION   AR364949
VERSION     AR364949.1  GI:34428169
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 5 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1007
AX048406/c
LOCUS       AX048406                  14 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 5 from Patent WO0071747.
ACCESSION   AX048406
VERSION     AX048406.1  GI:12225570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 5 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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  Best Local Similarity   92.3%;  Pred. No. 1.1e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 1008
AX827014
LOCUS       AX827014                  14 bp    RNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 11 from Patent EP1344835.
ACCESSION   AX827014
VERSION     AX827014.1  GI:39837221
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
            Liu,D.
  TITLE     Real-time nucleic acid detection processes and compositions
  JOURNAL   Patent: EP 1344835-A 11 17-SEP-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 1009
AX839906
LOCUS       AX839906                  14 bp    RNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 11 from Patent EP1348713.
ACCESSION   AX839906
VERSION     AX839906.1  GI:39978437
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Stavrianopoulos,J.G. and Rabbani,E.
  TITLE     Labeling reagents and labeled tabeled targets, target labeling
            processes and other processes for using same in nucleic acid
            determinations and analyses
  JOURNAL   Patent: EP 1348713-A 11 01-OCT-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1010
BD084127
LOCUS       BD084127                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084127
VERSION     BD084127.1  GI:22629737
KEYWORDS    JP 2001525663-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 15 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/15
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
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                     /db_xref="taxon:9606"

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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 1011
BD096963/c
LOCUS       BD096963                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096963
VERSION     BD096963.1  GI:22642551
KEYWORDS    JP 2001346579-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 2 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/2
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
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            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 1012
BD096965/c
LOCUS       BD096965                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096965
VERSION     BD096965.1  GI:22642553
KEYWORDS    JP 2001346579-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 4 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/4
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
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            FT   modified_base   1.
FEATURES             Location/Qualifiers
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  Query Match              0.3%;  Score 11.4;  DB 1;  Length 14;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 754 summaries

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SUMMARIES

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76		16	0.4	20	1	AL587727	ACCESSION:AL587727
77		16	0.4	20	1	CA853586	ACCESSION:CA853586
78		16	0.4	20	1	CF282002	ACCESSION:CF282002
79		16	0.4	20	1	CF297010	ACCESSION:CF297010
80		16	0.4	20	1	CF318278	ACCESSION:CF318278
81		16	0.4	20	1	CF320843	ACCESSION:CF320843
82	c	16	0.4	20	1	CF331733	ACCESSION:CF331733
83		16	0.4	20	1	CF333052	ACCESSION:CF333052
84		16	0.4	20	1	CF336815	ACCESSION:CF336815
85		16	0.4	20	1	AZ486787	ACCESSION:AZ486787
86	c	16	0.4	20	1	AZ579178	ACCESSION:AZ579178
87	c	16	0.4	20	1	AZ633741	ACCESSION:AZ633741
88		15.8	0.4	19	1	CF329136	ACCESSION:CF329136
89		15.8	0.4	19	1	AZ401252	ACCESSION:AZ401252
90	c	15.8	0.4	19	1	AZ401252	ACCESSION:AZ401252
91		15.8	0.4	19	1	AZ489586	ACCESSION:AZ489586
92		15.8	0.4	19	1	AZ510952	ACCESSION:AZ510952
93		15.8	0.4	19	1	AZ630416	ACCESSION:AZ630416
94	c	15.8	0.4	19	1	AZ630416	ACCESSION:AZ630416
95		15.8	0.4	19	1	AZ645841	ACCESSION:AZ645841
96	c	15.8	0.4	19	1	AZ650252	ACCESSION:AZ650252
97	c	15.8	0.4	19	1	AZ775624	ACCESSION:AZ775624
98		15.6	0.4	23	1	AZ862224	ACCESSION:AZ862224
99		15.4	0.4	17	1	AW246446	ACCESSION:AW246446
100		15.4	0.4	18	1	CF302409	ACCESSION:CF302409
101	c	15.4	0.4	18	1	CR786637	ACCESSION:CR786637
102	c	15.4	0.4	19	1	AZ450180	ACCESSION:AZ450180
103		15.4	0.4	19	1	AZ513919	ACCESSION:AZ513919
104		15	0.3	15	1	AJ690565	ACCESSION:AJ690565
105	c	15	0.3	15	1	BE230585	ACCESSION:BE230585
106		15	0.3	15	1	BQ582543	ACCESSION:BQ582543

	107	15	0.3	15	1	BQ585820	ACCESSION:BQ585820
	108	15	0.3	15	1	BQ590410	ACCESSION:BQ590410
	109	15	0.3	15	1	BQ590656	ACCESSION:BQ590656
	110	15	0.3	15	1	BQ591170	ACCESSION:BQ591170
	111	15	0.3	15	1	BQ591178	ACCESSION:BQ591178
	112	15	0.3	15	1	BQ591223	ACCESSION:BQ591223
	113	15	0.3	15	1	BQ594689	ACCESSION:BQ594689
	114	15	0.3	15	1	CF277319	ACCESSION:CF277319
	115	15	0.3	15	1	CF281923	ACCESSION:CF281923
	116	15	0.3	15	1	CF290920	ACCESSION:CF290920
	117	15	0.3	15	1	CF291029	ACCESSION:CF291029
	118	15	0.3	15	1	CF291103	ACCESSION:CF291103
	119	15	0.3	15	1	CF291717	ACCESSION:CF291717
	120	15	0.3	15	1	CF291798	ACCESSION:CF291798
	121	15	0.3	15	1	CF292458	ACCESSION:CF292458
	122	15	0.3	15	1	CF292461	ACCESSION:CF292461
	123	15	0.3	15	1	CF296652	ACCESSION:CF296652
	124	15	0.3	15	1	CF298148	ACCESSION:CF298148
	125	15	0.3	15	1	CF298630	ACCESSION:CF298630
	126	15	0.3	15	1	CF298733	ACCESSION:CF298733
	127	15	0.3	15	1	CF298805	ACCESSION:CF298805
	128	15	0.3	15	1	CF298889	ACCESSION:CF298889
	129	15	0.3	15	1	CF299602	ACCESSION:CF299602
	130	15	0.3	15	1	CF299608	ACCESSION:CF299608
	131	15	0.3	15	1	CF300121	ACCESSION:CF300121
	132	15	0.3	15	1	CF300361	ACCESSION:CF300361
	133	15	0.3	15	1	CF300992	ACCESSION:CF300992
	134	15	0.3	15	1	CF302034	ACCESSION:CF302034
	135	15	0.3	15	1	CF302124	ACCESSION:CF302124
	136	15	0.3	15	1	CF302182	ACCESSION:CF302182
	137	15	0.3	15	1	CF307923	ACCESSION:CF307923
	138	15	0.3	15	1	CF311159	ACCESSION:CF311159
	139	15	0.3	15	1	CF311907	ACCESSION:CF311907
	140	15	0.3	15	1	CF313319	ACCESSION:CF313319
c	141	15	0.3	15	1	CF313320	ACCESSION:CF313320
c	142	15	0.3	15	1	CF316251	ACCESSION:CF316251
	143	15	0.3	15	1	CF318035	ACCESSION:CF318035
	144	15	0.3	15	1	CF327434	ACCESSION:CF327434
	145	15	0.3	15	1	CF329379	ACCESSION:CF329379
	146	15	0.3	15	1	CF330195	ACCESSION:CF330195
	147	15	0.3	15	1	CF330668	ACCESSION:CF330668
	148	15	0.3	15	1	CF332178	ACCESSION:CF332178
	149	15	0.3	15	1	CF336202	ACCESSION:CF336202
c	150	15	0.3	15	1	CN751062	ACCESSION:CN751062
c	151	15	0.3	15	1	CN752390	ACCESSION:CN752390
c	152	15	0.3	15	1	CR547282	ACCESSION:CR547282
	153	15	0.3	16	1	BQ590166	ACCESSION:BQ590166
	154	15	0.3	16	1	BQ590507	ACCESSION:BQ590507
c	155	15	0.3	16	1	BQ592600	ACCESSION:BQ592600
	156	15	0.3	16	1	BQ592965	ACCESSION:BQ592965
	157	15	0.3	16	1	BQ595369	ACCESSION:BQ595369
c	158	15	0.3	16	1	BQ595717	ACCESSION:BQ595717
	159	15	0.3	16	1	CF279325	ACCESSION:CF279325
	160	15	0.3	16	1	CF296130	ACCESSION:CF296130
	161	15	0.3	16	1	CF311057	ACCESSION:CF311057
	162	15	0.3	16	1	CF314013	ACCESSION:CF314013
	163	15	0.3	16	1	CF314377	ACCESSION:CF314377
	164	15	0.3	16	1	CF315789	ACCESSION:CF315789
	165	15	0.3	16	1	CF316056	ACCESSION:CF316056
	166	15	0.3	16	1	CF317718	ACCESSION:CF317718
	167	15	0.3	16	1	CF320356	ACCESSION:CF320356
	168	15	0.3	16	1	CF327722	ACCESSION:CF327722
	169	15	0.3	16	1	CF329320	ACCESSION:CF329320
c	170	15	0.3	16	1	CF333386	ACCESSION:CF333386
c	171	15	0.3	16	1	CR786853	ACCESSION:CR786853
	172	15	0.3	17	1	BQ590128	ACCESSION:BQ590128
c	173	15	0.3	17	1	BQ590687	ACCESSION:BQ590687
	174	15	0.3	17	1	BQ591177	ACCESSION:BQ591177
	175	15	0.3	17	1	BQ591181	ACCESSION:BQ591181
	176	15	0.3	17	1	CF290854	ACCESSION:CF290854
	177	15	0.3	17	1	CF294668	ACCESSION:CF294668
	178	15	0.3	17	1	CF295988	ACCESSION:CF295988
	179	15	0.3	17	1	CF298589	ACCESSION:CF298589
	180	15	0.3	17	1	CF299997	ACCESSION:CF299997
	181	15	0.3	17	1	CF302447	ACCESSION:CF302447
	182	15	0.3	17	1	CF310219	ACCESSION:CF310219
	183	15	0.3	17	1	CF311499	ACCESSION:CF311499
	184	15	0.3	17	1	CF313013	ACCESSION:CF313013
	185	15	0.3	17	1	CF319075	ACCESSION:CF319075
	186	15	0.3	17	1	CF334566	ACCESSION:CF334566
	187	15	0.3	17	1	CF336950	ACCESSION:CF336950
c	188	15	0.3	18	1	AL038692	ACCESSION:AL038692
	189	15	0.3	18	1	BQ582676	ACCESSION:BQ582676
	190	15	0.3	18	1	BQ590027	ACCESSION:BQ590027
	191	15	0.3	18	1	CF277873	ACCESSION:CF277873
	192	15	0.3	18	1	CF297446	ACCESSION:CF297446
	193	15	0.3	18	1	CF298591	ACCESSION:CF298591
	194	15	0.3	18	1	CF299027	ACCESSION:CF299027
	195	15	0.3	18	1	CF299674	ACCESSION:CF299674
	196	15	0.3	18	1	CF300456	ACCESSION:CF300456
	197	15	0.3	18	1	CF301057	ACCESSION:CF301057
	198	15	0.3	18	1	CF301151	ACCESSION:CF301151
	199	15	0.3	18	1	CF301325	ACCESSION:CF301325
	200	15	0.3	18	1	CF301359	ACCESSION:CF301359
	201	15	0.3	18	1	CF301760	ACCESSION:CF301760
	202	15	0.3	18	1	CF309376	ACCESSION:CF309376
	203	15	0.3	18	1	CF320046	ACCESSION:CF320046
	204	15	0.3	18	1	CF320418	ACCESSION:CF320418
	205	15	0.3	18	1	CF329285	ACCESSION:CF329285
	206	15	0.3	18	1	CF329484	ACCESSION:CF329484
c	207	15	0.3	18	1	CF329485	ACCESSION:CF329485
c	208	15	0.3	32	1	BI259338	ACCESSION:BI259338
	209	14.8	0.3	18	1	AW248796	ACCESSION:AW248796
	210	14.8	0.3	18	1	BM658677	ACCESSION:BM658677
c	211	14.8	0.3	21	1	BX548564	ACCESSION:BX548564
	212	14.8	0.3	21	1	AZ625662	ACCESSION:AZ625662
	213	14.6	0.3	22	1	AZ316361	ACCESSION:AZ316361
	214	14.2	0.3	19	1	AZ360314	ACCESSION:AZ360314
	215	14.2	0.3	19	1	AZ764517	ACCESSION:AZ764517
c	216	14.2	0.3	20	1	AL587727	ACCESSION:AL587727
	217	14	0.3	14	1	BQ586422	ACCESSION:BQ586422
	218	14	0.3	14	1	BQ587890	ACCESSION:BQ587890
	219	14	0.3	14	1	BQ589191	ACCESSION:BQ589191
	220	14	0.3	14	1	BQ590242	ACCESSION:BQ590242
	221	14	0.3	14	1	BQ590261	ACCESSION:BQ590261
	222	14	0.3	14	1	BQ591168	ACCESSION:BQ591168
	223	14	0.3	14	1	BQ591176	ACCESSION:BQ591176
	224	14	0.3	14	1	BQ591207	ACCESSION:BQ591207
	225	14	0.3	14	1	BQ591380	ACCESSION:BQ591380
	226	14	0.3	14	1	BQ591482	ACCESSION:BQ591482
	227	14	0.3	14	1	BQ593052	ACCESSION:BQ593052
	228	14	0.3	14	1	CF277935	ACCESSION:CF277935
	229	14	0.3	14	1	CF278001	ACCESSION:CF278001
	230	14	0.3	14	1	CF278452	ACCESSION:CF278452
	231	14	0.3	14	1	CF279473	ACCESSION:CF279473
	232	14	0.3	14	1	CF279992	ACCESSION:CF279992
	233	14	0.3	14	1	CF281958	ACCESSION:CF281958
	234	14	0.3	14	1	CF282350	ACCESSION:CF282350
	235	14	0.3	14	1	CF294449	ACCESSION:CF294449
	236	14	0.3	14	1	CF295570	ACCESSION:CF295570
	237	14	0.3	14	1	CF296120	ACCESSION:CF296120
	238	14	0.3	14	1	CF297969	ACCESSION:CF297969
	239	14	0.3	14	1	CF298109	ACCESSION:CF298109
	240	14	0.3	14	1	CF299368	ACCESSION:CF299368
	241	14	0.3	14	1	CF300542	ACCESSION:CF300542
	242	14	0.3	14	1	CF301020	ACCESSION:CF301020
	243	14	0.3	14	1	CF301083	ACCESSION:CF301083
	244	14	0.3	14	1	CF301380	ACCESSION:CF301380
	245	14	0.3	14	1	CF302675	ACCESSION:CF302675
	246	14	0.3	14	1	CF302846	ACCESSION:CF302846
	247	14	0.3	14	1	CF308006	ACCESSION:CF308006
	248	14	0.3	14	1	CF308220	ACCESSION:CF308220
	249	14	0.3	14	1	CF308445	ACCESSION:CF308445
	250	14	0.3	14	1	CF308918	ACCESSION:CF308918
	251	14	0.3	14	1	CF310714	ACCESSION:CF310714
	252	14	0.3	14	1	CF311201	ACCESSION:CF311201

	253	14	0.3	14	1	CF311813	ACCESSION:CF311813
	254	14	0.3	14	1	CF318323	ACCESSION:CF318323
	255	14	0.3	14	1	CF318450	ACCESSION:CF318450
	256	14	0.3	14	1	CF319826	ACCESSION:CF319826
	257	14	0.3	14	1	CF321246	ACCESSION:CF321246
	258	14	0.3	14	1	CF327097	ACCESSION:CF327097
	259	14	0.3	14	1	CF327119	ACCESSION:CF327119
	260	14	0.3	14	1	CF327203	ACCESSION:CF327203
	261	14	0.3	14	1	CF327445	ACCESSION:CF327445
	262	14	0.3	14	1	CF328490	ACCESSION:CF328490
	263	14	0.3	14	1	CF328540	ACCESSION:CF328540
	264	14	0.3	14	1	CF328669	ACCESSION:CF328669
	265	14	0.3	14	1	CF328994	ACCESSION:CF328994
	266	14	0.3	14	1	CF329217	ACCESSION:CF329217
c	267	14	0.3	14	1	CF329990	ACCESSION:CF329990
	268	14	0.3	14	1	CF330784	ACCESSION:CF330784
	269	14	0.3	14	1	CF331272	ACCESSION:CF331272
	270	14	0.3	14	1	CF331861	ACCESSION:CF331861
	271	14	0.3	14	1	CF333214	ACCESSION:CF333214
c	272	14	0.3	14	1	CF333215	ACCESSION:CF333215
	273	14	0.3	14	1	CF333399	ACCESSION:CF333399
	274	14	0.3	14	1	CF334202	ACCESSION:CF334202
	275	14	0.3	14	1	CF334281	ACCESSION:CF334281
	276	14	0.3	14	1	CF334290	ACCESSION:CF334290
	277	14	0.3	14	1	CF335781	ACCESSION:CF335781
	278	14	0.3	14	1	CF336094	ACCESSION:CF336094
	279	14	0.3	14	1	CF336106	ACCESSION:CF336106
	280	14	0.3	14	1	CF336287	ACCESSION:CF336287
	281	14	0.3	14	1	CF336906	ACCESSION:CF336906
	282	14	0.3	15	1	AW250872	ACCESSION:AW250872
	283	14	0.3	15	1	CF295100	ACCESSION:CF295100
	284	14	0.3	15	1	CF301470	ACCESSION:CF301470
c	285	14	0.3	15	1	CR789161	ACCESSION:CR789161
c	286	14	0.3	16	1	CF291803	ACCESSION:CF291803
	287	14	0.3	17	1	BQ591588	ACCESSION:BQ591588
c	288	13.8	0.3	17	1	AW245664	ACCESSION:AW245664
c	289	13.8	0.3	17	1	AW248574	ACCESSION:AW248574
c	290	13.8	0.3	18	1	CF301359	ACCESSION:CF301359
	291	13.8	0.3	19	1	CF309858	ACCESSION:CF309858
c	292	13.8	0.3	20	1	AZ486787	ACCESSION:AZ486787
	293	13.6	0.3	20	1	AZ316368	ACCESSION:AZ316368
c	294	13.6	0.3	20	1	CF319428	ACCESSION:CF319428
c	295	13.4	0.3	15	1	CF301470	ACCESSION:CF301470
	296	13.4	0.3	15	1	CR789161	ACCESSION:CR789161
c	297	13.4	0.3	15	1	CF290849	ACCESSION:CF290849
c	298	13.4	0.3	15	1	CF291030	ACCESSION:CF291030
	299	13.4	0.3	16	1	AW245338	ACCESSION:AW245338
	300	13.4	0.3	16	1	CF317778	ACCESSION:CF317778
c	301	13.4	0.3	17	1	CF291802	ACCESSION:CF291802
	302	13.4	0.3	17	1	AW248574	ACCESSION:AW248574
c	303	13.4	0.3	19	1	CF291899	ACCESSION:CF291899
c	304	13.4	0.3	19	1	CF292072	ACCESSION:CF292072
c	305	13.4	0.3	19	1	CF292144	ACCESSION:CF292144
	306	13.4	0.3	19	1	CF310688	ACCESSION:CF310688
c	307	13.4	0.3	20	1	CF333052	ACCESSION:CF333052
	308	13.2	0.3	18	1	AL038692	ACCESSION:AL038692
c	309	13.2	0.3	18	1	BQ582676	ACCESSION:BQ582676
c	310	13.2	0.3	18	1	BQ590027	ACCESSION:BQ590027
c	311	13.2	0.3	18	1	CF277873	ACCESSION:CF277873
c	312	13.2	0.3	18	1	CF297446	ACCESSION:CF297446
c	313	13.2	0.3	18	1	CF299027	ACCESSION:CF299027
c	314	13.2	0.3	18	1	CF299674	ACCESSION:CF299674
c	315	13.2	0.3	18	1	CF301057	ACCESSION:CF301057
c	316	13.2	0.3	18	1	CF301325	ACCESSION:CF301325
c	317	13.2	0.3	18	1	CF301760	ACCESSION:CF301760
c	318	13.2	0.3	18	1	CF329285	ACCESSION:CF329285
c	319	13.2	0.3	19	1	CF293167	ACCESSION:CF293167
c	320	13.2	0.3	19	1	CF298396	ACCESSION:CF298396
c	321	13.2	0.3	19	1	CF302456	ACCESSION:CF302456
c	322	13.2	0.3	19	1	CF309821	ACCESSION:CF309821
c	323	13.2	0.3	19	1	CF311778	ACCESSION:CF311778
c	324	13.2	0.3	19	1	CF331361	ACCESSION:CF331361
c	325	13.2	0.3	19	1	CF335293	ACCESSION:CF335293
c	326	13.2	0.3	19	1	CN545923	ACCESSION:CN545923
c	327	13.2	0.3	19	1	AZ513919	ACCESSION:AZ513919
c	328	13.2	0.3	20	1	AL587572	ACCESSION:AL587572
c	329	13.2	0.3	20	1	CF316662	ACCESSION:CF316662
	330	13.2	0.3	20	1	AZ821905	ACCESSION:AZ821905
c	331	13.2	0.3	20	1	AJ666275	ACCESSION:AJ666275
	332	13.2	0.3	20	1	AL038460	ACCESSION:AL038460
c	333	13.2	0.3	20	1	CA853586	ACCESSION:CA853586
c	334	13.2	0.3	20	1	CF282002	ACCESSION:CF282002
c	335	13.2	0.3	20	1	CF318278	ACCESSION:CF318278
c	336	13.2	0.3	20	1	CF320843	ACCESSION:CF320843
	337	13.2	0.3	20	1	AZ579178	ACCESSION:AZ579178
	338	13.2	0.3	20	1	AZ633741	ACCESSION:AZ633741
c	339	13.2	0.3	21	1	CF276747	ACCESSION:CF276747
	340	13.2	0.3	22	1	AZ843648	ACCESSION:AZ843648
c	341	13.2	0.3	23	1	CF318266	ACCESSION:CF318266
c	342	13.2	0.3	25	1	CF308158	ACCESSION:CF308158
c	343	13	0.3	13	1	BQ583549	ACCESSION:BQ583549
	344	13	0.3	13	1	BQ589180	ACCESSION:BQ589180
c	345	13	0.3	13	1	BQ590337	ACCESSION:BQ590337
	346	13	0.3	13	1	CF278426	ACCESSION:CF278426
	347	13	0.3	13	1	CF280420	ACCESSION:CF280420
	348	13	0.3	13	1	CF280707	ACCESSION:CF280707
	349	13	0.3	13	1	CF280757	ACCESSION:CF280757
	350	13	0.3	13	1	CF282369	ACCESSION:CF282369
	351	13	0.3	13	1	CF290970	ACCESSION:CF290970
c	352	13	0.3	13	1	CF290971	ACCESSION:CF290971
	353	13	0.3	13	1	CF291011	ACCESSION:CF291011
	354	13	0.3	13	1	CF291060	ACCESSION:CF291060
c	355	13	0.3	13	1	CF291061	ACCESSION:CF291061
	356	13	0.3	13	1	CF291167	ACCESSION:CF291167
	357	13	0.3	13	1	CF291214	ACCESSION:CF291214
	358	13	0.3	13	1	CF291427	ACCESSION:CF291427
	359	13	0.3	13	1	CF291469	ACCESSION:CF291469
	360	13	0.3	13	1	CF291479	ACCESSION:CF291479
	361	13	0.3	13	1	CF291514	ACCESSION:CF291514
c	362	13	0.3	13	1	CF291515	ACCESSION:CF291515
	363	13	0.3	13	1	CF291596	ACCESSION:CF291596
c	364	13	0.3	13	1	CF291597	ACCESSION:CF291597
	365	13	0.3	13	1	CF291726	ACCESSION:CF291726
c	366	13	0.3	13	1	CF291903	ACCESSION:CF291903
	367	13	0.3	13	1	CF298590	ACCESSION:CF298590
	368	13	0.3	13	1	CF298592	ACCESSION:CF298592
	369	13	0.3	13	1	CF298736	ACCESSION:CF298736
	370	13	0.3	13	1	CF298764	ACCESSION:CF298764
	371	13	0.3	13	1	CF298795	ACCESSION:CF298795
	372	13	0.3	13	1	CF298908	ACCESSION:CF298908
	373	13	0.3	13	1	CF299133	ACCESSION:CF299133
	374	13	0.3	13	1	CF299359	ACCESSION:CF299359
	375	13	0.3	13	1	CF299937	ACCESSION:CF299937
	376	13	0.3	13	1	CF300118	ACCESSION:CF300118
	377	13	0.3	13	1	CF300587	ACCESSION:CF300587
	378	13	0.3	13	1	CF300658	ACCESSION:CF300658
	379	13	0.3	13	1	CF300929	ACCESSION:CF300929
	380	13	0.3	13	1	CF301247	ACCESSION:CF301247
	381	13	0.3	13	1	CF301286	ACCESSION:CF301286
	382	13	0.3	13	1	CF302158	ACCESSION:CF302158
	383	13	0.3	13	1	CF302830	ACCESSION:CF302830
	384	13	0.3	13	1	CF302898	ACCESSION:CF302898
	385	13	0.3	13	1	CF310516	ACCESSION:CF310516
c	386	13	0.3	13	1	CF310517	ACCESSION:CF310517
	387	13	0.3	13	1	CF312721	ACCESSION:CF312721
	388	13	0.3	13	1	CF313171	ACCESSION:CF313171
	389	13	0.3	13	1	CF314239	ACCESSION:CF314239
	390	13	0.3	13	1	CF314874	ACCESSION:CF314874
	391	13	0.3	13	1	CF315395	ACCESSION:CF315395
	392	13	0.3	13	1	CF316439	ACCESSION:CF316439
c	393	13	0.3	13	1	CF316440	ACCESSION:CF316440
	394	13	0.3	13	1	CF316637	ACCESSION:CF316637
	395	13	0.3	13	1	CF318290	ACCESSION:CF318290
	396	13	0.3	13	1	CF319066	ACCESSION:CF319066
	397	13	0.3	13	1	CF319531	ACCESSION:CF319531
c	398	13	0.3	13	1	CF319532	ACCESSION:CF319532

c	399	13	0.3	13	1	CF319919	ACCESSION:CF319919
	400	13	0.3	13	1	CF320017	ACCESSION:CF320017
c	401	13	0.3	13	1	CF320018	ACCESSION:CF320018
	402	13	0.3	13	1	CF320143	ACCESSION:CF320143
	403	13	0.3	13	1	CF320938	ACCESSION:CF320938
	404	13	0.3	13	1	CF326844	ACCESSION:CF326844
	405	13	0.3	13	1	CF327070	ACCESSION:CF327070
	406	13	0.3	13	1	CF327339	ACCESSION:CF327339
c	407	13	0.3	13	1	CF327340	ACCESSION:CF327340
	408	13	0.3	13	1	CF327576	ACCESSION:CF327576
	409	13	0.3	13	1	CF327888	ACCESSION:CF327888
	410	13	0.3	13	1	CF327939	ACCESSION:CF327939
	411	13	0.3	13	1	CF328153	ACCESSION:CF328153
	412	13	0.3	13	1	CF328228	ACCESSION:CF328228
	413	13	0.3	13	1	CF328807	ACCESSION:CF328807
	414	13	0.3	13	1	CF329075	ACCESSION:CF329075
c	415	13	0.3	13	1	CF329076	ACCESSION:CF329076
	416	13	0.3	13	1	CF329417	ACCESSION:CF329417
	417	13	0.3	13	1	CF329460	ACCESSION:CF329460
c	418	13	0.3	13	1	CF329729	ACCESSION:CF329729
	419	13	0.3	13	1	CF329800	ACCESSION:CF329800
c	420	13	0.3	13	1	CF329801	ACCESSION:CF329801
	421	13	0.3	13	1	CF329869	ACCESSION:CF329869
	422	13	0.3	13	1	CF329946	ACCESSION:CF329946
	423	13	0.3	13	1	CF329988	ACCESSION:CF329988
	424	13	0.3	13	1	CF330023	ACCESSION:CF330023
c	425	13	0.3	13	1	CF330725	ACCESSION:CF330725
	426	13	0.3	13	1	CF331041	ACCESSION:CF331041
	427	13	0.3	13	1	CF331266	ACCESSION:CF331266
c	428	13	0.3	13	1	CF331273	ACCESSION:CF331273
	429	13	0.3	13	1	CF331903	ACCESSION:CF331903
	430	13	0.3	13	1	CF332079	ACCESSION:CF332079
	431	13	0.3	13	1	CF332695	ACCESSION:CF332695
c	432	13	0.3	13	1	CF332696	ACCESSION:CF332696
	433	13	0.3	13	1	CF333486	ACCESSION:CF333486
	434	13	0.3	13	1	CF333972	ACCESSION:CF333972
c	435	13	0.3	13	1	CF333973	ACCESSION:CF333973
	436	13	0.3	13	1	CF334347	ACCESSION:CF334347
	437	13	0.3	13	1	CF337022	ACCESSION:CF337022
	438	13	0.3	13	1	CN546046	ACCESSION:CN546046
c	439	13	0.3	13	1	CN752228	ACCESSION:CN752228
c	440	13	0.3	13	1	CN752875	ACCESSION:CN752875
c	441	13	0.3	13	1	CN753196	ACCESSION:CN753196
	442	13	0.3	14	1	BQ591949	ACCESSION:BQ591949
	443	13	0.3	14	1	CF330198	ACCESSION:CF330198
	444	13	0.3	15	1	AW248644	ACCESSION:AW248644
	445	13	0.3	15	1	AW248954	ACCESSION:AW248954
	446	13	0.3	15	1	AW249757	ACCESSION:AW249757
c	447	13	0.3	15	1	CF543203	ACCESSION:CF543203
	448	13	0.3	16	1	CF312586	ACCESSION:CF312586
	449	13	0.3	17	1	AW245664	ACCESSION:AW245664
c	450	12.8	0.3	16	1	CF317778	ACCESSION:CF317778
c	451	12.8	0.3	16	1	AI684114	ACCESSION:AI684114
c	452	12.8	0.3	16	1	AI798250	ACCESSION:AI798250
	453	12.8	0.3	16	1	AW248540	ACCESSION:AW248540
c	454	12.8	0.3	16	1	CF319827	ACCESSION:CF319827
c	455	12.8	0.3	16	1	AJ592922	ACCESSION:AJ592922
c	456	12.8	0.3	17	1	CF299997	ACCESSION:CF299997
c	457	12.8	0.3	17	1	CF302447	ACCESSION:CF302447
c	458	12.8	0.3	17	1	CF313013	ACCESSION:CF313013
c	459	12.8	0.3	18	1	CF300456	ACCESSION:CF300456
c	460	12.8	0.3	18	1	CF320418	ACCESSION:CF320418
c	461	12.8	0.3	19	1	CF329136	ACCESSION:CF329136
c	462	12.8	0.3	21	1	CF309614	ACCESSION:CF309614
	463	12.6	0.3	19	1	AZ450180	ACCESSION:AZ450180
c	464	12.6	0.3	20	1	AZ343730	ACCESSION:AZ343730
c	465	12.6	0.3	20	1	CF330490	ACCESSION:CF330490
c	466	12.4	0.3	14	1	CF301021	ACCESSION:CF301021
c	467	12.4	0.3	15	1	CF329379	ACCESSION:CF329379
	468	12.4	0.3	16	1	CF291803	ACCESSION:CF291803
	469	12.4	0.3	19	1	CF311668	ACCESSION:CF311668
	470	12.4	0.3	20	1	CF331733	ACCESSION:CF331733
c	471	12.2	0.3	17	1	CF298341	ACCESSION:CF298341
	472	12.2	0.3	17	1	BQ590687	ACCESSION:BQ590687
c	473	12.2	0.3	17	1	BQ591177	ACCESSION:BQ591177
c	474	12.2	0.3	17	1	BQ591181	ACCESSION:BQ591181
c	475	12.2	0.3	17	1	CF290854	ACCESSION:CF290854
c	476	12.2	0.3	17	1	CF298589	ACCESSION:CF298589
c	477	12.2	0.3	17	1	CF310219	ACCESSION:CF310219
c	478	12.2	0.3	17	1	CF311499	ACCESSION:CF311499
c	479	12.2	0.3	17	1	CF319075	ACCESSION:CF319075
c	480	12.2	0.3	17	1	CF334566	ACCESSION:CF334566
c	481	12.2	0.3	17	1	BQ591588	ACCESSION:BQ591588
c	482	12.2	0.3	18	1	CF302409	ACCESSION:CF302409
	483	12.2	0.3	18	1	CR786637	ACCESSION:CR786637
c	484	12.2	0.3	18	1	CF301151	ACCESSION:CF301151
c	485	12.2	0.3	18	1	CF309376	ACCESSION:CF309376
c	486	12.2	0.3	18	1	CF320046	ACCESSION:CF320046
c	487	12.2	0.3	18	1	CF329484	ACCESSION:CF329484
	488	12.2	0.3	18	1	CF329485	ACCESSION:CF329485
	489	12.2	0.3	19	1	AZ509929	ACCESSION:AZ509929
c	490	12.2	0.3	19	1	CF291665	ACCESSION:CF291665
c	491	12.2	0.3	20	1	CF336815	ACCESSION:CF336815
c	492	12.2	0.3	21	1	CF333393	ACCESSION:CF333393
c	493	12.2	0.3	22	1	TA211D06P	ACCESSION:AL478564
	494	12.2	0.3	22	1	TA303G05P	ACCESSION:AL497383
c	495	12	0.3	20	1	CF298018	ACCESSION:CF298018
c	496	11.8	0.3	15	1	AJ690565	ACCESSION:AJ690565
	497	11.8	0.3	15	1	BE230585	ACCESSION:BE230585
c	498	11.8	0.3	15	1	BQ582543	ACCESSION:BQ582543
c	499	11.8	0.3	15	1	BQ585820	ACCESSION:BQ585820
c	500	11.8	0.3	15	1	BQ590410	ACCESSION:BQ590410
c	501	11.8	0.3	15	1	BQ590656	ACCESSION:BQ590656
c	502	11.8	0.3	15	1	BQ591170	ACCESSION:BQ591170
c	503	11.8	0.3	15	1	BQ591178	ACCESSION:BQ591178
c	504	11.8	0.3	15	1	BQ591223	ACCESSION:BQ591223
c	505	11.8	0.3	15	1	BQ594689	ACCESSION:BQ594689
c	506	11.8	0.3	15	1	CF277319	ACCESSION:CF277319
c	507	11.8	0.3	15	1	CF281923	ACCESSION:CF281923
c	508	11.8	0.3	15	1	CF290920	ACCESSION:CF290920
c	509	11.8	0.3	15	1	CF291029	ACCESSION:CF291029
c	510	11.8	0.3	15	1	CF291103	ACCESSION:CF291103
c	511	11.8	0.3	15	1	CF291717	ACCESSION:CF291717
c	512	11.8	0.3	15	1	CF291798	ACCESSION:CF291798
c	513	11.8	0.3	15	1	CF292458	ACCESSION:CF292458
c	514	11.8	0.3	15	1	CF292461	ACCESSION:CF292461
c	515	11.8	0.3	15	1	CF298148	ACCESSION:CF298148
c	516	11.8	0.3	15	1	CF298630	ACCESSION:CF298630
c	517	11.8	0.3	15	1	CF298733	ACCESSION:CF298733
c	518	11.8	0.3	15	1	CF298805	ACCESSION:CF298805
c	519	11.8	0.3	15	1	CF298889	ACCESSION:CF298889
c	520	11.8	0.3	15	1	CF299602	ACCESSION:CF299602
c	521	11.8	0.3	15	1	CF299608	ACCESSION:CF299608
c	522	11.8	0.3	15	1	CF300121	ACCESSION:CF300121
c	523	11.8	0.3	15	1	CF300361	ACCESSION:CF300361
c	524	11.8	0.3	15	1	CF300992	ACCESSION:CF300992
c	525	11.8	0.3	15	1	CF302034	ACCESSION:CF302034
c	526	11.8	0.3	15	1	CF302124	ACCESSION:CF302124
c	527	11.8	0.3	15	1	CF302182	ACCESSION:CF302182
c	528	11.8	0.3	15	1	CF307923	ACCESSION:CF307923
c	529	11.8	0.3	15	1	CF311159	ACCESSION:CF311159
c	530	11.8	0.3	15	1	CF311907	ACCESSION:CF311907
c	531	11.8	0.3	15	1	CF313319	ACCESSION:CF313319
	532	11.8	0.3	15	1	CF313320	ACCESSION:CF313320
	533	11.8	0.3	15	1	CF316251	ACCESSION:CF316251
c	534	11.8	0.3	15	1	CF318035	ACCESSION:CF318035
c	535	11.8	0.3	15	1	CF327434	ACCESSION:CF327434
c	536	11.8	0.3	15	1	CF330195	ACCESSION:CF330195
c	537	11.8	0.3	15	1	CF330668	ACCESSION:CF330668
c	538	11.8	0.3	15	1	CF332178	ACCESSION:CF332178
c	539	11.8	0.3	15	1	CF336202	ACCESSION:CF336202
	540	11.8	0.3	15	1	CR547282	ACCESSION:CR547282
	541	11.8	0.3	15	1	CF291030	ACCESSION:CF291030
	542	11.8	0.3	15	1	CF543203	ACCESSION:CF543203
c	543	11.8	0.3	16	1	BQ590207	ACCESSION:BQ590207
c	544	11.8	0.3	16	1	CF318894	ACCESSION:CF318894

c 545	11.8	0.3	16	1	CF327923	ACCESSION:CF327923
c 546	11.8	0.3	16	1	CF328223	ACCESSION:CF328223
547	11.8	0.3	16	1	CR786609	ACCESSION:CR786609
c 548	11.8	0.3	16	1	BQ590166	ACCESSION:BQ590166
c 549	11.8	0.3	16	1	BQ590507	ACCESSION:BQ590507
550	11.8	0.3	16	1	BQ592600	ACCESSION:BQ592600
c 551	11.8	0.3	16	1	BQ592965	ACCESSION:BQ592965
c 552	11.8	0.3	16	1	BQ595369	ACCESSION:BQ595369
553	11.8	0.3	16	1	BQ595717	ACCESSION:BQ595717
c 554	11.8	0.3	16	1	CF279325	ACCESSION:CF279325
c 555	11.8	0.3	16	1	CF296130	ACCESSION:CF296130
c 556	11.8	0.3	16	1	CF311057	ACCESSION:CF311057
c 557	11.8	0.3	16	1	CF314013	ACCESSION:CF314013
c 558	11.8	0.3	16	1	CF314377	ACCESSION:CF314377
c 559	11.8	0.3	16	1	CF315789	ACCESSION:CF315789
c 560	11.8	0.3	16	1	CF316056	ACCESSION:CF316056
c 561	11.8	0.3	16	1	CF317718	ACCESSION:CF317718
c 562	11.8	0.3	16	1	CF320356	ACCESSION:CF320356
c 563	11.8	0.3	16	1	CF327722	ACCESSION:CF327722
c 564	11.8	0.3	16	1	CF329320	ACCESSION:CF329320
565	11.8	0.3	16	1	CF333386	ACCESSION:CF333386
566	11.8	0.3	16	1	CR786853	ACCESSION:CR786853
c 567	11.8	0.3	17	1	CF295807	ACCESSION:CF295807
c 568	11.8	0.3	17	1	CF297251	ACCESSION:CF297251
c 569	11.8	0.3	17	1	CF299639	ACCESSION:CF299639
c 570	11.8	0.3	17	1	BQ590128	ACCESSION:BQ590128
c 571	11.8	0.3	17	1	CF294668	ACCESSION:CF294668
c 572	11.8	0.3	17	1	CF295988	ACCESSION:CF295988
c 573	11.8	0.3	17	1	CF336950	ACCESSION:CF336950
574	11.8	0.3	18	1	AJ725584	ACCESSION:AJ725584
575	11.8	0.3	18	1	AL048754	ACCESSION:AL048754
c 576	11.8	0.3	18	1	CF298591	ACCESSION:CF298591
c 577	11.8	0.3	18	1	BM658677	ACCESSION:BM658677
c 578	11.8	0.3	19	1	CF325356	ACCESSION:CF325356
c 579	11.8	0.3	19	1	CF327587	ACCESSION:CF327587
c 580	11.8	0.3	19	1	CF300236	ACCESSION:CF300236
c 581	11.8	0.3	19	1	CF309636	ACCESSION:CF309636
c 582	11.8	0.3	19	1	CF319596	ACCESSION:CF319596
c 583	11.8	0.3	19	1	AZ645841	ACCESSION:AZ645841
584	11.8	0.3	19	1	AZ650252	ACCESSION:AZ650252
585	11.8	0.3	20	1	AZ579122	ACCESSION:AZ579122
c 586	11.8	0.3	20	1	CL680297	ACCESSION:CL680297
587	11.8	0.3	21	1	CF282313	ACCESSION:CF282313
c 588	11.8	0.3	21	1	AZ963501	ACCESSION:AZ963501
c 589	11.8	0.3	22	1	AZ310057	ACCESSION:AZ310057
590	11.4	0.3	13	1	BQ583549	ACCESSION:BQ583549
c 591	11.4	0.3	13	1	BQ589180	ACCESSION:BQ589180
592	11.4	0.3	13	1	BQ590337	ACCESSION:BQ590337
c 593	11.4	0.3	13	1	CF278426	ACCESSION:CF278426
c 594	11.4	0.3	13	1	CF280420	ACCESSION:CF280420
c 595	11.4	0.3	13	1	CF280707	ACCESSION:CF280707
c 596	11.4	0.3	13	1	CF280757	ACCESSION:CF280757
c 597	11.4	0.3	13	1	CF282369	ACCESSION:CF282369
c 598	11.4	0.3	13	1	CF290970	ACCESSION:CF290970
599	11.4	0.3	13	1	CF290971	ACCESSION:CF290971
c 600	11.4	0.3	13	1	CF291011	ACCESSION:CF291011
c 601	11.4	0.3	13	1	CF291060	ACCESSION:CF291060
602	11.4	0.3	13	1	CF291061	ACCESSION:CF291061
c 603	11.4	0.3	13	1	CF291167	ACCESSION:CF291167
c 604	11.4	0.3	13	1	CF291214	ACCESSION:CF291214
c 605	11.4	0.3	13	1	CF291427	ACCESSION:CF291427
c 606	11.4	0.3	13	1	CF291469	ACCESSION:CF291469
c 607	11.4	0.3	13	1	CF291479	ACCESSION:CF291479
c 608	11.4	0.3	13	1	CF291514	ACCESSION:CF291514
609	11.4	0.3	13	1	CF291515	ACCESSION:CF291515
c 610	11.4	0.3	13	1	CF291596	ACCESSION:CF291596
611	11.4	0.3	13	1	CF291597	ACCESSION:CF291597
c 612	11.4	0.3	13	1	CF291726	ACCESSION:CF291726
613	11.4	0.3	13	1	CF291903	ACCESSION:CF291903
c 614	11.4	0.3	13	1	CF298590	ACCESSION:CF298590
c 615	11.4	0.3	13	1	CF298592	ACCESSION:CF298592
c 616	11.4	0.3	13	1	CF298736	ACCESSION:CF298736
c 617	11.4	0.3	13	1	CF298764	ACCESSION:CF298764
c 618	11.4	0.3	13	1	CF298795	ACCESSION:CF298795
c 619	11.4	0.3	13	1	CF298908	ACCESSION:CF298908
c 620	11.4	0.3	13	1	CF299133	ACCESSION:CF299133
c 621	11.4	0.3	13	1	CF299359	ACCESSION:CF299359
c 622	11.4	0.3	13	1	CF299937	ACCESSION:CF299937
c 623	11.4	0.3	13	1	CF300118	ACCESSION:CF300118
c 624	11.4	0.3	13	1	CF300587	ACCESSION:CF300587
c 625	11.4	0.3	13	1	CF300658	ACCESSION:CF300658
c 626	11.4	0.3	13	1	CF300929	ACCESSION:CF300929
c 627	11.4	0.3	13	1	CF301247	ACCESSION:CF301247
c 628	11.4	0.3	13	1	CF301286	ACCESSION:CF301286
c 629	11.4	0.3	13	1	CF302158	ACCESSION:CF302158
c 630	11.4	0.3	13	1	CF302830	ACCESSION:CF302830
c 631	11.4	0.3	13	1	CF302898	ACCESSION:CF302898
c 632	11.4	0.3	13	1	CF310516	ACCESSION:CF310516
633	11.4	0.3	13	1	CF310517	ACCESSION:CF310517
c 634	11.4	0.3	13	1	CF312721	ACCESSION:CF312721
c 635	11.4	0.3	13	1	CF313171	ACCESSION:CF313171
c 636	11.4	0.3	13	1	CF314239	ACCESSION:CF314239
c 637	11.4	0.3	13	1	CF314874	ACCESSION:CF314874
c 638	11.4	0.3	13	1	CF315395	ACCESSION:CF315395
c 639	11.4	0.3	13	1	CF316439	ACCESSION:CF316439
640	11.4	0.3	13	1	CF316440	ACCESSION:CF316440
c 641	11.4	0.3	13	1	CF316637	ACCESSION:CF316637
c 642	11.4	0.3	13	1	CF318290	ACCESSION:CF318290
c 643	11.4	0.3	13	1	CF319066	ACCESSION:CF319066
c 644	11.4	0.3	13	1	CF319531	ACCESSION:CF319531
645	11.4	0.3	13	1	CF319532	ACCESSION:CF319532
646	11.4	0.3	13	1	CF319919	ACCESSION:CF319919
c 647	11.4	0.3	13	1	CF320017	ACCESSION:CF320017
648	11.4	0.3	13	1	CF320018	ACCESSION:CF320018
c 649	11.4	0.3	13	1	CF320143	ACCESSION:CF320143
c 650	11.4	0.3	13	1	CF320938	ACCESSION:CF320938
c 651	11.4	0.3	13	1	CF326844	ACCESSION:CF326844
c 652	11.4	0.3	13	1	CF327070	ACCESSION:CF327070
c 653	11.4	0.3	13	1	CF327339	ACCESSION:CF327339
654	11.4	0.3	13	1	CF327340	ACCESSION:CF327340
c 655	11.4	0.3	13	1	CF327576	ACCESSION:CF327576
c 656	11.4	0.3	13	1	CF327888	ACCESSION:CF327888
c 657	11.4	0.3	13	1	CF327939	ACCESSION:CF327939
c 658	11.4	0.3	13	1	CF328153	ACCESSION:CF328153
c 659	11.4	0.3	13	1	CF328228	ACCESSION:CF328228
c 660	11.4	0.3	13	1	CF328807	ACCESSION:CF328807
c 661	11.4	0.3	13	1	CF329075	ACCESSION:CF329075
662	11.4	0.3	13	1	CF329076	ACCESSION:CF329076
c 663	11.4	0.3	13	1	CF329417	ACCESSION:CF329417
c 664	11.4	0.3	13	1	CF329460	ACCESSION:CF329460
665	11.4	0.3	13	1	CF329729	ACCESSION:CF329729
c 666	11.4	0.3	13	1	CF329800	ACCESSION:CF329800
667	11.4	0.3	13	1	CF329801	ACCESSION:CF329801
c 668	11.4	0.3	13	1	CF329869	ACCESSION:CF329869
c 669	11.4	0.3	13	1	CF329946	ACCESSION:CF329946
c 670	11.4	0.3	13	1	CF329988	ACCESSION:CF329988
c 671	11.4	0.3	13	1	CF330023	ACCESSION:CF330023
672	11.4	0.3	13	1	CF330725	ACCESSION:CF330725
c 673	11.4	0.3	13	1	CF331041	ACCESSION:CF331041
c 674	11.4	0.3	13	1	CF331266	ACCESSION:CF331266
675	11.4	0.3	13	1	CF331273	ACCESSION:CF331273
c 676	11.4	0.3	13	1	CF331903	ACCESSION:CF331903
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c 678	11.4	0.3	13	1	CF332695	ACCESSION:CF332695
679	11.4	0.3	13	1	CF332696	ACCESSION:CF332696
c 680	11.4	0.3	13	1	CF333486	ACCESSION:CF333486
c 681	11.4	0.3	13	1	CF333972	ACCESSION:CF333972
682	11.4	0.3	13	1	CF333973	ACCESSION:CF333973
c 683	11.4	0.3	13	1	CF334347	ACCESSION:CF334347
c 684	11.4	0.3	13	1	CF337022	ACCESSION:CF337022
c 685	11.4	0.3	13	1	CN546046	ACCESSION:CN546046
686	11.4	0.3	13	1	CN752228	ACCESSION:CN752228
687	11.4	0.3	13	1	CN752875	ACCESSION:CN752875
688	11.4	0.3	13	1	CN753196	ACCESSION:CN753196
c 689	11.4	0.3	14	1	BQ586422	ACCESSION:BQ586422
c 690	11.4	0.3	14	1	BQ587890	ACCESSION:BQ587890

c 691	11.4	0.3	14	1	BQ589191	ACCESSION:BQ589191
c 692	11.4	0.3	14	1	BQ590242	ACCESSION:BQ590242
c 693	11.4	0.3	14	1	BQ590261	ACCESSION:BQ590261
c 694	11.4	0.3	14	1	BQ591168	ACCESSION:BQ591168
c 695	11.4	0.3	14	1	BQ591176	ACCESSION:BQ591176
c 696	11.4	0.3	14	1	BQ591207	ACCESSION:BQ591207
c 697	11.4	0.3	14	1	BQ591380	ACCESSION:BQ591380
c 698	11.4	0.3	14	1	BQ591482	ACCESSION:BQ591482
c 699	11.4	0.3	14	1	BQ593052	ACCESSION:BQ593052
c 700	11.4	0.3	14	1	CF277935	ACCESSION:CF277935
c 701	11.4	0.3	14	1	CF278001	ACCESSION:CF278001
c 702	11.4	0.3	14	1	CF278452	ACCESSION:CF278452
c 703	11.4	0.3	14	1	CF279473	ACCESSION:CF279473
c 704	11.4	0.3	14	1	CF279992	ACCESSION:CF279992
c 705	11.4	0.3	14	1	CF281958	ACCESSION:CF281958
c 706	11.4	0.3	14	1	CF282350	ACCESSION:CF282350
c 707	11.4	0.3	14	1	CF294449	ACCESSION:CF294449
c 708	11.4	0.3	14	1	CF295570	ACCESSION:CF295570
c 709	11.4	0.3	14	1	CF296120	ACCESSION:CF296120
c 710	11.4	0.3	14	1	CF297969	ACCESSION:CF297969
c 711	11.4	0.3	14	1	CF298109	ACCESSION:CF298109
c 712	11.4	0.3	14	1	CF299368	ACCESSION:CF299368
c 713	11.4	0.3	14	1	CF300542	ACCESSION:CF300542
c 714	11.4	0.3	14	1	CF301020	ACCESSION:CF301020
c 715	11.4	0.3	14	1	CF301083	ACCESSION:CF301083
c 716	11.4	0.3	14	1	CF301380	ACCESSION:CF301380
c 717	11.4	0.3	14	1	CF302675	ACCESSION:CF302675
c 718	11.4	0.3	14	1	CF302846	ACCESSION:CF302846
c 719	11.4	0.3	14	1	CF308006	ACCESSION:CF308006
c 720	11.4	0.3	14	1	CF308220	ACCESSION:CF308220
c 721	11.4	0.3	14	1	CF308445	ACCESSION:CF308445
c 722	11.4	0.3	14	1	CF308918	ACCESSION:CF308918
c 723	11.4	0.3	14	1	CF310714	ACCESSION:CF310714
c 724	11.4	0.3	14	1	CF311201	ACCESSION:CF311201
c 725	11.4	0.3	14	1	CF311813	ACCESSION:CF311813
c 726	11.4	0.3	14	1	CF318323	ACCESSION:CF318323
c 727	11.4	0.3	14	1	CF318450	ACCESSION:CF318450
c 728	11.4	0.3	14	1	CF319826	ACCESSION:CF319826
c 729	11.4	0.3	14	1	CF321246	ACCESSION:CF321246
c 730	11.4	0.3	14	1	CF327097	ACCESSION:CF327097
c 731	11.4	0.3	14	1	CF327119	ACCESSION:CF327119
c 732	11.4	0.3	14	1	CF327203	ACCESSION:CF327203
c 733	11.4	0.3	14	1	CF327445	ACCESSION:CF327445
c 734	11.4	0.3	14	1	CF328490	ACCESSION:CF328490
c 735	11.4	0.3	14	1	CF328540	ACCESSION:CF328540
c 736	11.4	0.3	14	1	CF328669	ACCESSION:CF328669
c 737	11.4	0.3	14	1	CF328994	ACCESSION:CF328994
c 738	11.4	0.3	14	1	CF329217	ACCESSION:CF329217
739	11.4	0.3	14	1	CF329990	ACCESSION:CF329990
c 740	11.4	0.3	14	1	CF330784	ACCESSION:CF330784
c 741	11.4	0.3	14	1	CF331272	ACCESSION:CF331272
c 742	11.4	0.3	14	1	CF331861	ACCESSION:CF331861
c 743	11.4	0.3	14	1	CF333214	ACCESSION:CF333214
744	11.4	0.3	14	1	CF333215	ACCESSION:CF333215
c 745	11.4	0.3	14	1	CF333399	ACCESSION:CF333399
c 746	11.4	0.3	14	1	CF334202	ACCESSION:CF334202
c 747	11.4	0.3	14	1	CF334281	ACCESSION:CF334281
c 748	11.4	0.3	14	1	CF334290	ACCESSION:CF334290
c 749	11.4	0.3	14	1	CF335781	ACCESSION:CF335781
c 750	11.4	0.3	14	1	CF336094	ACCESSION:CF336094
c 751	11.4	0.3	14	1	CF336106	ACCESSION:CF336106
c 752	11.4	0.3	14	1	CF336287	ACCESSION:CF336287
c 753	11.4	0.3	14	1	CF336906	ACCESSION:CF336906
c 754	11.4	0.3	14	1	CF330198	ACCESSION:CF330198

ALIGNMENTS

RESULT 1
BI223563
LOCUS BI223563 42 bp mRNA linear EST 11-JUL-2001
DEFINITION 602941991F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5104919 5',
mRNA sequence.
ACCESSION BI223563
VERSION BI223563.1 GI:14677007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11253 row: f column: 24
High quality sequence stop: 42.

FEATURES Location/Qualifiers
source 1. .42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5104919"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

Query Match 1.0%; Score 42; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3294 AGAACCAGAGGGCATGCTGAATGCCCCCTGCTTACTTGGTGA 3335
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Db 1 AGAACCAGAGGGCATGCTGAATGCCCCCTGCTTACTTGGTGA 42

RESULT 2
BI259338
LOCUS BI259338 32 bp mRNA linear EST 17-JUL-2001
DEFINITION 602972590F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5111783 5',
mRNA sequence.
ACCESSION BI259338
VERSION BI259338.1 GI:14816575
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 32)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11271 row: d column: 24
High quality sequence stop: 32.

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FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5111783"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_12"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."

  Query Match             0.7%;  Score 32;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3304 GGCATGCTGAATGCCCCCTGCTTACTTGGTGA 3335
              ||||||||||||||||||||||||||||||||
Db          1 GGCATGCTGAATGCCCCCTGCTTACTTGGTGA 32


RESULT 3
CF308158
LOCUS       CF308158                 25 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-N19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--01-N19, mRNA sequence.
ACCESSION   CF308158
VERSION     CF308158.1  GI:33679919
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--01-N19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 7.3;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTTAAAAG 4525
              ||||||||||||||  | ||||||
Db          1 TTTTTTTTTTTTTTTAAGATAAAAG 25


RESULT 4
BI223563/c
LOCUS       BI223563                 42 bp    mRNA    linear   EST 11-JUL-2001
DEFINITION  602941991F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5104919 5',
            mRNA sequence.
ACCESSION   BI223563
VERSION     BI223563.1  GI:14677007
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11253  row: f  column: 24
            High quality sequence stop: 42.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5104919"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_12"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."

  Query Match             0.5%;  Score 19.8;  DB 1;  Length 42;
  Best Local Similarity   77.4%;  Pred. No. 57;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       3296 AACCAGAGGGCATGCTGAATGCCCCCTGCTT 3326
              || ||| |||||| | | |||||| ||| ||
Db         33 AAGCAGGGGGCATTCAGCATGCCCTCTGGTT 3


RESULT 5
AZ862224/c
LOCUS       AZ862224                 23 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0169N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0169N18 F, genomic survey sequence.
ACCESSION   AZ862224
VERSION     AZ862224.1  GI:13059330
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

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COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0169  row: N  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0169N18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 18.8;  DB 1;  Length 23;
  Best Local Similarity   90.9%;  Pred. No. 17;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4494 TTATAAGTTTTTTTTTTTTTTT 4515
              ||| || ||||||||||||||||
Db         23 TTAAAATTTTTTTTTTTTTTTT 2


RESULT 6
CF333393
LOCUS       CF333393                  21 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E09.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-E09, mRNA sequence.
ACCESSION   CF333393
VERSION     CF333393.1  GI:33815062
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--02-E09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 16;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||| ||||
Db          2 TTTTTTTTTTTTTTTTGGTT 21


RESULT 7
CF318266
LOCUS       CF318266                  23 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-F07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-F07, mRNA sequence.
ACCESSION   CF318266
VERSION     CF318266.1  GI:33690027
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--08-F07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
```

line."

Query Match 0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| ||||
Db          3 TTTTTTTTTTTTTTTGGTT 22
```

RESULT 8
CF325356
LOCUS CF325356 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-A08.g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA clone JMT1--03-A08, mRNA sequence.
ACCESSION CF325356
VERSION CF325356.1 GI:33798994
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT1--03-A08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.4%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTGGG 18
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RESULT 9
CF327587
LOCUS CF327587 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION CF327587
VERSION CF327587.1 GI:33803426
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-C04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          2 TTTTTTTTTTTTTTTGGG 19
```

RESULT 10
CF282313/c
LOCUS CF282313 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-M08, mRNA sequence.
ACCESSION CF282313
VERSION CF282313.1 GI:33659700
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

/clone="14ETL--09-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||||||||||||||||||
Db 21 TTTTTTTTTTTTTTTGGG 4

RESULT 11
AZ963501
LOCUS AZ963501 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0232M07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0232M07 R, genomic survey sequence.
ACCESSION AZ963501
VERSION AZ963501.1 GI:13834728
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0232 row: M column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0232M07"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTGGG 18

RESULT 12
AZ310057
LOCUS AZ310057 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0018A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018A15 R, genomic survey sequence.
ACCESSION AZ310057
VERSION AZ310057.1 GI:10351664
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: A column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0018A15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          2 TTTTTTTTTTTTTTTGGG 19
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RESULT 13
TA211D06P
LOCUS TA211D06P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 211d06, forward sequence, genomic survey sequence.
ACCESSION AL478564
VERSION AL478564.1 GI:11844523
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="211d06"

Query Match 0.4%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGGG 20
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RESULT 14
AZ316361/c
LOCUS AZ316361 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0034I16 F, genomic survey sequence.
ACCESSION AZ316361
VERSION AZ316361.1 GI:10364110
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: I column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034I16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       4495 TATAAGTTTTTTTTTTTTTTT 4515
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Db         22 TTTAAATTTTTTTTTTTTTTT 2
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RESULT 15
AZ633751
LOCUS AZ633751 22 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0489I11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0489I11 F, genomic survey sequence.
ACCESSION AZ633751
VERSION AZ633751.1 GI:11755941

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: I column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0489I11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 2 CTCTCTCTCTCTCTCTCTC 22

RESULT 16
AZ843648/c
LOCUS AZ843648 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0142B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142B07 R, genomic survey sequence.
ACCESSION AZ843648
VERSION AZ843648.1 GI:13013556
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: B column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142B07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2120 AGGGTTTTCTTTTCTTTTTTT 2140
||||||||| |||| |||||||
Db 22 AGGGTTTTTTTTTTTTTTTTT 2

RESULT 17
TA303G05P/c
LOCUS TA303G05P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence, genomic survey sequence.
ACCESSION AL497383
VERSION AL497383.1 GI:11865504
KEYWORDS GSS.
SOURCE Trypanosoma brucei

```
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Trypanosoma brucei"
                      /mol_type="genomic DNA"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="303g05"

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 31;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTTT 2144
              |||| |||||||||||| |||
Db         22 TTTTTTTTCTTTTTTTTTT 2


RESULT 18
AJ663023/c
LOCUS       AJ663023                 19 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ663023 CSEQRAN09 Sus scrofa cDNA clone C0000024_H21, mRNA
            sequence.
ACCESSION   AJ663023
VERSION     AJ663023.1  GI:49347146
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institite,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /clone="C0000024_H21"
                      /tissue_type="placenta"
                      /clone_lib="CSEQRAN09"
                      /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                      NotI; Single pass sequencing. Normalised library
                      constructed from pooled tissue from day 30 placentas."

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||| ||
Db         19 TTTTTTTTTTTTTGGTTT 1


RESULT 19
AZ316368/c
LOCUS       AZ316368                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034L22 F, genomic survey sequence.
ACCESSION   AZ316368
VERSION     AZ316368.1  GI:10364124
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: L  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0034L22"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4497 TAAGTTTTTTTTTTTTTTT 4515
              ||| |||||||||||||||
Db         19 TAAATTTTTTTTTTTTTTT 1
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RESULT 20
AZ343730
LOCUS AZ343730 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION AZ343730
VERSION AZ343730.1 GI:10422288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: E column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2124 TTTTCTTTTCTTTTTTTCT 2142
              ||||||||| |||||||||
Db          2 TTTTCTTTTTTTTTTTCT 20
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RESULT 21
CF276747
LOCUS CF276747 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--02-A06.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-A06, mRNA sequence.
ACCESSION CF276747
VERSION CF276747.1 GI:33654133
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              |||||||||||||||| |||
Db          3 TTTTTTTTTTTTTTTGGT 21
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RESULT 22
AL587572
LOCUS AL587572 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587572 BP Chicken Brain Library Gallus gallus cDNA clone ROS059B11, mRNA sequence.
ACCESSION AL587572
VERSION AL587572.1 GI:13192606

```
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS059B11"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 23
CF316662
LOCUS       CF316662                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--06-A20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--06-A20, mRNA sequence.
ACCESSION   CF316662
VERSION     CF316662.1  GI:33688423
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--06-A20"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 24
CF330490
LOCUS       CF330490                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-D16, mRNA
            sequence.
ACCESSION   CF330490
VERSION     CF330490.1  GI:33809214
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--06-D16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTGG 17
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RESULT 25
AZ821905/c
LOCUS       AZ821905                 20 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0094D20 R, genomic survey sequence.
ACCESSION   AZ821905
VERSION     AZ821905.1  GI:12991813
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0094  row: D  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0094D20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTGG 1
```

```
RESULT 26
CF309614
LOCUS       CF309614                 21 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-N20, mRNA sequence.
ACCESSION   CF309614
VERSION     CF309614.1  GI:33681375
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--03-N20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20
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```
RESULT 27
CF298018
LOCUS       CF298018                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA
            sequence.
ACCESSION   CF298018
VERSION     CF298018.1  GI:33669779
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
```

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--01-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 48;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||| | ||
Db          1 TTTTTTTTTTTTTTTTGATT 20


RESULT 28
AZ433566
LOCUS       AZ433566                 20 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0219C02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0219C02 R, genomic survey sequence.
ACCESSION   AZ433566
VERSION     AZ433566.1  GI:10557579
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0219  row: C  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0219C02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 48;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              |||||||||  |||  ||||||
Db          1 CTCTCTCTCTCTCTCTCTCT 20


RESULT 29
AZ492997
LOCUS       AZ492997                 20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0327K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0327K24 F, genomic survey sequence.
ACCESSION   AZ492997
VERSION     AZ492997.1  GI:10666247
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0327  row: K  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0327K24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20
```

RESULT 30
AZ579122/c
LOCUS AZ579122 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0363G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0363G19 F, genomic survey sequence.
ACCESSION AZ579122
VERSION AZ579122.1 GI:11693583
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: G column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363G19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||  ||
Db         20 TTTTTTTTTTTTTTTGTTTT 1
```

RESULT 31
AZ770557
LOCUS AZ770557 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0572N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0572N08 F, genomic survey sequence.
ACCESSION AZ770557
VERSION AZ770557.1 GI:12891863
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0572 row: N column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0572N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20
```

RESULT 32
CL680297
LOCUS CL680297 20 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0128c_G05_2 - PRI0128c.BR (20) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL680297
VERSION CL680297.1 GI:50187127
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .20
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2125 TTTCTTTTCTTTTTTTCTTT 2144
              ||| |||||||||||| |||
Db          1 TTTTTTTTCTTTTTTTTTTT 20
```

RESULT 33
BX548564
LOCUS BX548564 21 bp mRNA linear EST 10-OCT-2003
DEFINITION BX548564 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse101g03_p1c, mRNA sequence.
ACCESSION BX548564
VERSION BX548564.1 GI:33298798
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.
FEATURES Location/Qualifiers
source 1. .21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse101g03_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2124 TTTTCTTTTCTTTTTTTCTT 2143
              ||||||||| ||||||| ||
Db          2 TTTTCTTTTTTTTTTTTTTT 21
```

RESULT 34
AZ394897
LOCUS AZ394897 21 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0158H11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0158H11 R, genomic survey sequence.
ACCESSION AZ394897
VERSION AZ394897.1 GI:10509969
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0158 row: H column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0158H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db             1 TCTCTCTCTCTCTCTCTC 20
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RESULT 35
AZ589098/c
LOCUS AZ589098 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0397B19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0397B19 R, genomic survey sequence.
ACCESSION AZ589098
VERSION AZ589098.1 GI:11711288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: B column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0397B19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db             21 TCTCTCTCTCTCTCTCTC 2
```

RESULT 36
AZ597939
LOCUS AZ597939 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0412F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0412F22 F, genomic survey sequence.
ACCESSION AZ597939
VERSION AZ597939.1 GI:11720129
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

```
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0412  row: F  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0412F22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 57;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
              ||||||||| ||||||| ||
Db          2 ATATATATATATATATATAT 21


RESULT 37
AZ597939/c
LOCUS       AZ597939                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0412F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0412F22 F, genomic survey sequence.
ACCESSION   AZ597939
VERSION     AZ597939.1  GI:11720129
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0412  row: F  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0412F22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 57;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
              ||||||||| ||||||| ||
Db         21 ATATATATATATATATATAT 2


RESULT 38
AZ625662/c
LOCUS       AZ625662                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0465C23 F, genomic survey sequence.
ACCESSION   AZ625662
VERSION     AZ625662.1  GI:11747852
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0465  row: C  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0465C23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 57;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTTTTT 4514
              ||||  ||||||||||||||
Db         21 TATATATTTTTTTTTTTTTT 2


RESULT 39
AZ627978
LOCUS       AZ627978                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0476L04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0476L04 F, genomic survey sequence.
ACCESSION   AZ627978
VERSION     AZ627978.1  GI:11750168
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0476  row: L  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0476L04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 57;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 40
CF309858/c
LOCUS       CF309858                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-D16, mRNA sequence.
ACCESSION   CF309858
VERSION     CF309858.1  GI:33681619
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-D16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4497 TAAGTTTTTTTTTTTTTT 4514
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Db         19 TATGTTTTTTTTTTTTTT 2
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RESULT 41
AZ360314/c
LOCUS AZ360314 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0103G03 R, genomic survey sequence.
ACCESSION AZ360314
VERSION AZ360314.1 GI:10474014
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0103G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2124 TTTTCTTTTCTTTTTTTC 2141
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Db         18 TTTTTTTTTCTTTTTTTC 1
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RESULT 42
AZ509929/c
LOCUS AZ509929 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0354A07 F, genomic survey sequence.
ACCESSION AZ509929
VERSION AZ509929.1 GI:10691245
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: A column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4497 TAAGTTTTTTTTTTTTTT 4514
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Db         18 TAATTTTTTTTTTTTTTT 1
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RESULT 43
AZ764517/c
LOCUS AZ764517 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560L07 R, genomic survey sequence.
ACCESSION AZ764517
VERSION AZ764517.1 GI:12879561
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560L07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4498 AAGTTTTTTTTTTTTTTT 4515
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Db         19 AAATTTTTTTTTTTTTTT 2
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RESULT 44
CF319428
LOCUS CF319428 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-O20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-O20, mRNA sequence.
ACCESSION CF319428
VERSION CF319428.1 GI:33691189
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-O20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

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  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 65;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||| |
Db          3 TTTTTTTTTTTTTTGAG 20


RESULT 45
BQ590207
LOCUS       BQ590207                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-O15-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-O15 3-PRIME, mRNA sequence.
ACCESSION   BQ590207
VERSION     BQ590207.1  GI:26119790
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: O  column: 15
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189913"
                     /db_xref="taxon:161934"
                     /clone="024-019-O15"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 46
CF318894
LOCUS       CF318894                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--09-D06, mRNA sequence.
ACCESSION   CF318894
VERSION     CF318894.1  GI:33690655
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--09-D06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 47
CF327923
LOCUS       CF327923                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-J18, mRNA
            sequence.
ACCESSION   CF327923
VERSION     CF327923.1  GI:33804096
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

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          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--02-J18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 48
CF328223
LOCUS       CF328223                  16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-A10, mRNA
            sequence.
ACCESSION   CF328223
VERSION     CF328223.1  GI:33804692
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--03-A10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 49
CR786609/c
LOCUS       CR786609                  16 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468C2031_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468C2031 5', mRNA sequence.
ACCESSION   CR786609
VERSION     CR786609.1  GI:53705606
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
            Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468C2031
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="DKFZp468C2031"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTG 1


RESULT 50
CF291802
LOCUS       CF291802                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G05, mRNA
            sequence.
ACCESSION   CF291802
VERSION     CF291802.1  GI:33660835
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
```

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-G05"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 51
CF295807
LOCUS       CF295807                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--05-O12, mRNA
            sequence.
ACCESSION   CF295807
VERSION     CF295807.1  GI:33664840
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--05-O12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 52
CF297251
LOCUS       CF297251                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--07-P12, mRNA
            sequence.
ACCESSION   CF297251
VERSION     CF297251.1  GI:33666284
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="mRNA"
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                     /clone="30DGS--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 53
CF298341
LOCUS       CF298341                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K24, mRNA
            sequence.
ACCESSION   CF298341
VERSION     CF298341.1  GI:33670102
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
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  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--01-K24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 54
CF299639
LOCUS       CF299639                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L20, mRNA
            sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 55
AJ725584/c
LOCUS       AJ725584                 18 bp    mRNA    linear   EST 07-OCT-2004
DEFINITION  AJ725584 riken1 Gallus gallus cDNA clone 2c16r4, mRNA sequence.
ACCESSION   AJ725584
VERSION     AJ725584.1  GI:53890998
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J.,
            Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M.,
            Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
  TITLE     Full-length cDNAs from bursal lymphocytes to facilitate gene
            function analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Caldwell RB
            GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
            Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="2c16r4"
                     /cell_type="bursal lymphocyte"
                     /dev_stage="2-3 weeks old"
                     /clone_lib="riken1"
                     /note="CB inbred strain"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         17 TTTTTTTTTTTTTTTG 2


RESULT 56
AL048754/c
LOCUS       AL048754                 18 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION   AL048754
VERSION     AL048754.1  GI:4727825
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566L173"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         17 TTTTTTTTTTTTTTTG 2


RESULT 57
CF291665
LOCUS       CF291665                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-D01, mRNA
            sequence.
ACCESSION   CF291665
VERSION     CF291665.1  GI:33660698
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-D01"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 58
CF291899
LOCUS       CF291899                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I08.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I08, mRNA
            sequence.
ACCESSION   CF291899
VERSION     CF291899.1  GI:33660932
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-I08"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 59
CF292072
LOCUS       CF292072                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA
            sequence.
ACCESSION   CF292072
VERSION     CF292072.1  GI:33661105
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
```

```
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-M03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 60
CF292144
LOCUS       CF292144                  19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-N17, mRNA
            sequence.
ACCESSION   CF292144
VERSION     CF292144.1  GI:33661177
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-N17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 61
CF293167
LOCUS       CF293167                  19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--02-E02, mRNA
            sequence.
ACCESSION   CF293167
VERSION     CF293167.1  GI:33662200
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--02-E02"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 62
CF298396
LOCUS       CF298396                  19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M05, mRNA
            sequence.
ACCESSION   CF298396
VERSION     CF298396.1  GI:33670157
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--01-M05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          4 TTTTTTTTTTTTTTTG 19


RESULT 63
CF300236
LOCUS       CF300236                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-I24, mRNA
            sequence.
ACCESSION   CF300236
VERSION     CF300236.1  GI:33671997
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-I24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 64
CF302456
LOCUS       CF302456                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA
            sequence.
ACCESSION   CF302456
VERSION     CF302456.1  GI:33674217
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-P22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          4 TTTTTTTTTTTTTTTG 19


RESULT 65
CF309636
LOCUS       CF309636                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-O08.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-O08, mRNA sequence.
ACCESSION   CF309636
VERSION     CF309636.1  GI:33681397
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--03-O08"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 66
CF309821
LOCUS       CF309821                  19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-C17.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-C17, mRNA sequence.
ACCESSION   CF309821
VERSION     CF309821.1  GI:33681582
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--04-C17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 67
CF310688/c
LOCUS       CF310688                  19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-H18, mRNA sequence.
ACCESSION   CF310688
VERSION     CF310688.1  GI:33682449
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--05-H18"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db         18 GTTTTTTTTTTTTTTT 3


RESULT 68
CF311668/c
LOCUS       CF311668                  19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA
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library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-A05, mRNA sequence.
ACCESSION CF311668
VERSION CF311668.1 GI:33683429
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-A05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 17 GTTTTTTTTTTTTTTT 2

RESULT 69
CF311778
LOCUS CF311778 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-D01.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-D01, mRNA sequence.
ACCESSION CF311778
VERSION CF311778.1 GI:33683539
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-D01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 70
CF319596
LOCUS CF319596 19 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-C14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-C14, mRNA sequence.
ACCESSION CF319596
VERSION CF319596.1 GI:33691357
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--10-C14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

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  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 71
CF331361
LOCUS       CF331361                  19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-H08.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-H08, mRNA
            sequence.
ACCESSION   CF331361
VERSION     CF331361.1  GI:33810941
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--07-H08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 72
CF335293
LOCUS       CF335293                  19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--04-O17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--04-O17, mRNA sequence.
ACCESSION   CF335293
VERSION     CF335293.1  GI:33818938
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--04-O17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 73
CN545923
LOCUS       CN545923                  19 bp    mRNA    linear   EST 30-APR-2004
DEFINITION  EST 17867 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL006D08 3', mRNA sequence.
ACCESSION   CN545923
VERSION     CN545923.1  GI:46910548
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
  TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultivar="Cabernet Sauvignon"
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                     /db_xref="taxon:29760"
                     /clone="B3CS00RL006D08"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 74
AJ666275
LOCUS       AJ666275                 20 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ666275 CSEQRAN09 Sus scrofa cDNA clone C0000033_B07, mRNA
            sequence.
ACCESSION   AJ666275
VERSION     AJ666275.1  GI:49350726
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institite,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0000033_B07"
                     /tissue_type="placenta"
                     /clone_lib="CSEQRAN09"
                     /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pooled tissue from day 30 placentas."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 75
AL038460/c
LOCUS       AL038460                 20 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  DKFZp566B2246_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566B2246, mRNA sequence.
ACCESSION   AL038460
VERSION     AL038460.1  GI:49682131
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566B2246"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         17 TTTTTTTTTTTTTTTG 2


RESULT 76
AL587727
LOCUS       AL587727                 20 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS061D01, mRNA sequence.
ACCESSION   AL587727
VERSION     AL587727.1  GI:13192761
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS061D01"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
```

GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          5 TTTTTTTTTTTTTTTG 20
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RESULT 77
CA853586
LOCUS CA853586 20 bp mRNA linear EST 01-AUG-2003
DEFINITION B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone B09H12 5', mRNA sequence.
ACCESSION CA853586
VERSION CA853586.1 GI:33390391
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 20)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES Location/Qualifiers
source 1. .20
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B09H12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid. "

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17
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RESULT 78
CF282002
LOCUS CF282002 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F01, mRNA sequence.
ACCESSION CF282002
VERSION CF282002.1 GI:33659389
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16
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RESULT 79
CF297010
LOCUS CF297010 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--07-J24.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--07-J24, mRNA sequence.
ACCESSION CF297010
VERSION CF297010.1 GI:33666043
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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                     /clone="30DGS--07-J24"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTGG 16


RESULT 80
CF318278
LOCUS       CF318278                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-F13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-F13, mRNA sequence.
ACCESSION   CF318278
VERSION     CF318278.1  GI:33690039
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--08-F13"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 81
CF320843
LOCUS       CF320843                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-O01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-O01, mRNA sequence.
ACCESSION   CF320843
VERSION     CF320843.1  GI:33692604
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-O01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 82
CF331733/c
LOCUS       CF331733                  20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-P15, mRNA
            sequence.
ACCESSION   CF331733
VERSION     CF331733.1  GI:33811693
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--07-P15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db         16 GTTTTTTTTTTTTTTT 1


RESULT 83
CF333052
LOCUS       CF333052                  20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--01-M17, mRNA sequence.
ACCESSION   CF333052
VERSION     CF333052.1  GI:33814360
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--01-M17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          3 GTTTTTTTTTTTTTTT 18


RESULT 84
CF336815
LOCUS       CF336815                  20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--07-A04, mRNA sequence.
ACCESSION   CF336815
VERSION     CF336815.1  GI:33822012
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--07-A04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 85
AZ486787
LOCUS       AZ486787                  20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0315D23 F, genomic survey sequence.
ACCESSION   AZ486787
VERSION     AZ486787.1  GI:10653904
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
```

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 4 GTTTTTTTTTTTTTTT 19

RESULT 86
AZ579178/c
LOCUS AZ579178 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0363F11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0363F11 F, genomic survey sequence.
ACCESSION AZ579178
VERSION AZ579178.1 GI:11693523
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: F column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363F11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
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Db 16 TTTTTTTTTTTTTTTG 1

RESULT 87
AZ633741/c
LOCUS AZ633741 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0489G12 F, genomic survey sequence.
ACCESSION AZ633741
VERSION AZ633741.1 GI:11755931
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0489  row: G  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES              Location/Qualifiers
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                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0489G12"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db         16 GTTTTTTTTTTTTTTT 1


RESULT 88
CF329136
LOCUS       CF329136                 19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
            sequence.
ACCESSION   CF329136
VERSION     CF329136.1  GI:33806509
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="NACL--04-F15"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 87;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2126 TTCTTTTCTTTTTTTCTTT 2144
              || |||| ||||||||||||
Db          1 TTTTTTTTTTTTTTTCTTT 19


RESULT 89
AZ401252
LOCUS       AZ401252                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0167E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0167E20 R, genomic survey sequence.
ACCESSION   AZ401252
VERSION     AZ401252.1  GI:10516326
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0167  row: E  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0167E20"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2392 AAATATATATACATATATA 2410
              | ||||||||| |||||||
Db          1 ATATATATATATATATATA 19
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RESULT 90
AZ401252/c
LOCUS AZ401252 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0167E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0167E20 R, genomic survey sequence.
ACCESSION AZ401252
VERSION AZ401252.1 GI:10516326
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0167E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2395 TATATATACATATATACAT 2413
              |||||||| ||||||| ||
Db         19 TATATATATATATATATAT 1
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RESULT 91
AZ489586
LOCUS AZ489586 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0322C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0322C12 F, genomic survey sequence.
ACCESSION AZ489586
VERSION AZ489586.1 GI:10659481
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0322 row: C column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0322C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3181 CTCTCTCTCCCTCCCTCTC 3199
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Db          1 CTCTCTCTCTCTCTCTCTC 19
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RESULT 92
AZ510952
LOCUS AZ510952 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0355G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0355G15 R, genomic survey sequence.
ACCESSION AZ510952
VERSION AZ510952.1 GI:10692268
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: G column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0355G15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3182 TCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCT 19
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RESULT 93
AZ630416
LOCUS AZ630416 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0484B03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0484B03 F, genomic survey sequence.
ACCESSION AZ630416
VERSION AZ630416.1 GI:11752606
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2392 AAATATATATACATATATA 2410
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Db          1 ATATATATATATATATATA 19
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RESULT 94
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LOCUS AZ630416 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0484B03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0484B03 F, genomic survey sequence.
ACCESSION AZ630416
VERSION AZ630416.1 GI:11752606
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2395 TATATATACATATATACAT 2413
                |||||||| ||||||| ||
Db         19 TATATATATATATATATAT 1
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RESULT 95
AZ645841
LOCUS AZ645841 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0511G04 R, genomic survey sequence.
ACCESSION AZ645841
VERSION AZ645841.1 GI:11775726
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2125 TTTCTTTTCTTTTTTTCTT 2143
              ||| |||||||||||| ||
Db          1 TTTTTTTTCTTTTTTTTTT 19
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RESULT 96
AZ650252/c
LOCUS AZ650252 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0520N17 F, genomic survey sequence.
ACCESSION AZ650252
VERSION AZ650252.1 GI:11784550
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: N column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520N17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| ||
Db         19 TTTTTTTTTTTTTTGTTTT 1
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RESULT 97
AZ775624/c
LOCUS AZ775624 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0008E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0008E01 R, genomic survey sequence.
ACCESSION AZ775624
VERSION AZ775624.1 GI:12902356
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: E column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008E01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 87;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||| || ||
Db         19 TTTTTTTTTTTTTGTGTGT 1
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RESULT 98
AZ862224

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LOCUS       AZ862224                 23 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0169N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0169N18 F, genomic survey sequence.
ACCESSION   AZ862224
VERSION     AZ862224.1  GI:13059330
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0169  row: N  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0169N18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

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  Query Match             0.4%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAATTTGA 3627
              |||||| ||||| | ||||| |
Db          1 AAAAAAAAAAAAAAAAATTTTA 22
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RESULT 99
AW246446

```
LOCUS       AW246446                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821601.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821601 3',
            mRNA sequence.
ACCESSION   AW246446
VERSION     AW246446.1  GI:6589439
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821601.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM7  row: D  column: 18
            High quality sequence stop: 9.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821601"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
```

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4506 TTTTTTTTTTGGGTTAA 4522
              ||||||||||| |||||
Db          1 TTTTTTTTTGTGTTAA 17
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RESULT 100
CF302409
LOCUS CF302409 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-N19, mRNA sequence.
ACCESSION CF302409
VERSION CF302409.1 GI:33674170
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-N19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||| |
Db          2 TTTTTTTTTTTTTTAG 18
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RESULT 101
CR786637/c
LOCUS CR786637 18 bp mRNA linear EST 01-OCT-2004
DEFINITION DKFZp468J2331_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone DKFZp468J2331 5', mRNA sequence.
ACCESSION CR786637
VERSION CR786637.1 GI:53705634
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J2331
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
FEATURES Location/Qualifiers
source 1. .18
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp468J2331"
/tissue_type="heart"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="468 (synonym: phrt1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4499 AGTTTTTTTTTTTTTT 4515
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Db         17 ATTTTTTTTTTTTTTT 1
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RESULT 102
AZ450180/c
LOCUS AZ450180 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0248K13 R, genomic survey sequence.
ACCESSION AZ450180
VERSION AZ450180.1 GI:10604710
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: K column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0248K13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  |
Db         17 TTTTTTTTTTTTTTAG 1


RESULT 103
AZ513919
LOCUS       AZ513919                19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0360E13 F, genomic survey sequence.
ACCESSION   AZ513919
VERSION     AZ513919.1  GI:10695235
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0360  row: E  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0360E13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTT 2140
              ||||  ||||||||||||
Db          3 TTTTTTTTTCTTTTTT 19


RESULT 104
AJ690565
LOCUS       AJ690565                15 bp    mRNA    linear   EST 29-JUN-2004
DEFINITION  AJ690565 KN261 Bos taurus cDNA clone KN261-054_B13, mRNA sequence.
ACCESSION   AJ690565
VERSION     AJ690565.1  GI:49423173
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
            R. Site2: SmaI 3' Seq Primer M13F Normalised library constructed
            from bovine ovary. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
            EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="KN261-054_B13"
                     /tissue_type="ovary"
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                     /clone_lib="KN261"
                     /note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
                     SmaI; Single pass sequencing. Normalised library
                     constructed from bovine ovary."

  Query Match              0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 105
BE230585/c
LOCUS       BE230585                 15 bp    mRNA    linear   EST 07-JUL-2000
DEFINITION  99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
            (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION   BE230585
VERSION     BE230585.1  GI:8956782
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
            Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of ESTs from Rice Seedling
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Milyang 23"
                     /db_xref="taxon:39946"
                     /clone="99AS799"
                     /dev_stage="5 days after pollination"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Directional cDNA library inserted into lambda ZAPII
                     vector at 5'end with EcoRI and 3' end with Xho I site"

  Query Match              0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 106
BQ582543
LOCUS       BQ582543                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013300-024-007-B02-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION   BQ582543
VERSION     BQ582543.1  GI:26112120
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 7  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184162"
                     /db_xref="taxon:161934"
                     /clone="024-007-B02"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 107
BQ585820
LOCUS       BQ585820                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012533-024-014-H17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-014-H17 5-PRIME, mRNA sequence.
ACCESSION   BQ585820
VERSION     BQ585820.1  GI:26115402
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
```

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   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 14  row: H  column: 17
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187164"
                     /db_xref="taxon:161934"
                     /clone="024-014-H17"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 108
BQ590410
LOCUS       BQ590410                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M08-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION   BQ590410
VERSION     BQ590410.1  GI:26119993
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 19  row: M  column: 08
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189710"
                     /db_xref="taxon:161934"
                     /clone="024-019-M08"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 109
BQ590656
LOCUS       BQ590656                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S015086-024-018-L13-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION   BQ590656
VERSION     BQ590656.1  GI:26120239
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 18  row: L  column: 13
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189464"
                     /db_xref="taxon:161934"
                     /clone="024-018-L13"
                     /tissue_type="storage root"
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 110
BQ591170
LOCUS BQ591170 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-N18 3-PRIME, mRNA sequence.
ACCESSION BQ591170
VERSION BQ591170.1 GI:26120753
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: N column: 18
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188941"
/db_xref="taxon:161934"
/clone="024-017-N18"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 111
BQ591178
LOCUS BQ591178 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-F22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-F22 3-PRIME, mRNA sequence.
ACCESSION BQ591178
VERSION BQ591178.1 GI:26120761
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: F column: 22
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188949"
/db_xref="taxon:161934"
/clone="024-017-F22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

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RESULT 112
BQ591223
LOCUS       BQ591223                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H02 3-PRIME, mRNA sequence.
ACCESSION   BQ591223
VERSION     BQ591223.1  GI:26120806
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: H  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188901"
                     /db_xref="taxon:161934"
                     /clone="024-017-H02"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 113
BQ594689
LOCUS       BQ594689                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-024-M05 3-PRIME, mRNA sequence.
ACCESSION   BQ594689
VERSION     BQ594689.1  GI:26124272
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 24  row: M  column: 05
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:192163"
                     /db_xref="taxon:161934"
                     /clone="024-024-M05"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 114
CF277319
LOCUS       CF277319                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-M23,
            mRNA sequence.
ACCESSION   CF277319
VERSION     CF277319.1  GI:33654705
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
```

```
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--02-M23"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 115
CF281923
LOCUS       CF281923                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-D04,
            mRNA sequence.
ACCESSION   CF281923
VERSION     CF281923.1  GI:33659310
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--09-D04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 116
CF290920
LOCUS       CF290920                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-C09, mRNA
            sequence.
ACCESSION   CF290920
VERSION     CF290920.1  GI:33659953
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 117
CF291029
LOCUS       CF291029                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E19, mRNA
            sequence.
ACCESSION   CF291029
VERSION     CF291029.1  GI:33660062
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-E19"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 118
CF291103
LOCUS CF291103 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G10, mRNA sequence.
ACCESSION CF291103
VERSION CF291103.1 GI:33660136
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-G10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 119
CF291717
LOCUS CF291717 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E04, mRNA sequence.
ACCESSION CF291717
VERSION CF291717.1 GI:33660750
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-E04"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 120
CF291798
LOCUS CF291798 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G02, mRNA sequence.
ACCESSION CF291798
VERSION CF291798.1 GI:33660831

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KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-G02"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 121
CF292458
LOCUS       CF292458                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-E17, mRNA
            sequence.
ACCESSION   CF292458
VERSION     CF292458.1  GI:33661491
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--01-E17"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 122
CF292461
LOCUS       CF292461                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-E19, mRNA
            sequence.
ACCESSION   CF292461
VERSION     CF292461.1  GI:33661494
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--01-E19"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 123
CF296652
LOCUS       CF296652                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
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            sativa (japonica cultivar-group) cDNA clone 30DGS--07-C02, mRNA
            sequence.
ACCESSION   CF296652
VERSION     CF296652.1  GI:33665685
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--07-C02"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTG 15


RESULT 124
CF298148
LOCUS       CF298148                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G17, mRNA
            sequence.
ACCESSION   CF298148
VERSION     CF298148.1  GI:33669909
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--01-G17"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 125
CF298630
LOCUS       CF298630                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-B23, mRNA
            sequence.
ACCESSION   CF298630
VERSION     CF298630.1  GI:33670391
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-B23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 126
CF298733
LOCUS       CF298733                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E20, mRNA
            sequence.
ACCESSION   CF298733
VERSION     CF298733.1  GI:33670494
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="7LEAF--02-E20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 127
CF298805
LOCUS       CF298805                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-G20, mRNA
            sequence.
ACCESSION   CF298805
VERSION     CF298805.1  GI:33670566
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-G20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 128
CF298889
LOCUS       CF298889                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-J09, mRNA
            sequence.
ACCESSION   CF298889
VERSION     CF298889.1  GI:33670650
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="7LEAF--02-J09"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
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              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 129
CF299602
LOCUS       CF299602                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L01, mRNA
            sequence.
ACCESSION   CF299602
VERSION     CF299602.1  GI:33671363
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-L01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 130
CF299608
LOCUS       CF299608                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L04, mRNA
            sequence.
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-L04"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 131
CF300121
LOCUS       CF300121                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G12, mRNA
            sequence.
ACCESSION   CF300121
VERSION     CF300121.1  GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-G12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
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  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 132
CF300361
LOCUS       CF300361                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L16, mRNA
            sequence.
ACCESSION   CF300361
VERSION     CF300361.1  GI:33672122
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 133
CF300992
LOCUS       CF300992                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K19, mRNA
            sequence.
ACCESSION   CF300992
VERSION     CF300992.1  GI:33672753
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-K19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 134
CF302034
LOCUS       CF302034                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C24, mRNA
            sequence.
ACCESSION   CF302034
VERSION     CF302034.1  GI:33673795
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="7LEAF--07-C24"
                     /tissue_type="leaf"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTTTT 15
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RESULT 135
CF302124
LOCUS CF302124 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-F16, mRNA sequence.
ACCESSION CF302124
VERSION CF302124.1 GI:33673885
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTTTT 15
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RESULT 136
CF302182
LOCUS CF302182 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-H20, mRNA sequence.
ACCESSION CF302182
VERSION CF302182.1 GI:33673943
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
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Db          1 TTTTTTTTTTTTTTT 15
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RESULT 137
CF307923
LOCUS CF307923 15 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-I15, mRNA sequence.
ACCESSION CF307923
VERSION CF307923.1 GI:33679684
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--01-I15"
/tissue_type="leaf"

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                     /dev_stage="14 days after germination"
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 138
CF311159
LOCUS       CF311159                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--06-E11, mRNA sequence.
ACCESSION   CF311159
VERSION     CF311159.1  GI:33682920
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--06-E11"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
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                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 139
CF311907
LOCUS       CF311907                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--07-G04, mRNA sequence.
ACCESSION   CF311907
VERSION     CF311907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
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Qy       4501 TTTTTTTTTTTTTTT 4515
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 140
CF313319
LOCUS       CF313319                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--01-G13, mRNA sequence.
ACCESSION   CF313319
VERSION     CF313319.1  GI:33685080
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

```
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 141
CF313320/c
LOCUS       CF313320                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-G13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--01-G13, mRNA sequence.
ACCESSION   CF313320
VERSION     CF313320.1  GI:33685081
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
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Db         15 TTTTTTTTTTTTTTT 1


RESULT 142
CF316251/c
LOCUS       CF316251                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-H15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-H15, mRNA sequence.
ACCESSION   CF316251
VERSION     CF316251.1  GI:33688012
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
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Db         15 TTTTTTTTTTTTTTT 1


RESULT 143
CF318035
LOCUS       CF318035                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-P06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--07-P06, mRNA sequence.
ACCESSION   CF318035
VERSION     CF318035.1  GI:33689796
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KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="HD--07-P06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 144
CF327434
LOCUS       CF327434                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-O18, mRNA
            sequence.
ACCESSION   CF327434
VERSION     CF327434.1  GI:33803127
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--01-O18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 145
CF329379
LOCUS       CF329379                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-K23, mRNA
            sequence.
ACCESSION   CF329379
VERSION     CF329379.1  GI:33806995
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-K23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          1 GTTTTTTTTTTTTTT 15


RESULT 146
```

```
CF330195
LOCUS       CF330195                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-N03, mRNA
            sequence.
ACCESSION   CF330195
VERSION     CF330195.1  GI:33808618
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-N03"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 147
CF330668
LOCUS       CF330668                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-H16, mRNA
            sequence.
ACCESSION   CF330668
VERSION     CF330668.1  GI:33809572
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--06-H16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 148
CF332178
LOCUS       CF332178                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-J10, mRNA
            sequence.
ACCESSION   CF332178
VERSION     CF332178.1  GI:33812580
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--08-J10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
```

```
Db          1 TTTTTTTTTTTTTTT 15


RESULT 149
CF336202
LOCUS       CF336202                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-C20, mRNA sequence.
ACCESSION   CF336202
VERSION     CF336202.1  GI:33820794
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--06-C20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 150
CN751062/c
LOCUS       CN751062                 15 bp    mRNA    linear   EST 19-MAY-2004
DEFINITION  ApHL3SD-I-F8 ApHL3SD Acyrthosiphon pisum cDNA clone ApHL3SDIF8 5',
            mRNA sequence.
ACCESSION   CN751062
VERSION     CN751062.1  GI:47516059
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
  ORGANISM  Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
  TITLE     An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
  JOURNAL   Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR PRimers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: I  row: F  column: 8.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Acyrthosiphon pisum"
                     /mol_type="mRNA"
                     /cultivar="yr2"
                     /db_xref="taxon:7029"
                     /clone="ApHL3SDIF8"
                     /tissue_type="head"
                     /dev_stage="third instar nymph (L3)"
                     /lab_host="TOP10"
                     /clone_lib="ApHL3SD"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
                     Sample name: ApHL3SD ; Plant growth place: INRA-Rennes,
                     UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
                     conditions: peat ; Sowing date: 20/03/2003 ; Harvesting
                     date: 10/04/2003 ; Stress date: no stress ; Description:
                     aphids inoculated on one-week old Vicia faba germinations
                     under non sterile conditions. ; experimental condition:
                     short photoperiod (12-hr light/12-hr dark at 18 c)"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGG 4518
             |||||||||||||||
Db         15 TTTTTTTTTTTTGGG 1


RESULT 151
CN752390/c
LOCUS       CN752390                 15 bp    mRNA    linear   EST 19-MAY-2004
DEFINITION  ApHL3SD-XXXII-B2 ApHL3SD Acyrthosiphon pisum cDNA clone
            ApHL3SDXXXIIB2 5', mRNA sequence.
ACCESSION   CN752390
VERSION     CN752390.1  GI:47517387
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
  ORGANISM  Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
  TITLE     An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
  JOURNAL   Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR PRimers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXXII  row: B  column: 2.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Acyrthosiphon pisum"
                     /mol_type="mRNA"
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                     /cultivar="yr2"
                     /db_xref="taxon:7029"
                     /clone="ApHL3SDXXXIIB2"
                     /tissue_type="head"
                     /dev_stage="third instar nymph (L3)"
                     /lab_host="TOP10"
                     /clone_lib="ApHL3SD"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
                     Sample name: ApHL3SD ; Plant growth place: INRA-Rennes,
                     UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
                     conditions: peat ; Sowing date: 20/03/2003 ; Harvesting
                     date: 10/04/2003 ; Stress date: no stress ; Description:
                     aphids inoculated on one-week old Vicia faba germinations
                     under non sterile conditions. ; experimental condition:
                     short photoperiod (12-hr light/12-hr dark at 18 c)"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGG 4518
              |||||||||||||||
Db         15 TTTTTTTTTTTTGGG 1


RESULT 152
CR547282/c
LOCUS       CR547282                 15 bp    mRNA    linear   EST 12-JUL-2004
DEFINITION  DKFZp468I112_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468I112 5', mRNA sequence.
ACCESSION   CR547282
VERSION     CR547282.1  GI:50240938
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
            Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Bloecker,H., Boecher,M., Brandt,P., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National
            Research Centre for Biotechnology Ltd., Braunschweig/Germany)
            within the cDNA sequencing consortium of the German Genome Project.
            This clone (DKFZp468I112) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468I112"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 153
BQ590166
LOCUS       BQ590166                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-K18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-K18 3-PRIME, mRNA sequence.
ACCESSION   BQ590166
VERSION     BQ590166.1  GI:26119749
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: K  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189955"
                     /db_xref="taxon:161934"
                     /clone="024-019-K18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         1 TTTTTTTTTTTTTTT 15


RESULT 154
BQ590507
LOCUS       BQ590507                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION   BQ590507
VERSION     BQ590507.1  GI:26120090
```

```
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: M  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189608"
                     /db_xref="taxon:161934"
                     /clone="024-019-M04"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 155
BQ592600/c
LOCUS       BQ592600                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013686-024-028-F08-SP6R MPIZ-ADIS-024-developing root Beta
            vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION   BQ592600
VERSION     BQ592600.1  GI:26122183
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: F  column: 08
            Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:194262"
                     /db_xref="taxon:161934"
                     /clone="024-028-F08"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 156
BQ592965
LOCUS       BQ592965                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013324-024-028-A01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION   BQ592965
VERSION     BQ592965.1  GI:26122548
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
```

```
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: A  column: 01
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:193895"
                      /db_xref="taxon:161934"
                      /clone="024-028-A01"
                      /tissue_type="developing root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-developing root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 157
BQ595369
LOCUS       BQ595369                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION   BQ595369
VERSION     BQ595369.1  GI:26124952
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 22  row: P  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:191489"
                      /db_xref="taxon:161934"
                      /clone="024-022-P02"
                      /tissue_type="developing root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-developing root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 158
BQ595717/c
LOCUS       BQ595717                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012692-024-022-H07-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-H07 5-PRIME, mRNA sequence.
ACCESSION   BQ595717
VERSION     BQ595717.1  GI:26125300
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 22  row: H  column: 07
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:191134"
                      /db_xref="taxon:161934"
                      /clone="024-022-H07"
                      /tissue_type="developing root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-developing root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
```

orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2
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RESULT 159
CF279325
LOCUS CF279325 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09, mRNA sequence.
ACCESSION CF279325
VERSION CF279325.1 GI:33656711
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--05-J09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 160
CF296130
LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION CF296130
VERSION CF296130.1 GI:33665163
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-F22"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 161
CF311057
LOCUS CF311057 16 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION CF311057
VERSION CF311057.1 GI:33682818
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa (japonica cultivar-group)"

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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--06-C03"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 162
CF314013
LOCUS       CF314013                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-G01, mRNA sequence.
ACCESSION   CF314013
VERSION     CF314013.1  GI:33685774
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--02-G01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 163
CF314377
LOCUS       CF314377                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-O01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-O01, mRNA sequence.
ACCESSION   CF314377
VERSION     CF314377.1  GI:33686138
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--02-O01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 164
CF315789
LOCUS       CF315789                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-N10.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--04-N10, mRNA sequence.
ACCESSION   CF315789
VERSION     CF315789.1  GI:33687550
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
```

```
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="HD--04-N10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 165
CF316056
LOCUS       CF316056                16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-D07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-D07, mRNA sequence.
ACCESSION   CF316056
VERSION     CF316056.1  GI:33687817
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--05-D07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 166
CF317718
LOCUS       CF317718                16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-I05.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--07-I05, mRNA sequence.
ACCESSION   CF317718
VERSION     CF317718.1  GI:33689479
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--07-I05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 167
CF320356
LOCUS       CF320356                16 bp    mRNA    linear   EST 15-AUG-2003
```

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DEFINITION  HD--11-D14.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-D14, mRNA sequence.
ACCESSION   CF320356
VERSION     CF320356.1  GI:33692117
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-D14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 168
CF327722
LOCUS       CF327722                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA
            sequence.
ACCESSION   CF327722
VERSION     CF327722.1  GI:33803695
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-F06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 169
CF329320
LOCUS       CF329320                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
            sequence.
ACCESSION   CF329320
VERSION     CF329320.1  GI:33806877
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-J17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
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                    ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 170
CF333386/c
LOCUS       CF333386                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-E05, mRNA sequence.
ACCESSION   CF333386
VERSION     CF333386.1  GI:33815044
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--02-E05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 2


RESULT 171
CR786853/c
LOCUS       CR786853                 16 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468E2231_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468E2231 5', mRNA sequence.
ACCESSION   CR786853
VERSION     CR786853.1  GI:53705850
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
            Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468E2231
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468E2231"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 2


RESULT 172
BQ590128
LOCUS       BQ590128                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION   BQ590128
VERSION     BQ590128.1  GI:26119711
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189986"
                     /db_xref="taxon:161934"
                     /clone="024-019-E19"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
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/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
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Db          1 TTTTTTTTTTTTTTT 15
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RESULT 173
BQ590687/c
LOCUS BQ590687 17 bp mRNA linear EST 06-DEC-2002
DEFINITION S013717-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION BQ590687
VERSION BQ590687.1 GI:26120270
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
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Db         17 TTTTTTTTTTTTTTT 3
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RESULT 174
BQ591177
LOCUS BQ591177 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION BQ591177
VERSION BQ591177.1 GI:26120760
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: B column: 22
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188948"
/db_xref="taxon:161934"
/clone="024-017-B22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTTTT 15
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RESULT 175
BQ591181
LOCUS       BQ591181                  17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H16-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H16 3-PRIME, mRNA sequence.
ACCESSION   BQ591181
VERSION     BQ591181.1  GI:26120764
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 17  row: H  column: 16
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188932"
                     /db_xref="taxon:161934"
                     /clone="024-017-H16"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 176
CF290854
LOCUS       CF290854                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A21, mRNA
            sequence.
ACCESSION   CF290854
VERSION     CF290854.1  GI:33659887
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-A21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 177
CF294668
LOCUS       CF294668                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
            sequence.
ACCESSION   CF294668
VERSION     CF294668.1  GI:33663701
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
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/clone="30DGS--04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 178
CF295988
LOCUS CF295988 17 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 179
CF298589
LOCUS CF298589 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION CF298589
VERSION CF298589.1 GI:33670350
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--02-A18"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 180
CF299997
LOCUS CF299997 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-D19, mRNA sequence.
ACCESSION CF299997
VERSION CF299997.1 GI:33671758
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-D19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 181
CF302447
LOCUS CF302447 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA sequence.
ACCESSION CF302447
VERSION CF302447.1 GI:33674208
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-P11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 182
CF310219
LOCUS CF310219 17 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION CF310219
VERSION CF310219.1 GI:33681980
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-M02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 183
CF311499
LOCUS CF311499 17 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION CF311499
VERSION CF311499.1 GI:33683260
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-L20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 184
CF313013
LOCUS CF313013 17 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-P19, mRNA sequence.
ACCESSION CF313013
VERSION CF313013.1 GI:33684774
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 185
CF319075
LOCUS CF319075 17 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-H06, mRNA sequence.
ACCESSION CF319075
VERSION CF319075.1 GI:33690836
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 186
CF334566
LOCUS CF334566 17 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-O13, mRNA sequence.
ACCESSION CF334566
VERSION CF334566.1 GI:33817460

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KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--03-O13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 187
CF336950
LOCUS       CF336950                 17 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--07-D04, mRNA sequence.
ACCESSION   CF336950
VERSION     CF336950.1  GI:33822280
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--07-D04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 188
AL038692/c
LOCUS       AL038692                 18 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  DKFZp566J0846_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566J0846, mRNA sequence.
ACCESSION   AL038692
VERSION     AL038692.1  GI:49682190
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566J0846"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 189
BQ582676
LOCUS       BQ582676                 18 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012281-024-007-P18-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-P18 5-PRIME, mRNA sequence.
ACCESSION   BQ582676
VERSION     BQ582676.1  GI:26112253
KEYWORDS    EST.
SOURCE      Beta vulgaris
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  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 18   Std Error: 0.00
            Plate: 7  row: P  column: 18
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:184018"
                      /db_xref="taxon:161934"
                      /clone="024-007-P18"
                      /tissue_type="inflorescence"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-inflorescence"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 190
BQ590027
LOCUS       BQ590027                 18 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-E24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E24 3-PRIME, mRNA sequence.
ACCESSION   BQ590027
VERSION     BQ590027.1  GI:26119610
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 18   Std Error: 0.00
            Plate: 19  row: E  column: 24
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .18
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                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:190095"
                      /db_xref="taxon:161934"
                      /clone="024-019-E24"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 191
CF277873
LOCUS       CF277873                 18 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-J04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-J04,
            mRNA sequence.
ACCESSION   CF277873
VERSION     CF277873.1  GI:33655259
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Oryza sativa (japonica cultivar-group)"
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--03-J04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 192
CF297446
LOCUS CF297446 18 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--08-F02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--08-F02, mRNA sequence.
ACCESSION CF297446
VERSION CF297446.1 GI:33666479
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--08-F02"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 193
CF298591
LOCUS CF298591 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA sequence.
ACCESSION CF298591
VERSION CF298591.1 GI:33670352
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--02-A20"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 194
CF299027
LOCUS CF299027 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-N14, mRNA sequence.
ACCESSION CF299027
VERSION CF299027.1 GI:33670788
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-N14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 195
CF299674
LOCUS       CF299674                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA
            sequence.
ACCESSION   CF299674
VERSION     CF299674.1  GI:33671435
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-M14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 196
CF300456
LOCUS       CF300456                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA
            sequence.
ACCESSION   CF300456
VERSION     CF300456.1  GI:33672217
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-N23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 197
CF301057
LOCUS       CF301057                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M05, mRNA
            sequence.
ACCESSION   CF301057
VERSION     CF301057.1  GI:33672818
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
```

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          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 198
CF301151
LOCUS       CF301151                18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-O05.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-O05, mRNA
            sequence.
ACCESSION   CF301151
VERSION     CF301151.1  GI:33672912
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-O05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 199
CF301325
LOCUS       CF301325                18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-C12, mRNA
            sequence.
ACCESSION   CF301325
VERSION     CF301325.1  GI:33673086
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="7LEAF--06-C12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 200
CF301359
LOCUS       CF301359                18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D05, mRNA
            sequence.
ACCESSION   CF301359
VERSION     CF301359.1  GI:33673120
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39947"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 201
CF301760
LOCUS       CF301760                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
            sequence.
ACCESSION   CF301760
VERSION     CF301760.1  GI:33673521
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="7LEAF--06-L22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 202
CF309376
LOCUS       CF309376                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-I19, mRNA sequence.
ACCESSION   CF309376
VERSION     CF309376.1  GI:33681137
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--03-I19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 203
CF320046
LOCUS       CF320046                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-M11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-M11, mRNA sequence.
ACCESSION   CF320046
VERSION     CF320046.1  GI:33691807
KEYWORDS    EST.
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SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--10-M11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 204
CF320418
LOCUS       CF320418                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-E22.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-E22, mRNA sequence.
ACCESSION   CF320418
VERSION     CF320418.1  GI:33692179
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-E22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 205
CF329285
LOCUS       CF329285                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-I22, mRNA
            sequence.
ACCESSION   CF329285
VERSION     CF329285.1  GI:33806806
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-I22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

```
RESULT 206
CF329484
LOCUS       CF329484                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA
            sequence.
ACCESSION   CF329484
VERSION     CF329484.1  GI:33807207
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 207
CF329485/c
LOCUS       CF329485                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA
            sequence.
ACCESSION   CF329485
VERSION     CF329485.1  GI:33807209
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 208
BI259338/c
LOCUS       BI259338                 32 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602972590F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5111783 5',
            mRNA sequence.
ACCESSION   BI259338
VERSION     BI259338.1  GI:14816575
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11271  row: d  column: 24
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5111783"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_12"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."

  Query Match             0.3%;  Score 15;  DB 1;  Length 32;
  Best Local Similarity   78.3%;  Pred. No. 3.6e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy       3296 AACCAGAGGGCATGCTGAATGCC 3318
              || ||| |||||| | | |||||
Db         23 AAGCAGGGGGCATTCAGCATGCC 1


RESULT 209
AW248796
LOCUS       AW248796                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820768.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820768 3',
            mRNA sequence.
ACCESSION   AW248796
VERSION     AW248796.1  GI:6591789
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820768.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 12
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: B  column: 1
            High quality sequence stop: 12.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820768"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4506 TTTTTTTTTTGGGTTAAA 4523
              ||||||||||||  |||
Db          1 TTTTTTTTTGGGGAAAA 18


RESULT 210
BM658677
```

```
LOCUS       BM658677                 18 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658677
VERSION     BM658677.1  GI:18958948
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2125 TTTCTTTTCTTTTTTTCT 2142
              ||| ||||||||||||| |
Db          1 TTTTTTTTCTTTTTTTT 18


RESULT 211
BX548564/c
LOCUS       BX548564                 21 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX548564 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse101g03_p1c, mRNA sequence.
ACCESSION   BX548564
VERSION     BX548564.1  GI:33298798
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
```

University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES Location/Qualifiers
source 1. .21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse101g03_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| ||||
Db 21 AAAAAAAAAAAAAAAGAA 4

RESULT 212
AZ625662
LOCUS AZ625662 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0465C23 F, genomic survey sequence.
ACCESSION AZ625662
VERSION AZ625662.1 GI:11747852
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0465 row: C column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0465C23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2385 AAAAATAAAATATATATA 2402
||||| |||| |||||||
Db 4 AAAAAAAAAAAATATATA 21

RESULT 213
AZ316361
LOCUS AZ316361 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0034I16 F, genomic survey sequence.
ACCESSION AZ316361
VERSION AZ316361.1 GI:10364110
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: I column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034I16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.3%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 2.9e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGAATTTGA 3627
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Db          1 AAAAAAAAAAAAAAAATTTAA 21
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RESULT 214
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LOCUS       AZ360314                 19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0103G03 R, genomic survey sequence.
ACCESSION   AZ360314
VERSION     AZ360314.1  GI:10474014
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: G  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0103G03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.3%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              |||||||| ||||| | ||
Db          1 GAAAAAAAGAAAAAAAAAA 19
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RESULT 215
AZ764517
LOCUS       AZ764517                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560L07 R, genomic survey sequence.
ACCESSION   AZ764517
VERSION     AZ764517.1  GI:12879561
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0560  row: L  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0560L07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3607 AAAAACAAAAACAGAATTT 3625
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Db          1 AAAAAAAAAAAAAAAATTT 19
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RESULT 216
AL587727/c
LOCUS AL587727 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone ROS061D01, mRNA sequence.
ACCESSION AL587727
VERSION AL587727.1 GI:13192761
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-
Seq primer: M13F.
FEATURES Location/Qualifiers
source 1. .20
/organism="Gallus gallus"
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/db_xref="taxon:9031"
/clone="ROS061D01"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGAAT 3623
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Db         19 AAAAAAAAAAAAAAAAAAT 1
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RESULT 217
BQ586422
LOCUS BQ586422 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013307-024-013-O02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-013-O02 3-PRIME, mRNA sequence.
ACCESSION BQ586422
VERSION BQ586422.1 GI:26116004
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 13 row: O column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:186441"
/db_xref="taxon:161934"
/clone="024-013-O02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 218
BQ587890
LOCUS BQ587890 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013302-024-009-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-009-B02 3-PRIME, mRNA sequence.
ACCESSION BQ587890
VERSION BQ587890.1 GI:26117472
KEYWORDS EST.

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SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 9  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184980"
                     /db_xref="taxon:161934"
                     /clone="024-009-B02"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TTTTTTTTTTTTTT 14


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LOCUS       BQ589191                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014009-024-015-I20-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-I20 3-PRIME, mRNA sequence.
ACCESSION   BQ589191
VERSION     BQ589191.1  GI:26118774
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 15  row: I  column: 20
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                     /clone="024-015-I20"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
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Db          1 TTTTTTTTTTTTTT 14


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LOCUS       BQ590242                  14 bp    mRNA    linear   EST 06-DEC-2002
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            cDNA clone 024-019-E16 5-PRIME, mRNA sequence.
ACCESSION   BQ590242
VERSION     BQ590242.1  GI:26119825
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
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                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TTTTTTTTTTTTTT 14


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ACCESSION   BQ590261
VERSION     BQ590261.1  GI:26119844
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 19  row: K  column: 14
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
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                     line)"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 222
BQ591168
LOCUS       BQ591168                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H18 3-PRIME, mRNA sequence.
ACCESSION   BQ591168
VERSION     BQ591168.1  GI:26120751
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: H  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188939"
                     /db_xref="taxon:161934"
                     /clone="024-017-H18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
```

SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14
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RESULT 223
BQ591176
LOCUS BQ591176 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-N20-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-N20 3-PRIME, mRNA sequence.
ACCESSION BQ591176
VERSION BQ591176.1 GI:26120759
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: N column: 20
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188947"
/db_xref="taxon:161934"
/clone="024-017-N20"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14
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RESULT 224
BQ591207
LOCUS BQ591207 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-B04-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION BQ591207
VERSION BQ591207.1 GI:26120790
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 04
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188904"
/db_xref="taxon:161934"
/clone="024-017-B04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14
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RESULT 225
BQ591380
LOCUS BQ591380 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012714-024-017-B15-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-B15 3-PRIME, mRNA sequence.

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ACCESSION   BQ591380
VERSION     BQ591380.1  GI:26120963
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: B  column: 15
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188734"
                     /db_xref="taxon:161934"
                     /clone="024-017-B15"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 226
BQ591482
LOCUS       BQ591482                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012713-024-017-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION   BQ591482
VERSION     BQ591482.1  GI:26121065
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: M  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188633"
                     /db_xref="taxon:161934"
                     /clone="024-017-M04"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 227
BQ593052
LOCUS       BQ593052                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012375-024-028-C03-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-C03 5-PRIME, mRNA sequence.
ACCESSION   BQ593052
VERSION     BQ593052.1  GI:26122635
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
```

```
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaa@mpiz-koeln.mpg.de
          Insert Length: 14   Std Error: 0.00
          Plate: 28  row: C  column: 03
          Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:193808"
                     /db_xref="taxon:161934"
                     /clone="024-028-C03"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 228
CF277935
LOCUS       CF277935                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-K11,
            mRNA sequence.
ACCESSION   CF277935
VERSION     CF277935.1  GI:33655321
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--03-K11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 229
CF278001
LOCUS       CF278001                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-L21,
            mRNA sequence.
ACCESSION   CF278001
VERSION     CF278001.1  GI:33655387
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--03-L21"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 230
CF278452
LOCUS       CF278452                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F22,
            mRNA sequence.
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ACCESSION   CF278452
VERSION     CF278452.1  GI:33655838
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--04-F22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 231
CF279473
LOCUS       CF279473                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-M14,
            mRNA sequence.
ACCESSION   CF279473
VERSION     CF279473.1  GI:33656859
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="14ETL--05-M14"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 232
CF279992
LOCUS       CF279992                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--06-I01,
            mRNA sequence.
ACCESSION   CF279992
VERSION     CF279992.1  GI:33657378
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 233
CF281958
LOCUS       CF281958                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-D24,
            mRNA sequence.
ACCESSION   CF281958
VERSION     CF281958.1  GI:33659345
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 234
CF282350
LOCUS       CF282350                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,
            mRNA sequence.
ACCESSION   CF282350
VERSION     CF282350.1  GI:33659737
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="14ETL--09-N05"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 235
CF294449
LOCUS       CF294449                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--03-P15, mRNA
            sequence.
ACCESSION   CF294449
VERSION     CF294449.1  GI:33663482
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 236
CF295570
LOCUS       CF295570                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--05-J06, mRNA
            sequence.
ACCESSION   CF295570
VERSION     CF295570.1  GI:33664603
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="30DGS--05-J06"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 237
CF296120
LOCUS       CF296120                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-F17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--06-F17, mRNA
            sequence.
ACCESSION   CF296120
VERSION     CF296120.1  GI:33665153
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 238
CF297969
LOCUS       CF297969                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-C16, mRNA
            sequence.
ACCESSION   CF297969
VERSION     CF297969.1  GI:33669730
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
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RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTT 4514
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Db 1 TTTTTTTTTTTTTT 14

RESULT 239
CF298109
LOCUS CF298109 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-F19, mRNA sequence.
ACCESSION CF298109
VERSION CF298109.1 GI:33669870
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTT 4514
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Db 1 TTTTTTTTTTTTTT 14

RESULT 240
CF299368
LOCUS CF299368 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F21, mRNA sequence.
ACCESSION CF299368
VERSION CF299368.1 GI:33671129
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTT 4514
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Db 1 TTTTTTTTTTTTTT 14

RESULT 241
CF300542
LOCUS CF300542 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION CF300542
VERSION CF300542.1 GI:33672303
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-B01"
/tissue_type="leaf"
/dev_stage="7 days after germination"

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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 242
CF301020
LOCUS       CF301020                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-L10, mRNA
            sequence.
ACCESSION   CF301020
VERSION     CF301020.1  GI:33672781
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="7LEAF--05-L10"
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 243
CF301083
LOCUS       CF301083                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M19, mRNA
            sequence.
ACCESSION   CF301083
VERSION     CF301083.1  GI:33672844
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="7LEAF--05-M19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 244
CF301380
LOCUS       CF301380                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
            sequence.
ACCESSION   CF301380
VERSION     CF301380.1  GI:33673141
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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/clone="7LEAF--06-D16"
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTTTTTTTTTTTT 14

RESULT 245
CF302675
LOCUS CF302675 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-G18, mRNA sequence.
ACCESSION CF302675
VERSION CF302675.1 GI:33674436
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTT 4514
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Db 1 TTTTTTTTTTTTTT 14

RESULT 246
CF302846
LOCUS CF302846 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-M05, mRNA sequence.
ACCESSION CF302846
VERSION CF302846.1 GI:33674607
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTT 4514
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Db 1 TTTTTTTTTTTTTT 14

RESULT 247
CF308006
LOCUS CF308006 14 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-K10, mRNA sequence.
ACCESSION CF308006
VERSION CF308006.1 GI:33679767
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers

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                    element binding transcription factor 3 overexpression
                    line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 248
CF308220
LOCUS       CF308220                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--01-P06, mRNA sequence.
ACCESSION   CF308220
VERSION     CF308220.1  GI:33679981
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 249
CF308445
LOCUS       CF308445                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--02-E10, mRNA sequence.
ACCESSION   CF308445
VERSION     CF308445.1  GI:33680206
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 250
CF308918
LOCUS       CF308918                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--02-O16, mRNA sequence.
ACCESSION   CF308918
VERSION     CF308918.1  GI:33680679
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 251
CF310714
LOCUS       CF310714                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-I11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-I11, mRNA sequence.
ACCESSION   CF310714
VERSION     CF310714.1  GI:33682475
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 252
CF311201
LOCUS       CF311201                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--06-F09, mRNA sequence.
ACCESSION   CF311201
VERSION     CF311201.1  GI:33682962
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--06-F09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 253
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CF311813
LOCUS       CF311813                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--07-D22, mRNA sequence.
ACCESSION   CF311813
VERSION     CF311813.1  GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--07-D22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 254
CF318323
LOCUS       CF318323                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-G13, mRNA sequence.
ACCESSION   CF318323
VERSION     CF318323.1  GI:33690084
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--08-G13"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 255
CF318450
LOCUS       CF318450                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-J08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-J08, mRNA sequence.
ACCESSION   CF318450
VERSION     CF318450.1  GI:33690211
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--08-J08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
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derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 256
CF319826
LOCUS CF319826 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-H16, mRNA sequence.
ACCESSION CF319826
VERSION CF319826.1 GI:33691587
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--10-H16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 257
CF321246
LOCUS CF321246 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--12-G24.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--12-G24, mRNA sequence.
ACCESSION CF321246
VERSION CF321246.1 GI:33693007
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--12-G24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 258
CF327097
LOCUS CF327097 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-H01, mRNA sequence.
ACCESSION CF327097
VERSION CF327097.1 GI:33802449
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14

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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--01-H01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 259
CF327119
LOCUS       CF327119                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-H14, mRNA
            sequence.
ACCESSION   CF327119
VERSION     CF327119.1  GI:33802493
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39947"
                     /clone="NACL--01-H14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 260
CF327203
LOCUS       CF327203                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-J16, mRNA
            sequence.
ACCESSION   CF327203
VERSION     CF327203.1  GI:33802665
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTG 4516
              ||||||||||||||
Db          1 TTTTTTTTTTTTTG 14


RESULT 261
CF327445
LOCUS       CF327445                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-O24, mRNA
            sequence.
ACCESSION   CF327445
VERSION     CF327445.1  GI:33803149
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--01-O24"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 262
CF328490
LOCUS       CF328490                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-G21, mRNA
            sequence.
ACCESSION   CF328490
VERSION     CF328490.1  GI:33805226
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 263
CF328540
LOCUS       CF328540                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-H24, mRNA
            sequence.
ACCESSION   CF328540
VERSION     CF328540.1  GI:33805324
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 264
CF328669
LOCUS       CF328669                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-K23, mRNA
            sequence.
ACCESSION   CF328669
VERSION     CF328669.1  GI:33805587
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
```

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           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="NACL--03-K23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 265
CF328994
LOCUS       CF328994                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-C11, mRNA
            sequence.
ACCESSION   CF328994
VERSION     CF328994.1  GI:33806228
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 266
CF329217
LOCUS       CF329217                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-H10, mRNA
            sequence.
ACCESSION   CF329217
VERSION     CF329217.1  GI:33806672
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 267
CF329990/c
LOCUS       CF329990                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-I11, mRNA
            sequence.
ACCESSION   CF329990
VERSION     CF329990.1  GI:33808202
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db         14 TTTTTTTTTTTTTT 1


RESULT 268
CF330784
LOCUS       CF330784                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-K10, mRNA
            sequence.
ACCESSION   CF330784
VERSION     CF330784.1  GI:33809790
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="NACL--06-K10"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db         1 TTTTTTTTTTTTTT 14


RESULT 269
CF331272
LOCUS       CF331272                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
            sequence.
ACCESSION   CF331272
VERSION     CF331272.1  GI:33810755
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="NACL--07-F09"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db         1 TTTTTTTTTTTTTT 14


RESULT 270
CF331861
LOCUS       CF331861                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-C10, mRNA
            sequence.
ACCESSION   CF331861
VERSION     CF331861.1  GI:33811945
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 271
CF333214
LOCUS       CF333214                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-A10, mRNA sequence.
ACCESSION   CF333214
VERSION     CF333214.1  GI:33814707
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39947"
                     /clone="JMT--02-A10"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 272
CF333215/c
LOCUS       CF333215                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-A10, mRNA sequence.
ACCESSION   CF333215
VERSION     CF333215.1  GI:33814709
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
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                     pepared from Arabidopsis Jasmoinate Carboxyl
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Db         14 TTTTTTTTTTTTTT 1


RESULT 273
CF333399
LOCUS       CF333399                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
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library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-E12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
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Db 1 TTTTTTTTTTTTTT 14

RESULT 274
CF334202
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DEFINITION JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-G11, mRNA sequence.
ACCESSION CF334202
VERSION CF334202.1 GI:33816736
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
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Db 1 TTTTTTTTTTTTTT 14

RESULT 275
CF334281
LOCUS CF334281 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-I05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-I05, mRNA sequence.
ACCESSION CF334281
VERSION CF334281.1 GI:33816894
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTTT 14


RESULT 276
CF334290
LOCUS       CF334290                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-I11, mRNA sequence.
ACCESSION   CF334290
VERSION     CF334290.1  GI:33816914
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="JMT--03-I11"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
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                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
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Qy       4501 TTTTTTTTTTTTTT 4514
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Db          1 TTTTTTTTTTTTTT 14


RESULT 277
CF335781
LOCUS       CF335781                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--05-J13, mRNA sequence.
ACCESSION   CF335781
VERSION     CF335781.1  GI:33819936
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
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Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 278
CF336094
LOCUS       CF336094                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-A10, mRNA sequence.
ACCESSION   CF336094
VERSION     CF336094.1  GI:33820566
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 279
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LOCUS CF336106 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--06-A17, mRNA sequence.
ACCESSION CF336106
VERSION CF336106.1 GI:33820590
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
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RESULT 280
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ACCESSION CF336287
VERSION CF336287.1 GI:33820962
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 281
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DEFINITION JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--07-C05, mRNA sequence.
ACCESSION CF336906
VERSION CF336906.1 GI:33822182
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES             Location/Qualifiers
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  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
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Db          1 TTTTTTTTTTTTTT 14


RESULT 282
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LOCUS       AW250872                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821138.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821138 3',
            mRNA sequence.
ACCESSION   AW250872
VERSION     AW250872.1  GI:6593865
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821138.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 15 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
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            High quality sequence stop: 8.
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                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGG 4518
              ||||||||||| ||||
Db          1 TTTTTTTTTTNTGGG 15


RESULT 283
CF295100
LOCUS       CF295100                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-O02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--04-O02, mRNA
            sequence.
ACCESSION   CF295100
VERSION     CF295100.1  GI:33664133
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--04-O02"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 284
CF301470
LOCUS       CF301470                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-F15, mRNA
```

```
            sequence.
ACCESSION   CF301470
VERSION     CF301470.1  GI:33673231
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--06-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTT 4513
              ||||||||||||||
Db          2 GTTTTTTTTTTTTT 15


RESULT 285
CR789161/c
LOCUS       CR789161                 15 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468J1632_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468J1632 5', mRNA sequence.
ACCESSION   CR789161
VERSION     CR789161.1  GI:53708043
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
            RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J1632
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468J1632"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTT 4513
              ||||||||||||||
Db         14 GTTTTTTTTTTTTT 1


RESULT 286
CF291803/c
LOCUS       CF291803                 16 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G05, mRNA
            sequence.
ACCESSION   CF291803
VERSION     CF291803.1  GI:33660836
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-G05"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         16 TTTTTTTTTTTTTT 3


RESULT 287
BQ591588
```

```
LOCUS       BQ591588                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012616-024-017-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-C15 5-PRIME, mRNA sequence.
ACCESSION   BQ591588
VERSION     BQ591588.1  GI:26121171
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 17  row: C  column: 15
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188532"
                     /db_xref="taxon:161934"
                     /clone="024-017-C15"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          4 TTTTTTTTTTTTTT 17


RESULT 288
AW245664/c
LOCUS       AW245664                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION   AW245664
VERSION     AW245664.1  GI:6588657
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence.
            Plate: LLCM10  row: N  column: 19.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822994"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| |||||||| |
Db         17 AAAAAAAAAAAACAGGA 1


RESULT 289
AW248574/c
LOCUS       AW248574                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3',
            mRNA sequence.
ACCESSION   AW248574
VERSION     AW248574.1  GI:6591567
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821096.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
```

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          be found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
          Scores: PHRED from University of Washington Genome Center. Vector
          Trimming: cross_match from University of Washington Genome Center
          PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
          Drosophila Genome Project. University of Washington Genome Center:
          http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
          PHRED high quality bases following vector sequence. Very Low
          Quality Sequence: Trace file contained 17 contiguous distinct peaks
          following vector sequence. Polyadenylation: Based upon the presence
          of a XhoI site followed by a run of 14 or more T residues at the
          beginning of the sequence, this cDNA insert was polyadenylated.
          Plate: LLCM5  row: O  column: 17
          High quality sequence stop: 8.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821096"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              ||||||||||||  | ||
Db         17 AAAAAACAAAAAAAAAA 1


RESULT 290
CF301359/c
LOCUS       CF301359                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D05, mRNA
            sequence.
ACCESSION   CF301359
VERSION     CF301359.1  GI:33673120
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--06-D05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              |||||||||  |||||  |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 291
CF309858
LOCUS       CF309858                  19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-D16, mRNA sequence.
ACCESSION   CF309858
VERSION     CF309858.1  GI:33681619
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--04-D16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              |||||||  |||||||  |
Db          3 AAAAAAAAAAAAACATA 19


RESULT 292
```

```
AZ486787/c
LOCUS       AZ486787                 20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0315D23 F, genomic survey sequence.
ACCESSION   AZ486787
VERSION     AZ486787.1  GI:10653904
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0315  row: D  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0315D23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||||| |
Db         17 AAAAAAAAAAAAACAAA 1


RESULT 293
AZ316368
```

```
LOCUS       AZ316368                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034L22 F, genomic survey sequence.
ACCESSION   AZ316368
VERSION     AZ316368.1  GI:10364124
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: L  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0034L22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3608 AAAACAAAAACAGAATTTGA 3627
              |||| ||||| | ||||| |
Db          1 AAAAAAAAAAAAAAATTTAA 20


RESULT 294
CF319428/c
LOCUS       CF319428                 20 bp    mRNA    linear   EST 15-AUG-2003
```

```
DEFINITION  HD--09-O20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--09-O20, mRNA sequence.
ACCESSION   CF319428
VERSION     CF319428.1  GI:33691189
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--09-O20"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAACAG 3620
              ||  ||||||| ||||| ||
Db         20 CTCAAAAAAAAAAAAAAAAG 1


RESULT 295
CF301470/c
LOCUS       CF301470                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-F15, mRNA
            sequence.
ACCESSION   CF301470
VERSION     CF301470.1  GI:33673231
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--06-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         15 AAAAAAAAAAAAACA 1


RESULT 296
CR789161
LOCUS       CR789161                 15 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468J1632_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468J1632 5', mRNA sequence.
ACCESSION   CR789161
VERSION     CR789161.1  GI:53708043
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
            RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J1632
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468J1632"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
```

```
Db          1 AAAAAAAAAAAAACA 15


RESULT 297
CF290849/c
LOCUS       CF290849                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A17, mRNA
            sequence.
ACCESSION   CF290849
VERSION     CF290849.1  GI:33659882
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-A17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||| |||||
Db         15 TTTTTTTTATTTTT 1


RESULT 298
CF291030/c
LOCUS       CF291030                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E19, mRNA
            sequence.
ACCESSION   CF291030
VERSION     CF291030.1  GI:33660063
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-E19"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||| |||||||
Db         15 TTTTTTTATTTTTTT 1


RESULT 299
AW245338
LOCUS       AW245338                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822905.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822905 3',
            mRNA sequence.
ACCESSION   AW245338
VERSION     AW245338.1  GI:6588331
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822905.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM10  row: K  column: 2
            High quality sequence stop: 15.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="IMAGE:2822905"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4506 TTTTTTTTTGGGTT 4520
||||||||||| |||
Db 1 TTTTTTTTTGTGTT 15

RESULT 300
CF317778
LOCUS CF317778 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-J13, mRNA sequence.
ACCESSION CF317778
VERSION CF317778.1 GI:33689539
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-J13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||| ||||||||||||

Db 1 TTTGTTTTTTTTTTT 15

RESULT 301
CF291802/c
LOCUS CF291802 17 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION CF291802
VERSION CF291802.1 GI:33660835
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-G05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| |||||||
Db 15 AAAAAAAAAAAAACA 1

RESULT 302
AW248574
LOCUS AW248574 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3', mRNA sequence.
ACCESSION AW248574
VERSION AW248574.1 GI:6591567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821096.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 8 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM5 row: O column: 17
High quality sequence stop: 8.

```
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821096"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 3.2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||| ||||
Db          1 TTTTTTTTTGTTTT 15


RESULT 303
CF291899/c
LOCUS       CF291899                19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I08.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I08, mRNA
            sequence.
ACCESSION   CF291899
VERSION     CF291899.1  GI:33660932
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-I08"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         15 AAAAAAAAAAAAACA 1


RESULT 304
CF292072/c
LOCUS       CF292072                19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA
            sequence.
ACCESSION   CF292072
VERSION     CF292072.1  GI:33661105
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-M03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         15 AAAAAAAAAAAAACA 1


RESULT 305
```

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CF292144/c
LOCUS       CF292144                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-N17, mRNA
            sequence.
ACCESSION   CF292144
VERSION     CF292144.1  GI:33661177
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-N17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         15 AAAAAAAAAAAAACA 1


RESULT 306
CF310688
LOCUS       CF310688                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-H18, mRNA sequence.
ACCESSION   CF310688
VERSION     CF310688.1  GI:33682449
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--05-H18"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db          5 AAAAAAAAAAAAACA 19


RESULT 307
CF333052/c
LOCUS       CF333052                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--01-M17, mRNA sequence.
ACCESSION   CF333052
VERSION     CF333052.1  GI:33814360
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--01-M17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 20;
```

```
  Best Local Similarity   93.3%;  Pred. No. 4.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         16 AAAAAAAAAAAAACA 2


RESULT 308
AL038692
LOCUS       AL038692                 18 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  DKFZp566J0846_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566J0846, mRNA sequence.
ACCESSION   AL038692
VERSION     AL038692.1  GI:49682190
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566J0846"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 309
BQ582676/c
LOCUS       BQ582676                 18 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012281-024-007-P18-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-P18 5-PRIME, mRNA sequence.
ACCESSION   BQ582676
VERSION     BQ582676.1  GI:26112253
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 18   Std Error: 0.00
            Plate: 7  row: P  column: 18
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184018"
                     /db_xref="taxon:161934"
                     /clone="024-007-P18"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 310
BQ590027/c
LOCUS       BQ590027                 18 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-E24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E24 3-PRIME, mRNA sequence.
ACCESSION   BQ590027
VERSION     BQ590027.1  GI:26119610
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 18   Std Error: 0.00
            Plate: 19  row: E  column: 24
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Beta vulgaris"
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:190095"
/db_xref="taxon:161934"
/clone="024-019-E24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 311
CF277873/c
LOCUS CF277873 18 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--03-J04.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-J04, mRNA sequence.
ACCESSION CF277873
VERSION CF277873.1 GI:33655259
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--03-J04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 312
CF297446/c
LOCUS CF297446 18 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--08-F02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--08-F02, mRNA sequence.
ACCESSION CF297446
VERSION CF297446.1 GI:33666479
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--08-F02"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 313
CF299027/c
LOCUS CF299027 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-N14, mRNA sequence.
ACCESSION CF299027
VERSION CF299027.1 GI:33670788
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-N14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 314
CF299674/c
LOCUS       CF299674                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA
            sequence.
ACCESSION   CF299674
VERSION     CF299674.1  GI:33671435
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-M14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 315
CF301057/c
LOCUS       CF301057                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M05, mRNA
            sequence.
ACCESSION   CF301057
VERSION     CF301057.1  GI:33672818
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-M05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 316
CF301325/c
LOCUS       CF301325                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-C12, mRNA
            sequence.
ACCESSION   CF301325
VERSION     CF301325.1  GI:33673086
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnahm@ggbio.com, bnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="7LEAF--06-C12"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 317
CF301760/c
LOCUS       CF301760                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
            sequence.
ACCESSION   CF301760
VERSION     CF301760.1  GI:33673521
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnahm@ggbio.com, bnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="7LEAF--06-L22"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 318
CF329285/c
LOCUS       CF329285                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-I22, mRNA
            sequence.
ACCESSION   CF329285
VERSION     CF329285.1  GI:33806806
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnahm@ggbio.com, bnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="NACL--04-I22"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
              | |||||||| ||||| |
Db         18 TAGAAAAAAAAAAAAAAA 1


RESULT 319
CF293167/c
LOCUS       CF293167                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--02-E02, mRNA
            sequence.
ACCESSION   CF293167
VERSION     CF293167.1  GI:33662200
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KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--02-E02"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 320
CF298396/c
LOCUS       CF298396                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M05, mRNA
            sequence.
ACCESSION   CF298396
VERSION     CF298396.1  GI:33670157
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--01-M05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 321
CF302456/c
LOCUS       CF302456                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA
            sequence.
ACCESSION   CF302456
VERSION     CF302456.1  GI:33674217
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-P22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 322
CF309821/c
LOCUS       CF309821                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-C17.g1 ABF3-overexpressing transgenic rice plasmid cDNA
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library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--04-C17, mRNA sequence.
ACCESSION CF309821
VERSION CF309821.1 GI:33681582
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-C17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 323
CF311778/c
LOCUS CF311778 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-D01.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-D01, mRNA sequence.
ACCESSION CF311778
VERSION CF311778.1 GI:33683539
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-D01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 324
CF331361/c
LOCUS CF331361 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-H08.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-H08, mRNA sequence.
ACCESSION CF331361
VERSION CF331361.1 GI:33810941
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--07-H08"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 325
CF335293/c
LOCUS       CF335293                 19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--04-O17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--04-O17, mRNA sequence.
ACCESSION   CF335293
VERSION     CF335293.1  GI:33818938
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--04-O17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 326
CN545923/c
LOCUS       CN545923                 19 bp    mRNA    linear   EST 30-APR-2004
DEFINITION  EST 17867 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL006D08 3', mRNA sequence.
ACCESSION   CN545923
VERSION     CN545923.1  GI:46910548
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
  TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultivar="Cabernet Sauvignon"
                     /db_xref="taxon:29760"
                     /clone="B3CS00RL006D08"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 327
AZ513919/c
LOCUS       AZ513919                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0360E13 F, genomic survey sequence.
ACCESSION   AZ513919
VERSION     AZ513919.1  GI:10695235
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0360  row: E  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0360E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAGAAAAAAAAAA 2
```

RESULT 328
AL587572/c
LOCUS AL587572 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587572 BP Chicken Brain Library Gallus gallus cDNA clone ROS059B11, mRNA sequence.
ACCESSION AL587572
VERSION AL587572.1 GI:13192606
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-
Seq primer: M13F.
FEATURES Location/Qualifiers
source 1. .20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 329
CF316662/c
LOCUS CF316662 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--06-A20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--06-A20, mRNA sequence.
ACCESSION CF316662
VERSION CF316662.1 GI:33688423
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-A20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 330
AZ821905
LOCUS AZ821905 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0094D20 R, genomic survey sequence.
ACCESSION AZ821905

```
VERSION     AZ821905.1  GI:12991813
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0094  row: D  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0094D20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          3 AAAAAAAAAAAAAAAAAA 20


RESULT 331
AJ666275/c
LOCUS       AJ666275                 20 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ666275 CSEQRAN09 Sus scrofa cDNA clone C0000033_B07, mRNA
            sequence.
ACCESSION   AJ666275
VERSION     AJ666275.1  GI:49350726
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institite,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0000033_B07"
                     /tissue_type="placenta"
                     /clone_lib="CSEQRAN09"
                     /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pooled tissue from day 30 placentas."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         20 AAAAAAAAAAAAAAAAAA 3


RESULT 332
AL038460
LOCUS       AL038460                 20 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  DKFZp566B2246_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566B2246, mRNA sequence.
ACCESSION   AL038460
VERSION     AL038460.1  GI:49682131
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566B2246"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          3 AAAAAAAAAAAAAAAAAA 20


RESULT 333
CA853586/c
LOCUS       CA853586                 20 bp    mRNA    linear   EST 01-AUG-2003
DEFINITION  B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
            B09H12 5', mRNA sequence.
ACCESSION   CA853586
VERSION     CA853586.1  GI:33390391
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Alkharouf,N.W., Khan,R. and Matthews,B.F.
  TITLE     Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharon@ba.ars.usda.gov.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Peking"
                     /db_xref="taxon:3847"
                     /clone="B09H12"
                     /tissue_type="Roots"
                     /dev_stage="Seedlings"
                     /clone_lib="cDNA Peking library 12hr SCN3"
                     /note="Vector: pBluescript SK-; cDNA clones from mRNA
                     extracted from roots of soybean cv. Peking 12  hrs after
                     infection by SCN race 3. These are cloned in pBluescript
                     SK- phagemid. "

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         20 AAAAAAAAAAAAAAAAAA 3


RESULT 334
CF282002/c
LOCUS       CF282002                 20 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F01,
            mRNA sequence.
ACCESSION   CF282002
VERSION     CF282002.1  GI:33659389
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--09-F01"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 335
CF318278/c
LOCUS       CF318278                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-F13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-F13, mRNA sequence.
ACCESSION   CF318278
VERSION     CF318278.1  GI:33690039
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--08-F13"
                     /tissue_type="callus"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         20 AAAAAAAAAAAAAAAAAA 3


RESULT 336
CF320843/c
LOCUS       CF320843                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-O01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-O01, mRNA sequence.
ACCESSION   CF320843
VERSION     CF320843.1  GI:33692604
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-O01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 337
AZ579178
LOCUS       AZ579178                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0363F11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0363F11 F, genomic survey sequence.
ACCESSION   AZ579178
VERSION     AZ579178.1  GI:11693523
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0363  row: F  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0363F11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          2 AAAAAAAAAAAAAAAAAA 19


RESULT 338
AZ633741
```

```
LOCUS       AZ633741                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0489G12 F, genomic survey sequence.
ACCESSION   AZ633741
VERSION     AZ633741.1  GI:11755931
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0489  row: G  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0489G12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||||  ||
Db          3 AAAAAAAAAAAAACCAAA 20


RESULT 339
CF276747/c
LOCUS       CF276747                 21 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--02-A06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-A06,
            mRNA sequence.
ACCESSION   CF276747
VERSION     CF276747.1  GI:33654133
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--02-A06"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 4.9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 340
AZ843648
LOCUS       AZ843648                 22 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0142B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0142B07 R, genomic survey sequence.
ACCESSION   AZ843648
VERSION     AZ843648.1  GI:13013556
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: B column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142B07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 13.2; DB 1; Length 22;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 341
CF318266/c
LOCUS CF318266 23 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-F07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-F07, mRNA sequence.
ACCESSION CF318266
VERSION CF318266.1 GI:33690027
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-F07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13.2; DB 1; Length 23;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 342
CF308158/c
LOCUS CF308158 25 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-N19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-N19, mRNA sequence.
ACCESSION CF308158
VERSION CF308158.1 GI:33679919
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--01-N19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13.2; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;

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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAA 3617
              |||  ||||||| |||||
Db         19 TCTTAAAAAAAAAAAAAA 2


RESULT 343
BQ583549/c
LOCUS       BQ583549                  13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011978-024-005-C14-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION   BQ583549
VERSION     BQ583549.1  GI:26113126
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 5  row: C  column: 14
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:183152"
                     /db_xref="taxon:161934"
                     /clone="024-005-C14"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 344
BQ589180
LOCUS       BQ589180                  13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014009-024-015-I22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-I22 3-PRIME, mRNA sequence.
ACCESSION   BQ589180
VERSION     BQ589180.1  GI:26118763
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 15  row: I  column: 22
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187886"
                     /db_xref="taxon:161934"
                     /clone="024-015-I22"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         1 TTTTTTTTTTTTT 13


RESULT 345
BQ590337/c
LOCUS       BQ590337                  13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012840-024-019-G12-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-G12 5-PRIME, mRNA sequence.
ACCESSION   BQ590337
VERSION     BQ590337.1  GI:26119920
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
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REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 19  row: G  column: 12
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="taxon:161934"
                     /clone="024-019-G12"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db         13 TTTTTTTTTTTTT 1


RESULT 346
CF278426
LOCUS       CF278426                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F09,
            mRNA sequence.
ACCESSION   CF278426
VERSION     CF278426.1  GI:33655812
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--04-F09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 347
CF280420
LOCUS       CF280420                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-B11,
            mRNA sequence.
ACCESSION   CF280420
VERSION     CF280420.1  GI:33657806
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 348
CF280707
LOCUS       CF280707                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H19,
            mRNA sequence.
ACCESSION   CF280707
VERSION     CF280707.1  GI:33658093
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 349
CF280757
LOCUS       CF280757                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-I21.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-I21,
            mRNA sequence.
ACCESSION   CF280757
VERSION     CF280757.1  GI:33658143
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     (14ETL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 350
CF282369
LOCUS       CF282369                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N16.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N16,
            mRNA sequence.
ACCESSION   CF282369
VERSION     CF282369.1  GI:33659756
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /clone="14ETL--09-N16"
                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 351
CF290970
LOCUS       CF290970                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
            sequence.
ACCESSION   CF290970
VERSION     CF290970.1  GI:33660003
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 352
CF290971/c
LOCUS       CF290971                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
            sequence.
ACCESSION   CF290971
VERSION     CF290971.1  GI:33660004
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 353
CF291011
LOCUS       CF291011                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E10, mRNA
            sequence.
ACCESSION   CF291011
VERSION     CF291011.1  GI:33660044
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-E10"
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
||||||||||||||
Db 1 TTTTTTTTTTTTT 13

RESULT 354
CF291060
LOCUS CF291060 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION CF291060
VERSION CF291060.1 GI:33660093
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F11"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
||||||||||||||
Db 1 TTTTTTTTTTTTT 13

RESULT 355
CF291061/c
LOCUS CF291061 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION CF291061
VERSION CF291061.1 GI:33660094
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F11"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
||||||||||||||
Db 13 TTTTTTTTTTTTT 1

RESULT 356
CF291167
LOCUS CF291167 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION CF291167
VERSION CF291167.1 GI:33660200
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"

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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-H20"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 357
CF291214
LOCUS       CF291214                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-I22, mRNA
            sequence.
ACCESSION   CF291214
VERSION     CF291214.1  GI:33660247
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-I22"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 358
CF291427
LOCUS       CF291427                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-N14, mRNA
            sequence.
ACCESSION   CF291427
VERSION     CF291427.1  GI:33660460
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-N14"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 359
CF291469
LOCUS       CF291469                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-O12, mRNA
            sequence.
ACCESSION   CF291469
VERSION     CF291469.1  GI:33660502
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
```

```
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-O12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 360
CF291479
LOCUS       CF291479                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-O17, mRNA
            sequence.
ACCESSION   CF291479
VERSION     CF291479.1  GI:33660512
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-O17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 361
CF291514
LOCUS       CF291514                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
            sequence.
ACCESSION   CF291514
VERSION     CF291514.1  GI:33660547
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-P13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 362
CF291515/c
LOCUS       CF291515                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
            sequence.
ACCESSION   CF291515
VERSION     CF291515.1  GI:33660548
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /clone="14ROOT--01-P13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy       4501 TTTTTTTTTTTTT 4513
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Db         13 TTTTTTTTTTTTT 1


RESULT 363
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LOCUS       CF291596                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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            sequence.
ACCESSION   CF291596
VERSION     CF291596.1  GI:33660629
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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                     with oligoribonucleotides and then used as templates for
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Db         13 TTTTTTTTTTTTT 1


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CF291597/c
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DEFINITION  14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B12, mRNA
            sequence.
ACCESSION   CF291597
VERSION     CF291597.1  GI:33660630
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Db         13 TTTTTTTTTTTTT 1


RESULT 365
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LOCUS       CF291726                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E10, mRNA
            sequence.
ACCESSION   CF291726
VERSION     CF291726.1  GI:33660759
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db          1 TTTTTTTTTTTTT 13


RESULT 366
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LOCUS       CF291903                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I10, mRNA
            sequence.
ACCESSION   CF291903
VERSION     CF291903.1  GI:33660936
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db          1 TTTTTTTTTTTTT 13


RESULT 367
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LOCUS       CF298590                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF298590
VERSION     CF298590.1  GI:33670351
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 368
CF298592
LOCUS       CF298592                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF298592
VERSION     CF298592.1  GI:33670353
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TTTTTTTTTTTTT 13


RESULT 369
CF298736
LOCUS       CF298736                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF298736
VERSION     CF298736.1  GI:33670497
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Db          1 TTTTTTTTTTTTT 13


RESULT 370
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LOCUS       CF298764                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF298764
VERSION     CF298764.1  GI:33670525
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Db          1 TTTTTTTTTTTTT 13


RESULT 371
CF298795
LOCUS       CF298795                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF298795
VERSION     CF298795.1  GI:33670556
KEYWORDS    EST.
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 372
CF298908
LOCUS       CF298908                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF298908
VERSION     CF298908.1  GI:33670669
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
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Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 373
CF299133
LOCUS       CF299133                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-A06, mRNA
            sequence.
ACCESSION   CF299133
VERSION     CF299133.1  GI:33670894
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 374
CF299359
LOCUS       CF299359                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F15, mRNA
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            sequence.
ACCESSION   CF299359
VERSION     CF299359.1  GI:33671120
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 375
CF299937
LOCUS       CF299937                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C12, mRNA
            sequence.
ACCESSION   CF299937
VERSION     CF299937.1  GI:33671698
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 376
CF300118
LOCUS       CF300118                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G10, mRNA
            sequence.
ACCESSION   CF300118
VERSION     CF300118.1  GI:33671879
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 377
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CF300587
LOCUS       CF300587                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-C01, mRNA
            sequence.
ACCESSION   CF300587
VERSION     CF300587.1  GI:33672348
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 378
CF300658
LOCUS       CF300658                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-D14, mRNA
            sequence.
ACCESSION   CF300658
VERSION     CF300658.1  GI:33672419
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 379
CF300929
LOCUS       CF300929                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J11, mRNA
            sequence.
ACCESSION   CF300929
VERSION     CF300929.1  GI:33672690
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 380
CF301247
LOCUS       CF301247                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sequence.
ACCESSION   CF301247
VERSION     CF301247.1  GI:33673008
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 381
CF301286
LOCUS       CF301286                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-B15, mRNA
            sequence.
ACCESSION   CF301286
VERSION     CF301286.1  GI:33673047
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 382
CF302158
LOCUS       CF302158                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-G20, mRNA
            sequence.
ACCESSION   CF302158
VERSION     CF302158.1  GI:33673919
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 383
CF302830
LOCUS       CF302830                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--08-L16, mRNA
            sequence.
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--08-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 384
CF302898
LOCUS       CF302898                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--08-N08, mRNA
            sequence.
ACCESSION   CF302898
VERSION     CF302898.1  GI:33674659
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 385
CF310516
LOCUS       CF310516                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-D09, mRNA sequence.
ACCESSION   CF310516
VERSION     CF310516.1  GI:33682277
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="ABF--05-D09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13
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RESULT 386
CF310517/c
LOCUS CF310517 13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION CF310517
VERSION CF310517.1 GI:33682278
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 387
CF312721
LOCUS CF312721 13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-J13, mRNA sequence.
ACCESSION CF312721
VERSION CF312721.1 GI:33684482
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13
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RESULT 388
CF313171
LOCUS CF313171 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-D10.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--01-D10, mRNA sequence.
ACCESSION CF313171
VERSION CF313171.1 GI:33684932
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
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                     /clone="HD--01-D10"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 389
CF314239
LOCUS       CF314239                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-L01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-L01, mRNA sequence.
ACCESSION   CF314239
VERSION     CF314239.1  GI:33686000
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 390
CF314874
LOCUS       CF314874                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-J07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--03-J07, mRNA sequence.
ACCESSION   CF314874
VERSION     CF314874.1  GI:33686635
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="callus"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
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                     line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 391
CF315395
LOCUS       CF315395                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-E20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--04-E20, mRNA sequence.
ACCESSION   CF315395
VERSION     CF315395.1  GI:33687156
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 392
CF316439
LOCUS       CF316439                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-L17, mRNA sequence.
ACCESSION   CF316439
VERSION     CF316439.1  GI:33688200
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 393
CF316440/c
LOCUS       CF316440                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-L17, mRNA sequence.
ACCESSION   CF316440
VERSION     CF316440.1  GI:33688201
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                      line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
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Qy       4501 TTTTTTTTTTTTT 4513
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Db         13 TTTTTTTTTTTTT 1
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RESULT 394
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DEFINITION  HD--06-A04.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--06-A04, mRNA sequence.
ACCESSION   CF316637
VERSION     CF316637.1  GI:33688398
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     line."

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Db          1 TTTTTTTTTTTTT 13


RESULT 395
CF318290
LOCUS       CF318290                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-F19.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-F19, mRNA sequence.
ACCESSION   CF318290
VERSION     CF318290.1  GI:33690051
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     line."

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Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 396
CF319066
LOCUS       CF319066                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H02.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--09-H02, mRNA sequence.
ACCESSION   CF319066
VERSION     CF319066.1  GI:33690827
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTT 13
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LOCUS CF319531 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-B03.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-B03, mRNA sequence.
ACCESSION CF319531
VERSION CF319531.1 GI:33691292
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2e+02;
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RESULT 398
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LOCUS CF319532 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-B03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-B03, mRNA sequence.
ACCESSION CF319532
VERSION CF319532.1 GI:33691293
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Query Match 0.3%; Score 13; DB 1; Length 13;
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Db         13 TTTTTTTTTTTTT 1
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RESULT 399
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LOCUS CF319919 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-J17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-J17, mRNA sequence.
ACCESSION CF319919
VERSION CF319919.1 GI:33691680
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers

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                    line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 400
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LOCUS       CF320017                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-L20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-L20, mRNA sequence.
ACCESSION   CF320017
VERSION     CF320017.1  GI:33691778
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 401
CF320018/c
LOCUS       CF320018                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-L20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-L20, mRNA sequence.
ACCESSION   CF320018
VERSION     CF320018.1  GI:33691779
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Qy       4501 TTTTTTTTTTTTT 4513
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Db         13 TTTTTTTTTTTTT 1


RESULT 402
CF320143
LOCUS       CF320143                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-O13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
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            HD--10-O13, mRNA sequence.
ACCESSION   CF320143
VERSION     CF320143.1  GI:33691904
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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                     line."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TTTTTTTTTTTTT 13


RESULT 403
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LOCUS       CF320938                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-A06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
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            HD--12-A06, mRNA sequence.
ACCESSION   CF320938
VERSION     CF320938.1  GI:33692699
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--12-A06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 404
CF326844
LOCUS       CF326844                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-B12, mRNA
            sequence.
ACCESSION   CF326844
VERSION     CF326844.1  GI:33801943
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
                     /clone="NACL--01-B12"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 405
CF327070
LOCUS       CF327070                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
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sativa (japonica cultivar-group) cDNA clone NACL--01-G09, mRNA sequence.
ACCESSION CF327070
VERSION CF327070.1 GI:33802396
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
||||||||||||||
Db 1 TTTTTTTTTTTTT 13

RESULT 406
CF327339
LOCUS CF327339 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION CF327339
VERSION CF327339.1 GI:33802936
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
||||||||||||||
Db 1 TTTTTTTTTTTTT 13

RESULT 407
CF327340/c
LOCUS CF327340 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION CF327340
VERSION CF327340.1 GI:33802938
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
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Db 13 TTTTTTTTTTTTT 1

RESULT 408
CF327576
LOCUS CF327576 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-B22, mRNA sequence.
ACCESSION CF327576
VERSION CF327576.1 GI:33803404
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/mol_type="mRNA"
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/clone="NACL--02-B22"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
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Qy 4501 TTTTTTTTTTTTT 4513
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Db 1 TTTTTTTTTTTTT 13

RESULT 409
CF327888
LOCUS CF327888 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-I22, mRNA sequence.
ACCESSION CF327888
VERSION CF327888.1 GI:33804024
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone="NACL--02-I22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513
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Db 1 TTTTTTTTTTTTT 13

RESULT 410
CF327939
LOCUS CF327939 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-K02, mRNA sequence.
ACCESSION CF327939
VERSION CF327939.1 GI:33804127
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="NACL--02-K02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTT 4513

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              ||||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 411
CF328153
LOCUS       CF328153                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-O19, mRNA
            sequence.
ACCESSION   CF328153
VERSION     CF328153.1  GI:33804556
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-O19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 412
CF328228
LOCUS       CF328228                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-A13, mRNA
            sequence.
ACCESSION   CF328228
VERSION     CF328228.1  GI:33804702
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 413
CF328807
LOCUS       CF328807                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-O07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-O07, mRNA
            sequence.
ACCESSION   CF328807
VERSION     CF328807.1  GI:33805856
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 414
CF329075
LOCUS       CF329075                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
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            sequence.
ACCESSION   CF329075
VERSION     CF329075.1  GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 415
CF329076/c
LOCUS       CF329076                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-E07, mRNA
            sequence.
ACCESSION   CF329076
VERSION     CF329076.1  GI:33806395
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 416
CF329417
LOCUS       CF329417                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-L19, mRNA
            sequence.
ACCESSION   CF329417
VERSION     CF329417.1  GI:33807072
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-L19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13
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RESULT 417
CF329460
LOCUS CF329460 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-M18, mRNA sequence.
ACCESSION CF329460
VERSION CF329460.1 GI:33807156
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-M18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13
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RESULT 418
CF329729/c
LOCUS CF329729 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-C14, mRNA sequence.
ACCESSION CF329729
VERSION CF329729.1 GI:33807674
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/mol_type="mRNA"
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/clone="NACL--05-C14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 419
CF329800
LOCUS CF329800 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION CF329800
VERSION CF329800.1 GI:33807817
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-E04"
/tissue_type="callus"

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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 420
CF329801/c
LOCUS       CF329801                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-E04, mRNA
            sequence.
ACCESSION   CF329801
VERSION     CF329801.1  GI:33807819
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-E04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 421
CF329869
LOCUS       CF329869                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-F18, mRNA
            sequence.
ACCESSION   CF329869
VERSION     CF329869.1  GI:33807959
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--05-F18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 422
CF329946
LOCUS       CF329946                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-H12, mRNA
            sequence.
ACCESSION   CF329946
VERSION     CF329946.1  GI:33808114
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-H12"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 423
CF329988
LOCUS       CF329988                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-I10, mRNA
            sequence.
ACCESSION   CF329988
VERSION     CF329988.1  GI:33808198
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-I10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 424
CF330023
LOCUS       CF330023                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-J05, mRNA
            sequence.
ACCESSION   CF330023
VERSION     CF330023.1  GI:33808268
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-J05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 425
CF330725/c
LOCUS       CF330725                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-J01, mRNA
            sequence.
ACCESSION   CF330725
VERSION     CF330725.1  GI:33809672
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--06-J01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db         13 TTTTTTTTTTTTT 1


RESULT 426
CF331041
LOCUS       CF331041                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-A04, mRNA
            sequence.
ACCESSION   CF331041
VERSION     CF331041.1  GI:33810299
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 427
CF331266
LOCUS       CF331266                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-F06, mRNA
            sequence.
ACCESSION   CF331266
VERSION     CF331266.1  GI:33810744
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 428
CF331273/c
LOCUS       CF331273                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
            sequence.
ACCESSION   CF331273
VERSION     CF331273.1  GI:33810757
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 429
CF331903
LOCUS       CF331903                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-D07, mRNA
            sequence.
ACCESSION   CF331903
VERSION     CF331903.1  GI:33812027
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         1 TTTTTTTTTTTTT 13


RESULT 430
CF332079
LOCUS       CF332079                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-H04, mRNA
            sequence.
ACCESSION   CF332079
VERSION     CF332079.1  GI:33812379
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db         1 TTTTTTTTTTTTT 13


RESULT 431
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LOCUS       CF332695                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--01-E21, mRNA sequence.
ACCESSION   CF332695
VERSION     CF332695.1  GI:33813618
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 432
CF332696/c
LOCUS       CF332696                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--01-E21, mRNA sequence.
ACCESSION   CF332696
VERSION     CF332696.1  GI:33813620
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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Qy       4501 TTTTTTTTTTTTT 4513
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Db         13 TTTTTTTTTTTTT 1


RESULT 433
CF333486
LOCUS       CF333486                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-G11, mRNA sequence.
ACCESSION   CF333486
VERSION     CF333486.1  GI:33815268
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 434
CF333972
LOCUS       CF333972                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-B12, mRNA sequence.
ACCESSION   CF333972
VERSION     CF333972.1  GI:33816249
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KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
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Db          1 TTTTTTTTTTTTT 13


RESULT 435
CF333973/c
LOCUS       CF333973                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-B12, mRNA sequence.
ACCESSION   CF333973
VERSION     CF333973.1  GI:33816251
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--03-B12"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 436
CF334347
LOCUS       CF334347                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-J19, mRNA sequence.
ACCESSION   CF334347
VERSION     CF334347.1  GI:33817022
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--03-J19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13
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RESULT 437
CF337022
LOCUS       CF337022                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--07-E22, mRNA sequence.
ACCESSION   CF337022
VERSION     CF337022.1  GI:33822426
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--07-E22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 438
CN546046
LOCUS       CN546046                  13 bp    mRNA    linear   EST 30-APR-2004
DEFINITION  EST 17998 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL007H03 3', mRNA sequence.
ACCESSION   CN546046
VERSION     CN546046.1  GI:46910671
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
  TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultivar="Cabernet Sauvignon"
                     /db_xref="taxon:29760"
                     /clone="B3CS00RL007H03"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

  Query Match             0.3%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 439
CN752228/c
LOCUS       CN752228                  13 bp    mRNA    linear   EST 19-MAY-2004
DEFINITION  ApHL3SD-XXVIII-A5 ApHL3SD Acyrthosiphon pisum cDNA clone
            ApHL3SDXXVIIIA5 5', mRNA sequence.
ACCESSION   CN752228
VERSION     CN752228.1  GI:47517225
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
  ORGANISM  Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
  TITLE     An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
  JOURNAL   Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR PRimers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXVIII  row: A  column: 5.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Acyrthosiphon pisum"
                     /mol_type="mRNA"
                     /cultivar="yr2"
                     /db_xref="taxon:7029"
                     /clone="ApHL3SDXXVIIIA5"
                     /tissue_type="head"
                     /dev_stage="third instar nymph (L3)"
                     /lab_host="TOP10"
                     /clone_lib="ApHL3SD"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
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Sample name: ApHL3SD ; Plant growth place: INRA-Rennes, UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 20/03/2003 ; Harvesting date: 10/04/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 440
CN752875/c
LOCUS CN752875 13 bp mRNA linear EST 19-MAY-2004
DEFINITION ApHL3LD-VII-H10 ApHL3LD Acyrthosiphon pisum cDNA clone ApHL3LDVIIH10 5', mRNA sequence.
ACCESSION CN752875
VERSION CN752875.1 GI:47517872
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 13)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts.
PCR PRimers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: VII row: H column: 10.
FEATURES Location/Qualifiers
source 1. .13
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ApHL3LDVIIH10"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="ApHL3LD"
/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB; Sample name: ApHL3LD ; Plant growth place: INRA-Rennes, UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 18/01/2003 ; Harvesting date: 03/02/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 441
CN753196/c
LOCUS CN753196 13 bp mRNA linear EST 19-MAY-2004
DEFINITION ApHL3LD-XVI-A12 ApHL3LD Acyrthosiphon pisum cDNA clone ApHL3LDXVIA12 5', mRNA sequence.
ACCESSION CN753196
VERSION CN753196.1 GI:47518193
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 13)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts.
PCR PRimers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: XVI row: A column: 12.
FEATURES Location/Qualifiers
source 1. .13
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ApHL3LDXVIA12"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="ApHL3LD"
/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB; Sample name: ApHL3LD ; Plant growth place: INRA-Rennes, UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 18/01/2003 ; Harvesting date: 03/02/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 442
BQ591949
LOCUS BQ591949 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012580-024-016-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-016-C15 5-PRIME, mRNA sequence.
ACCESSION BQ591949
VERSION BQ591949.1 GI:26121532
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

```
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 16  row: C  column: 15
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188168"
                     /db_xref="taxon:161934"
                     /clone="024-016-C15"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTG 4516
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Db          2 TTTTTTTTTTTTG 14


RESULT 443
CF330198
LOCUS       CF330198                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-N04, mRNA
            sequence.
ACCESSION   CF330198
VERSION     CF330198.1  GI:33808624
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-N04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTT 4512
              |||||||||||||
Db          2 GTTTTTTTTTTTT 14


RESULT 444
AW248644
LOCUS       AW248644                  15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820747.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820747 3',
            mRNA sequence.
ACCESSION   AW248644
VERSION     AW248644.1  GI:6591637
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820747.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 15 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM5  row: A  column: 4
            High quality sequence stop: 6.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820747"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
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                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4506 TTTTTTTTTTGGG 4518
              |||||||||||||
Db          1 TTTTTTTTTTGGG 13


RESULT 445
AW248954
LOCUS       AW248954                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819408.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819408 3',
            mRNA sequence.
ACCESSION   AW248954
VERSION     AW248954.1  GI:6591947
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819408.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 15 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM1  row: I  column: 9
            High quality sequence stop: 8.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819408"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4506 TTTTTTTTTTGGG 4518
              |||||||||||||
Db          1 TTTTTTTTTTGGG 13


RESULT 446
AW249757
LOCUS       AW249757                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819607.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819607 3',
            mRNA sequence.
ACCESSION   AW249757
VERSION     AW249757.1  GI:6592750
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819607.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 15 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM2  row: A  column: 16
            High quality sequence stop: 8.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819607"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4506 TTTTTTTTTTGGG 4518
              |||||||||||||
```

```
Db          1 TTTTTTTTTTGGG 13


RESULT 447
CF543203/c
LOCUS       CF543203                 15 bp    mRNA    linear   EST 22-SEP-2003
DEFINITION  S014679-024-030-D05-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-030-D05 5-PRIME, mRNA sequence.
ACCESSION   CF543203
VERSION     CF543203.1  GI:34891643
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 30  row: D  column: 05
            Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:936579"
                     /db_xref="taxon:161934"
                     /clone="024-030-D05"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTG 4516
              |||||||||||||
Db         15 TTTTTTTTTTTTG 3


RESULT 448
CF312586
LOCUS       CF312586                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--08-G13, mRNA sequence.
ACCESSION   CF312586
VERSION     CF312586.1  GI:33684347
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--08-G13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 13;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 449
AW245664
LOCUS       AW245664                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION   AW245664
VERSION     AW245664.1  GI:6588657
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
```

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.
Plate: LLCM10 row: N column: 19.

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822994"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTT 4512
||||||||||||| |
Db 5 GTTTTTTTTTTTT 17

RESULT 450
CF317778/c
LOCUS CF317778 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-J13, mRNA sequence.
ACCESSION CF317778
VERSION CF317778.1 GI:33689539
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-J13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3606 AAAAAACAAAAACAGA 3621
|||||| ||||||| |
Db 16 AAAAAAAAAAAACAAA 1

RESULT 451
AI684114/c
LOCUS AI684114 16 bp mRNA linear EST 16-DEC-1999
DEFINITION tx79d02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2275779 3' similar to TR:Q09084 Q09084 EXTENSIN CLASS II PRECURSOR ;, mRNA sequence.
ACCESSION AI684114
VERSION AI684114.1 GI:4895408
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1454 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2275779"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4090 TGTGGGTGTGGGTGGG 4105
|||||| | |||||||
Db 16 TGTGGGGGGGGGTGGG 1

RESULT 452

```
AI798250/c
LOCUS       AI798250                 16 bp    mRNA    linear   EST 06-JUL-1999
DEFINITION  tr32b08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219991 3'
            similar to TR:O79354 O79354 CYTOCHROME OXIDASE SUBUNIT III. ;, mRNA
            sequence.
ACCESSION   AI798250
VERSION     AI798250.1  GI:5363722
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219991"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ov23"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||| ||||||||| ||
Db         16 TTTCTTTTTTTTTGTG 1


RESULT 453
AW248540
LOCUS       AW248540                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
            mRNA sequence.
ACCESSION   AW248540
VERSION     AW248540.1  GI:6591533
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820844.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: E  column: 5
            High quality sequence stop: 15.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820844"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2135 TTTTTTCTTTAATAAC 2150
              |||||| ||||| |||
Db          1 TTTTTTTTTTAAAAAC 16


RESULT 454
CF319827/c
LOCUS       CF319827                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-H16.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-H16, mRNA sequence.
ACCESSION   CF319827
VERSION     CF319827.1  GI:33691588
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
```

```
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--10-H16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              ||||||||||  |||
Db         16 GTTTTTTTTTAATTT 1


RESULT 455
AJ592922/c
LOCUS       AJ592922                  16 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            371G07, genomic survey sequence.
ACCESSION   AJ592922
VERSION     AJ592922.1  GI:37942546
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 16)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="371G07"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .16
                     /note="T-DNA flanking sequence
                     left border"

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.9e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2419 AGAACGTTAAACTATT 2434
              | || ||||||||||
Db         16 AAAATGTTAAACTATT 1


RESULT 456
CF299997/c
LOCUS       CF299997                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-D19, mRNA
            sequence.
ACCESSION   CF299997
VERSION     CF299997.1  GI:33671758
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4.4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 457
CF302447/c
LOCUS       CF302447                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
            sequence.
ACCESSION   CF302447
VERSION     CF302447.1  GI:33674208
```

```
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-P11"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4.4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 458
CF313013/c
LOCUS       CF313013                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--08-P19, mRNA sequence.
ACCESSION   CF313013
VERSION     CF313013.1  GI:33684774
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--08-P19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4.4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 459
CF300456/c
LOCUS       CF300456                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA
            sequence.
ACCESSION   CF300456
VERSION     CF300456.1  GI:33672217
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-N23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 4.8e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 460
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CF320418/c
LOCUS       CF320418                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-E22.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-E22, mRNA sequence.
ACCESSION   CF320418
VERSION     CF320418.1  GI:33692179
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-E22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 4.8e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 461
CF329136/c
LOCUS       CF329136                 19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
            sequence.
ACCESSION   CF329136
VERSION     CF329136.1  GI:33806509
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-F15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 462
CF309614/c
LOCUS       CF309614                 21 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-N20, mRNA sequence.
ACCESSION   CF309614
VERSION     CF309614.1  GI:33681375
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--03-N20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
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  Query Match             0.3%;  Score 12.8;  DB 1;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 5.4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         18 AAAAAAAAAAAAAAAG 3


RESULT 463
AZ450180
LOCUS       AZ450180                19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0248K13 R, genomic survey sequence.
ACCESSION   AZ450180
VERSION     AZ450180.1  GI:10604710
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0248  row: K  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0248K13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 5.5e+02;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAACA 3619
              ||  ||||||| ||||| |
Db          1 CTAAAAAAAAAAAAAAAAA 19


RESULT 464
AZ343730/c
LOCUS       AZ343730                20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION   AZ343730
VERSION     AZ343730.1  GI:10422288
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0077  row: E  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0077E20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 5.6e+02;
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```
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              ||||||||  ||||  | ||
Db         19 GAAAAAAAAAAAAGAAAAA 1


RESULT 465
CF330490/c
LOCUS       CF330490                  20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-D16, mRNA
            sequence.
ACCESSION   CF330490
VERSION     CF330490.1  GI:33809214
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--06-D16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 5.6e+02;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2336 TTCCAAACATCCAAAAAAA 2354
              |||||||  |   |||||||
Db         19 TTCCAAAAAAAAAAAAAAA 1


RESULT 466
CF301021/c
LOCUS       CF301021                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-L10, mRNA
            sequence.
ACCESSION   CF301021
VERSION     CF301021.1  GI:33672782
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-L10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||| ||||||
Db         14 TTTTTTTATTTTTT 1


RESULT 467
CF329379/c
LOCUS       CF329379                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-K23, mRNA
            sequence.
ACCESSION   CF329379
VERSION     CF329379.1  GI:33806995
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-K23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
```

RT-PCR."

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1
```

RESULT 468
CF291803
LOCUS CF291803 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION CF291803
VERSION CF291803.1 GI:33660836
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-G05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3604 GAAAAAAACAAAAA 3617
              |||||||| |||||
Db          2 GAAAAAAAAAAAAA 15
```

RESULT 469
CF311668
LOCUS CF311668 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-A05, mRNA sequence.
ACCESSION CF311668
VERSION CF311668.1 GI:33683429
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-A05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db          4 AAAAAAAAAAAAAC 17
```

RESULT 470
CF331733
LOCUS CF331733 20 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-P15, mRNA sequence.
ACCESSION CF331733
VERSION CF331733.1 GI:33811693
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

/clone="NACL--07-P15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 12.4; DB 1; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db          3 AAAAAAAAAAAAAC 16
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RESULT 471
CF298341/c
LOCUS CF298341 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION CF298341
VERSION CF298341.1 GI:33670102
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-K24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         17 GCAAAAAAAAAAAAAAA 1
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RESULT 472
BQ590687
LOCUS BQ590687 17 bp mRNA linear EST 06-DEC-2002
DEFINITION S013717-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION BQ590687
VERSION BQ590687.1 GI:26120270
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAAAAAA 17
```

RESULT 473
BQ591177/c
LOCUS BQ591177 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION BQ591177
VERSION BQ591177.1 GI:26120760
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

```
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 17  row: B  column: 22
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188948"
                     /db_xref="taxon:161934"
                     /clone="024-017-B22"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 474
BQ591181/c
LOCUS       BQ591181                  17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H16-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H16 3-PRIME, mRNA sequence.
ACCESSION   BQ591181
VERSION     BQ591181.1  GI:26120764
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 17  row: H  column: 16
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188932"
                     /db_xref="taxon:161934"
                     /clone="024-017-H16"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAA 3982
              ||||| || ||||| ||
Db         17 ATAAAAAAAAAAAAAAA 1


RESULT 475
CF290854/c
LOCUS       CF290854                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A21, mRNA
            sequence.
ACCESSION   CF290854
VERSION     CF290854.1  GI:33659887
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-A21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1
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RESULT 476
CF298589/c
LOCUS CF298589 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION CF298589
VERSION CF298589.1 GI:33670350
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--02-A18"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1
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RESULT 477
CF310219/c
LOCUS CF310219 17 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION CF310219
VERSION CF310219.1 GI:33681980
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-M02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1
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RESULT 478
CF311499/c
LOCUS CF311499 17 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION CF311499
VERSION CF311499.1 GI:33683260
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17

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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--06-L20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         17 GTAAAAAAAAAAAAAAA 1


RESULT 479
CF319075/c
LOCUS       CF319075                17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--09-H06, mRNA sequence.
ACCESSION   CF319075
VERSION     CF319075.1  GI:33690836
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--09-H06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAA 3982
              ||||| || ||||| ||
Db         17 ATAAAAAAAAAAAAAAA 1


RESULT 480
CF334566/c
LOCUS       CF334566                17 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-O13, mRNA sequence.
ACCESSION   CF334566
VERSION     CF334566.1  GI:33817460
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--03-O13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 481
BQ591588/c
LOCUS       BQ591588                17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012616-024-017-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-C15 5-PRIME, mRNA sequence.
ACCESSION   BQ591588
VERSION     BQ591588.1  GI:26121171
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
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            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 17  row: C  column: 15
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188532"
                     /db_xref="taxon:161934"
                     /clone="024-017-C15"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| | ||
Db         17 AAAAAAAAAAAAAATAA 1


RESULT 482
CF302409/c
LOCUS       CF302409                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-N19, mRNA
            sequence.
ACCESSION   CF302409
VERSION     CF302409.1  GI:33674170
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-N19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAA 3617
              ||  ||||||| |||||
Db         18 CTAAAAAAAAAAAAAAA 2


RESULT 483
CR786637
LOCUS       CR786637                 18 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468J2331_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468J2331 5', mRNA sequence.
ACCESSION   CR786637
VERSION     CR786637.1  GI:53705634
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
            Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J2331
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468J2331"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3607 AAAAACAAAAACAGAAT 3623
              ||||| ||||| | |||
Db         1 AAAAAAAAAAAAAAAAT 17


RESULT 484
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```
CF301151/c
LOCUS       CF301151                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-O05.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-O05, mRNA
            sequence.
ACCESSION   CF301151
VERSION     CF301151.1  GI:33672912
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-O05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 485
CF309376/c
LOCUS       CF309376                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-I19, mRNA sequence.
ACCESSION   CF309376
VERSION     CF309376.1  GI:33681137
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--03-I19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         17 GTAAAAAAAAAAAAAAA 1


RESULT 486
CF320046/c
LOCUS       CF320046                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-M11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-M11, mRNA sequence.
ACCESSION   CF320046
VERSION     CF320046.1  GI:33691807
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--10-M11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
```

```
  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAA 3982
              ||||| || ||||| ||
Db         18 ATAAAAAAAAAAAAAAA 2


RESULT 487
CF329484/c
LOCUS       CF329484                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA
            sequence.
ACCESSION   CF329484
VERSION     CF329484.1  GI:33807207
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         17 GTAAAAAAAAAAAAAAA 1


RESULT 488
CF329485
LOCUS       CF329485                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA
            sequence.
ACCESSION   CF329485
VERSION     CF329485.1  GI:33807209
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db          2 GTAAAAAAAAAAAAAAA 18


RESULT 489
AZ509929
LOCUS       AZ509929                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354A07 F, genomic survey sequence.
ACCESSION   AZ509929
VERSION     AZ509929.1  GI:10691245
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: A  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3608 AAAACAAAAACAGAATT 3624
|||| ||||| | ||||
Db 1 AAAAAAAAAAAAAAATT 17

RESULT 490
CF291665/c
LOCUS CF291665 19 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-D01, mRNA sequence.
ACCESSION CF291665
VERSION CF291665.1 GI:33660698
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-D01"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGA 3621
||||||| ||||| | |
Db 17 AAAAAAAAAAAAAAAAA 1

RESULT 491
CF336815/c
LOCUS CF336815 20 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--07-A04, mRNA sequence.
ACCESSION CF336815
VERSION CF336815.1 GI:33822012
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S.; Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-A04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACA 3619
| ||||||| ||||| |
Db 17 GCAAAAAAAAAAAAAAA 1

RESULT 492
CF333393/c
LOCUS CF333393 21 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-E09.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-E09, mRNA sequence.
ACCESSION CF333393
VERSION CF333393.1 GI:33815062
KEYWORDS EST.

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SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--02-E09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.8e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 493
TA211D06P/c
LOCUS       TA211D06P                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 211d06, forward sequence,
            genomic survey sequence.
ACCESSION   AL478564
VERSION     AL478564.1  GI:11844523
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="211d06"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.6e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 494
TA303G05P
LOCUS       TA303G05P                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 303g05, forward sequence,
            genomic survey sequence.
ACCESSION   AL497383
VERSION     AL497383.1  GI:11865504
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="303g05"

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.6e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| | ||
Db          1 AAAAAAAAAAAAGAAAA 17


RESULT 495
CF298018/c
LOCUS       CF298018                  20 bp    mRNA    linear   EST 15-AUG-2003
```

```
DEFINITION  7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA
            sequence.
ACCESSION   CF298018
VERSION     CF298018.1  GI:33669779
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--01-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 6e+02;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3598 AGTCTGGAAAAAAACAAAAA 3617
              | ||   ||||||| |||||
Db         20 AATCAAAAAAAAAAAAAAAA 1


RESULT 496
AJ690565/c
LOCUS       AJ690565                 15 bp    mRNA    linear   EST 29-JUN-2004
DEFINITION  AJ690565 KN261 Bos taurus cDNA clone KN261-054_B13, mRNA sequence.
ACCESSION   AJ690565
VERSION     AJ690565.1  GI:49423173
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
            R. Site2: SmaI 3' Seq Primer M13F Normalised library constructed
            from bovine ovary. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
            EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="KN261-054_B13"
                     /tissue_type="ovary"
                     /clone_lib="KN261"
                     /note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
                     SmaI; Single pass sequencing. Normalised library
                     constructed from bovine ovary."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 497
BE230585
LOCUS       BE230585                 15 bp    mRNA    linear   EST 07-JUL-2000
DEFINITION  99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
            (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION   BE230585
VERSION     BE230585.1  GI:8956782
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
            Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of ESTs from Rice Seedling
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Milyang 23"
                     /db_xref="taxon:39946"
                     /clone="99AS799"
                     /dev_stage="5 days after pollination"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Directional cDNA library inserted into lambda ZAPII
                     vector at 5'end with EcoRI and 3' end with Xho I site"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 498
BQ582543/c
```

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LOCUS       BQ582543                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013300-024-007-B02-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION   BQ582543
VERSION     BQ582543.1  GI:26112120
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 7  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184162"
                     /db_xref="taxon:161934"
                     /clone="024-007-B02"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 499
BQ585820/c
LOCUS       BQ585820                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012533-024-014-H17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-014-H17 5-PRIME, mRNA sequence.
ACCESSION   BQ585820
VERSION     BQ585820.1  GI:26115402
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 14  row: H  column: 17
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187164"
                     /db_xref="taxon:161934"
                     /clone="024-014-H17"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 500
BQ590410/c
LOCUS       BQ590410                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M08-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION   BQ590410
VERSION     BQ590410.1  GI:26119993
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
```

```
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 19  row: M  column: 08
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189710"
                     /db_xref="taxon:161934"
                     /clone="024-019-M08"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 501
BQ590656/c
LOCUS       BQ590656                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S015086-024-018-L13-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION   BQ590656
VERSION     BQ590656.1  GI:26120239
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 18  row: L  column: 13
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189464"
                     /db_xref="taxon:161934"
                     /clone="024-018-L13"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 502
BQ591170/c
LOCUS       BQ591170                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-N18 3-PRIME, mRNA sequence.
ACCESSION   BQ591170
VERSION     BQ591170.1  GI:26120753
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: N  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188941"
                     /db_xref="taxon:161934"
                     /clone="024-017-N18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
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/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 15 AAAAAAAAAAAAAAA 1

RESULT 503
BQ591178/c
LOCUS BQ591178 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-F22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-F22 3-PRIME, mRNA sequence.
ACCESSION BQ591178
VERSION BQ591178.1 GI:26120761
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: F column: 22
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188949"
/db_xref="taxon:161934"
/clone="024-017-F22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 15 AAAAAAAAAAAAAAA 1

RESULT 504
BQ591223/c
LOCUS BQ591223 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-H02 3-PRIME, mRNA sequence.
ACCESSION BQ591223
VERSION BQ591223.1 GI:26120806
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: H column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188901"
/db_xref="taxon:161934"
/clone="024-017-H02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 15 AAAAAAAAAAAAAAA 1

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RESULT 505
BQ594689/c
LOCUS       BQ594689                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-024-M05 3-PRIME, mRNA sequence.
ACCESSION   BQ594689
VERSION     BQ594689.1  GI:26124272
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 24  row: M  column: 05
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:192163"
                     /db_xref="taxon:161934"
                     /clone="024-024-M05"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 506
CF277319/c
LOCUS       CF277319                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-M23,
            mRNA sequence.
ACCESSION   CF277319
VERSION     CF277319.1  GI:33654705
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--02-M23"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 507
CF281923/c
LOCUS       CF281923                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-D04,
            mRNA sequence.
ACCESSION   CF281923
VERSION     CF281923.1  GI:33659310
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /db_xref="taxon:39947"
                     /clone="14ETL-09-D04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 508
CF290920/c
LOCUS       CF290920                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-C09, mRNA
            sequence.
ACCESSION   CF290920
VERSION     CF290920.1  GI:33659953
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 509
CF291029/c
LOCUS       CF291029                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E19, mRNA
            sequence.
ACCESSION   CF291029
VERSION     CF291029.1  GI:33660062
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-E19"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 510
CF291103/c
LOCUS       CF291103                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G10, mRNA
            sequence.
ACCESSION   CF291103
VERSION     CF291103.1  GI:33660136
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-G10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 511
CF291717/c
LOCUS       CF291717                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E04, mRNA
            sequence.
ACCESSION   CF291717
VERSION     CF291717.1  GI:33660750
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-E04"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 512
CF291798/c
LOCUS       CF291798                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G02, mRNA
            sequence.
ACCESSION   CF291798
VERSION     CF291798.1  GI:33660831
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-G02"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 513
CF292458/c
LOCUS       CF292458                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-E17, mRNA
            sequence.
ACCESSION   CF292458
VERSION     CF292458.1  GI:33661491
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .15
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                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="30DGS--01-E17"
                      /tissue_type="leaf"
                      /dev_stage="30 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 514
CF292461/c
LOCUS       CF292461                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-E19, mRNA
            sequence.
ACCESSION   CF292461
VERSION     CF292461.1  GI:33661494
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /clone="30DGS--01-E19"
                      /tissue_type="leaf"
                      /dev_stage="30 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 515
CF298148/c
LOCUS       CF298148                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G17, mRNA
            sequence.
ACCESSION   CF298148
VERSION     CF298148.1  GI:33669909
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa (japonica cultivar-group)"
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                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                      RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 516
CF298630/c
LOCUS       CF298630                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-B23, mRNA
            sequence.
ACCESSION   CF298630
VERSION     CF298630.1  GI:33670391
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 517
CF298733/c
LOCUS       CF298733                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E20, mRNA
            sequence.
ACCESSION   CF298733
VERSION     CF298733.1  GI:33670494
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 518
CF298805/c
LOCUS       CF298805                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-G20, mRNA
            sequence.
ACCESSION   CF298805
VERSION     CF298805.1  GI:33670566
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 519
CF298889/c
LOCUS       CF298889                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-J09, mRNA
            sequence.
ACCESSION   CF298889
VERSION     CF298889.1  GI:33670650
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 520
CF299602/c
LOCUS       CF299602                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L01, mRNA
            sequence.
ACCESSION   CF299602
VERSION     CF299602.1  GI:33671363
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="7 days after germination"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 521
CF299608/c
LOCUS       CF299608                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L04, mRNA
            sequence.
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 522
CF300121/c
LOCUS       CF300121                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G12, mRNA
            sequence.
ACCESSION   CF300121
VERSION     CF300121.1  GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
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  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 523
CF300361/c
LOCUS       CF300361                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L16, mRNA
            sequence.
ACCESSION   CF300361
VERSION     CF300361.1  GI:33672122
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 524
CF300992/c
LOCUS       CF300992                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K19, mRNA
            sequence.
ACCESSION   CF300992
VERSION     CF300992.1  GI:33672753
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-K19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 525
CF302034/c
LOCUS       CF302034                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C24, mRNA
            sequence.
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ACCESSION   CF302034
VERSION     CF302034.1  GI:33673795
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-C24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 526
CF302124/c
LOCUS       CF302124                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-F16, mRNA
            sequence.
ACCESSION   CF302124
VERSION     CF302124.1  GI:33673885
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-F16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 527
CF302182/c
LOCUS       CF302182                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-H20, mRNA
            sequence.
ACCESSION   CF302182
VERSION     CF302182.1  GI:33673943
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--07-H20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 528
CF307923/c
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LOCUS       CF307923                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--01-I15, mRNA sequence.
ACCESSION   CF307923
VERSION     CF307923.1  GI:33679684
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--01-I15"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 529
CF311159/c
LOCUS       CF311159                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--06-E11, mRNA sequence.
ACCESSION   CF311159
VERSION     CF311159.1  GI:33682920
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
                     /clone="ABF--06-E11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 530
CF311907/c
LOCUS       CF311907                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--07-G04, mRNA sequence.
ACCESSION   CF311907
VERSION     CF311907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--07-G04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
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line."

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1
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RESULT 531
CF313319/c
LOCUS CF313319 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--01-G13, mRNA sequence.
ACCESSION CF313319
VERSION CF313319.1 GI:33685080
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="HD--01-G13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACA 3619
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Db         15 AAAAAAAAAAAAAAA 1
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RESULT 532
CF313320
LOCUS CF313320 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-G13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--01-G13, mRNA sequence.
ACCESSION CF313320
VERSION CF313320.1 GI:33685081
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--01-G13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACA 3619
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Db          1 AAAAAAAAAAAAAAA 15
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RESULT 533
CF316251
LOCUS CF316251 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-H15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-H15, mRNA sequence.
ACCESSION CF316251
VERSION CF316251.1 GI:33688012
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-H15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 1 AAAAAAAAAAAAAAA 15

RESULT 534
CF318035/c
LOCUS CF318035 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-P06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-P06, mRNA sequence.
ACCESSION CF318035
VERSION CF318035.1 GI:33689796
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-P06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 15 AAAAAAAAAAAAAAA 1

RESULT 535
CF327434/c
LOCUS CF327434 15 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-O18, mRNA sequence.
ACCESSION CF327434
VERSION CF327434.1 GI:33803127
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-O18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 15 AAAAAAAAAAAAAAA 1

RESULT 536
CF330195/c
LOCUS CF330195 15 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-N03, mRNA sequence.
ACCESSION CF330195
VERSION CF330195.1 GI:33808618
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--05-N03"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 537
CF330668/c
LOCUS       CF330668                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-H16, mRNA
            sequence.
ACCESSION   CF330668
VERSION     CF330668.1  GI:33809572
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--06-H16"
                     /tissue_type="callus"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 538
CF332178/c
LOCUS       CF332178                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-J10, mRNA
            sequence.
ACCESSION   CF332178
VERSION     CF332178.1  GI:33812580
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--08-J10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 539
CF336202/c
LOCUS       CF336202                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-C20, mRNA sequence.
ACCESSION   CF336202
VERSION     CF336202.1  GI:33820794
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
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```
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
                     /clone="JMT--06-C20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 540
CR547282
LOCUS       CR547282                 15 bp    mRNA    linear   EST 12-JUL-2004
DEFINITION  DKFZp468I112_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468I112 5', mRNA sequence.
ACCESSION   CR547282
VERSION     CR547282.1  GI:50240938
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
            Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Bloecker,H., Boecher,M., Brandt,P., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National
            Research Centre for Biotechnology Ltd., Braunschweig/Germany)
            within the cDNA sequencing consortium of the German Genome Project.
            This clone (DKFZp468I112) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468I112"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         1 AAAAAAAAAAAAAAA 15


RESULT 541
CF291030
LOCUS       CF291030                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E19, mRNA
            sequence.
ACCESSION   CF291030
VERSION     CF291030.1  GI:33660063
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="14ROOT--01-E19"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         1 AAAAAAATAAAAAAA 15


RESULT 542
CF543203
LOCUS       CF543203                 15 bp    mRNA    linear   EST 22-SEP-2003
DEFINITION  S014679-024-030-D05-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-030-D05 5-PRIME, mRNA sequence.
ACCESSION   CF543203
VERSION     CF543203.1  GI:34891643
KEYWORDS    EST.
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SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 30  row: D  column: 05
            Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="GABI:936579"
                     /db_xref="taxon:161934"
                     /clone="024-030-D05"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2382 GTCAAAAATAAAATA 2396
              ||||||| |||| |
Db          1 GTCAAAAAAAAAAAA 15


RESULT 543
BQ590207/c
LOCUS       BQ590207                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-O15-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-O15 3-PRIME, mRNA sequence.
ACCESSION   BQ590207
VERSION     BQ590207.1  GI:26119790
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:161934"
                     /clone="024-019-O15"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 544
CF318894/c
LOCUS       CF318894                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--09-D06, mRNA sequence.
ACCESSION   CF318894
VERSION     CF318894.1  GI:33690655
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 545
CF327923/c
LOCUS       CF327923                  16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-J18, mRNA
            sequence.
ACCESSION   CF327923
VERSION     CF327923.1  GI:33804096
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-J18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 546
CF328223/c
LOCUS       CF328223                  16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-A10, mRNA
            sequence.
ACCESSION   CF328223
VERSION     CF328223.1  GI:33804692
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--03-A10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 547
CR786609
LOCUS       CR786609                  16 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468C2031_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468C2031 5', mRNA sequence.
ACCESSION   CR786609
VERSION     CR786609.1  GI:53705606
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
```

```
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
            Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468C2031
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES              Location/Qualifiers
     source           1. .16
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                      /mol_type="mRNA"
                      /db_xref="taxon:9600"
                      /clone="DKFZp468C2031"
                      /tissue_type="heart"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="468 (synonym: phrt1)"
                      /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          2 AAAAAAAAAAAAAAA 16


RESULT 548
BQ590166/c
LOCUS       BQ590166                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-K18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-K18 3-PRIME, mRNA sequence.
ACCESSION   BQ590166
VERSION     BQ590166.1  GI:26119749
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: K  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:189955"
                      /db_xref="taxon:161934"
                      /clone="024-019-K18"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 549
BQ590507/c
LOCUS       BQ590507                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION   BQ590507
VERSION     BQ590507.1  GI:26120090
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: M  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:189608"
                      /db_xref="taxon:161934"
                      /clone="024-019-M04"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 550
BQ592600
LOCUS       BQ592600                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013686-024-028-F08-SP6R MPIZ-ADIS-024-developing root Beta
            vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION   BQ592600
VERSION     BQ592600.1  GI:26122183
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: F  column: 08
            Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
FEATURES             Location/Qualifiers
     source          1. .16
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="GABI:194262"
                     /db_xref="taxon:161934"
                     /clone="024-028-F08"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 551
BQ592965/c
LOCUS       BQ592965                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013324-024-028-A01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION   BQ592965
VERSION     BQ592965.1  GI:26122548
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: A  column: 01
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:193895"
                     /db_xref="taxon:161934"
                     /clone="024-028-A01"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 552
BQ595369/c
LOCUS       BQ595369                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION   BQ595369
VERSION     BQ595369.1  GI:26124952
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
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REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 22  row: P  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     line)"
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                     /db_xref="taxon:161934"
                     /clone="024-022-P02"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 553
BQ595717
LOCUS       BQ595717                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012692-024-022-H07-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-H07 5-PRIME, mRNA sequence.
ACCESSION   BQ595717
VERSION     BQ595717.1  GI:26125300
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 22  row: H  column: 07
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .16
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:191134"
                     /db_xref="taxon:161934"
                     /clone="024-022-H07"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         1 AAAAAAAAAAAAAAA 15


RESULT 554
CF279325/c
LOCUS       CF279325                  16 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
            mRNA sequence.
ACCESSION   CF279325
VERSION     CF279325.1  GI:33656711
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--05-J09"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 16 AAAAAAAAAAAAAAA 2

RESULT 555
CF296130/c
LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION CF296130
VERSION CF296130.1 GI:33665163
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-F22"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 15 AAAAAAAAAAAAAAA 1

RESULT 556
CF311057/c
LOCUS CF311057 16 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION CF311057
VERSION CF311057.1 GI:33682818
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-C03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 16 AAAAAAAAAAAAAAA 2

RESULT 557
CF314013/c
LOCUS CF314013 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--02-G01, mRNA sequence.
ACCESSION CF314013
VERSION CF314013.1 GI:33685774
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

```
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="HD--02-G01"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 558
CF314377/c
LOCUS       CF314377                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-O01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-O01, mRNA sequence.
ACCESSION   CF314377
VERSION     CF314377.1  GI:33686138
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--02-O01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 559
CF315789/c
LOCUS       CF315789                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-N10.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--04-N10, mRNA sequence.
ACCESSION   CF315789
VERSION     CF315789.1  GI:33687550
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--04-N10"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 560
CF316056/c
LOCUS       CF316056                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-D07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-D07, mRNA sequence.
ACCESSION   CF316056
VERSION     CF316056.1  GI:33687817
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--05-D07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 561
CF317718/c
LOCUS       CF317718                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-I05.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--07-I05, mRNA sequence.
ACCESSION   CF317718
VERSION     CF317718.1  GI:33689479
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="HD--07-I05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 562
CF320356/c
LOCUS       CF320356                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-D14.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-D14, mRNA sequence.
ACCESSION   CF320356
VERSION     CF320356.1  GI:33692117
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-D14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2
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RESULT 563
CF327722/c
LOCUS       CF327722                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA
            sequence.
ACCESSION   CF327722
VERSION     CF327722.1  GI:33803695
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-F06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 564
CF329320/c
LOCUS       CF329320                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
            sequence.
ACCESSION   CF329320
VERSION     CF329320.1  GI:33806877
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-J17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 565
CF333386
LOCUS       CF333386                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-E05, mRNA sequence.
ACCESSION   CF333386
VERSION     CF333386.1  GI:33815044
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--02-E05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 566
CR786853
LOCUS       CR786853                 16 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp468E2231_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
            DKFZp468E2231 5', mRNA sequence.
ACCESSION   CR786853
VERSION     CR786853.1  GI:53705850
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
            Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468E2231
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp468E2231"
                     /tissue_type="heart"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="468 (synonym: phrt1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6.1e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 567
CF295807/c
LOCUS       CF295807                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--05-O12, mRNA
            sequence.
ACCESSION   CF295807
VERSION     CF295807.1  GI:33664840
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--05-O12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 568
CF297251/c
LOCUS       CF297251                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--07-P12, mRNA
            sequence.
ACCESSION   CF297251
VERSION     CF297251.1  GI:33666284
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="30DGS--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 569
CF299639/c
LOCUS       CF299639                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L20, mRNA
            sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 570
BQ590128/c
LOCUS       BQ590128                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION   BQ590128
VERSION     BQ590128.1  GI:26119711
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 19  row: E  column: 19
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189986"
                     /db_xref="taxon:161934"
                     /clone="024-019-E19"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 571
CF294668/c
LOCUS       CF294668                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
            sequence.
ACCESSION   CF294668
VERSION     CF294668.1  GI:33663701
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
```

```
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--04-E17"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 572
CF295988/c
LOCUS       CF295988                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
            sequence.
ACCESSION   CF295988
VERSION     CF295988.1  GI:33665021
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--06-C17"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 573
CF336950/c
LOCUS       CF336950                 17 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--07-D04, mRNA sequence.
ACCESSION   CF336950
VERSION     CF336950.1  GI:33822280
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--07-D04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 574
AJ725584
LOCUS       AJ725584                 18 bp    mRNA    linear   EST 07-OCT-2004
DEFINITION  AJ725584 riken1 Gallus gallus cDNA clone 2c16r4, mRNA sequence.
ACCESSION   AJ725584
VERSION     AJ725584.1  GI:53890998
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J.,
            Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M.,
            Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
  TITLE     Full-length cDNAs from bursal lymphocytes to facilitate gene
            function analysis
```

```
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Caldwell RB
            GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
            Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="2c16r4"
                     /cell_type="bursal lymphocyte"
                     /dev_stage="2-3 weeks old"
                     /clone_lib="riken1"
                     /note="CB inbred strain"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          3 AAAAAAAAAAAAAAA 17


RESULT 575
AL048754
LOCUS       AL048754                 18 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION   AL048754
VERSION     AL048754.1  GI:4727825
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566L173"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          3 AAAAAAAAAAAAAAA 17


RESULT 576
CF298591/c
LOCUS       CF298591                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA
            sequence.
ACCESSION   CF298591
VERSION     CF298591.1  GI:33670352
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-A20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 577
BM658677/c
LOCUS       BM658677                 18 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658677
VERSION     BM658677.1  GI:18958948
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
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(5'-NNN. . .NNNinsert)
GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG. non-normalized library, sequenced 3' with M13R primer."

Query Match 0.3%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAGAAAAAAA 2
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RESULT 578
CF325356/c
LOCUS CF325356 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-A08.g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA clone JMT1--03-A08, mRNA sequence.
ACCESSION CF325356
VERSION CF325356.1 GI:33798994
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT1--03-A08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 6.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1
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RESULT 579
CF327587/c
LOCUS CF327587 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION CF327587
VERSION CF327587.1 GI:33803426
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-C04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 6.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2
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RESULT 580
CF300236/c
LOCUS CF300236 19 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-I24, mRNA sequence.
ACCESSION CF300236
VERSION CF300236.1 GI:33671997
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa (japonica cultivar-group)"

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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--04-I24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 6.3e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 581
CF309636/c
LOCUS       CF309636                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-O08.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-O08, mRNA sequence.
ACCESSION   CF309636
VERSION     CF309636.1  GI:33681397
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--03-O08"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 6.3e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 582
CF319596/c
LOCUS       CF319596                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-C14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-C14, mRNA sequence.
ACCESSION   CF319596
VERSION     CF319596.1  GI:33691357
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--10-C14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 6.3e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 583
AZ645841/c
LOCUS       AZ645841                19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0511G04 R, genomic survey sequence.
ACCESSION   AZ645841
VERSION     AZ645841.1  GI:11775726
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0511  row: G  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0511G04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 6.3e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAGAAAAAAA 2


RESULT 584
AZ650252
LOCUS       AZ650252                 19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0520N17 F, genomic survey sequence.
ACCESSION   AZ650252
VERSION     AZ650252.1  GI:11784550
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0520  row: N  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0520N17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 6.3e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3608 AAAACAAAAACAGAA 3622
              |||||||||| | ||
Db          1 AAAACAAAAAAAAAA 15


RESULT 585
AZ579122
LOCUS       AZ579122                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0363G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0363G19 F, genomic survey sequence.
ACCESSION   AZ579122
VERSION     AZ579122.1  GI:11693583
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: G column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363G19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 11.8; DB 1; Length 20;
Best Local Similarity 86.7%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3608 AAAACAAAAACAGAA 3622
|||||||||| | ||
Db 1 AAAACAAAAAAAAAA 15

RESULT 586
CL680297/c
LOCUS CL680297 20 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0128c_G05_2 - PRI0128c.BR (20) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL680297
VERSION CL680297.1 GI:50187127
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES Location/Qualifiers
source 1. .20
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.3%; Score 11.8; DB 1; Length 20;
Best Local Similarity 86.7%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 16 AAAAAAAGAAAAAAA 2

RESULT 587
CF282313
LOCUS CF282313 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-M08, mRNA sequence.
ACCESSION CF282313
VERSION CF282313.1 GI:33659700
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.8; DB 1; Length 21;
Best Local Similarity 86.7%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619

```
                ||||||| ||||| |
Db          7 AAAAAAAAAAAAAAA 21


RESULT 588
AZ963501/c
LOCUS       AZ963501                21 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0232M07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0232M07 R, genomic survey sequence.
ACCESSION   AZ963501
VERSION     AZ963501.1  GI:13834728
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0232M07"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 21;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 589
AZ310057/c
LOCUS       AZ310057                22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0018A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0018A15 R, genomic survey sequence.
ACCESSION   AZ310057
VERSION     AZ310057.1  GI:10351664
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0018  row: A  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0018A15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 22;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2
```

```
RESULT 590
BQ583549
LOCUS       BQ583549                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011978-024-005-C14-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION   BQ583549
VERSION     BQ583549.1  GI:26113126
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 5  row: C  column: 14
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:183152"
                     /db_xref="taxon:161934"
                     /clone="024-005-C14"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 591
BQ589180/c
LOCUS       BQ589180                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014009-024-015-I22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-I22 3-PRIME, mRNA sequence.
ACCESSION   BQ589180
VERSION     BQ589180.1  GI:26118763
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 15  row: I  column: 22
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187886"
                     /db_xref="taxon:161934"
                     /clone="024-015-I22"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          13 AAAAAAAAAAAAA 1


RESULT 592
BQ590337
LOCUS       BQ590337                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012840-024-019-G12-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-G12 5-PRIME, mRNA sequence.
ACCESSION   BQ590337
VERSION     BQ590337.1  GI:26119920
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
```

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            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 19  row: G  column: 12
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189780"
                     /db_xref="taxon:161934"
                     /clone="024-019-G12"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 593
CF278426/c
LOCUS       CF278426                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F09,
            mRNA sequence.
ACCESSION   CF278426
VERSION     CF278426.1  GI:33655812
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--04-F09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          13 AAAAAAAAAAAAA 1


RESULT 594
CF280420/c
LOCUS       CF280420                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-B11,
            mRNA sequence.
ACCESSION   CF280420
VERSION     CF280420.1  GI:33657806
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--07-B11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          13 AAAAAAAAAAAAA 1
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RESULT 595
CF280707/c
LOCUS       CF280707                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H19,
            mRNA sequence.
ACCESSION   CF280707
VERSION     CF280707.1  GI:33658093
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--07-H19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 596
CF280757/c
LOCUS       CF280757                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-I21.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-I21,
            mRNA sequence.
ACCESSION   CF280757
VERSION     CF280757.1  GI:33658143
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--07-I21"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 597
CF282369/c
LOCUS       CF282369                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N16.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N16,
            mRNA sequence.
ACCESSION   CF282369
VERSION     CF282369.1  GI:33659756
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="14ETL--09-N16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1
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  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 598
CF290970/c
LOCUS       CF290970                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
            sequence.
ACCESSION   CF290970
VERSION     CF290970.1  GI:33660003
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 599
CF290971
LOCUS       CF290971                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
            sequence.
ACCESSION   CF290971
VERSION     CF290971.1  GI:33660004
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-E10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13


RESULT 600
CF291011/c
LOCUS       CF291011                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E10, mRNA
            sequence.
ACCESSION   CF291011
VERSION     CF291011.1  GI:33660044
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--01-E10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1
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RESULT 601
CF291060/c
LOCUS CF291060 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION CF291060
VERSION CF291060.1 GI:33660093
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F11"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1
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RESULT 602
CF291061
LOCUS CF291061 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION CF291061
VERSION CF291061.1 GI:33660094
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F11"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13
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RESULT 603
CF291167/c
LOCUS CF291167 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION CF291167
VERSION CF291167.1 GI:33660200
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-H20"
/tissue_type="root"

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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 604
CF291214/c
LOCUS       CF291214                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-I22, mRNA
            sequence.
ACCESSION   CF291214
VERSION     CF291214.1  GI:33660247
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /cultivar="Nackdong"
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                     /clone="14ROOT--01-I22"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 605
CF291427/c
LOCUS       CF291427                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-N14, mRNA
            sequence.
ACCESSION   CF291427
VERSION     CF291427.1  GI:33660460
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /cultivar="Nackdong"
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                     /clone="14ROOT--01-N14"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 606
CF291469/c
LOCUS       CF291469                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-O12, mRNA
            sequence.
ACCESSION   CF291469
VERSION     CF291469.1  GI:33660502
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="14ROOT--01-O12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 607
CF291479/c
LOCUS       CF291479                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-O17, mRNA
            sequence.
ACCESSION   CF291479
VERSION     CF291479.1  GI:33660512
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 608
CF291514/c
LOCUS       CF291514                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
            sequence.
ACCESSION   CF291514
VERSION     CF291514.1  GI:33660547
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="14ROOT--01-P13"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

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  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 609
CF291515
LOCUS       CF291515                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
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            sequence.
ACCESSION   CF291515
VERSION     CF291515.1  GI:33660548
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
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                     /tissue_type="root"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 610
CF291596/c
LOCUS       CF291596                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B12, mRNA
            sequence.
ACCESSION   CF291596
VERSION     CF291596.1  GI:33660629
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /cultivar="Nackdong"
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                     /clone="14ROOT--02-B12"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 611
CF291597
LOCUS       CF291597                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B12, mRNA
            sequence.
ACCESSION   CF291597
VERSION     CF291597.1  GI:33660630
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-B12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
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Qy       3605 AAAAAAACAAAAA 3617
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Db          1 AAAAAAAAAAAAA 13


RESULT 612
CF291726/c
LOCUS       CF291726                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E10, mRNA
            sequence.
ACCESSION   CF291726
VERSION     CF291726.1  GI:33660759
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-E10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 613
CF291903
LOCUS       CF291903                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I10, mRNA
            sequence.
ACCESSION   CF291903
VERSION     CF291903.1  GI:33660936
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ROOT--02-I10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 614
CF298590/c
LOCUS       CF298590                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A19, mRNA
            sequence.
ACCESSION   CF298590
VERSION     CF298590.1  GI:33670351
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--02-A19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 615
CF298592/c
LOCUS       CF298592                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A21, mRNA
            sequence.
ACCESSION   CF298592
VERSION     CF298592.1  GI:33670353
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /cultivar="Nackdong"
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                     /clone="7LEAF--02-A21"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 616
CF298736/c
LOCUS       CF298736                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E22, mRNA
            sequence.
ACCESSION   CF298736
VERSION     CF298736.1  GI:33670497
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="7LEAF--02-E22"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 617
CF298764/c
LOCUS       CF298764                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-F20, mRNA
            sequence.
ACCESSION   CF298764
VERSION     CF298764.1  GI:33670525
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 618
CF298795/c
LOCUS       CF298795                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-G14, mRNA
            sequence.
ACCESSION   CF298795
VERSION     CF298795.1  GI:33670556
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="7LEAF--02-G14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 619
CF298908/c
LOCUS       CF298908                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--02-K03, mRNA
            sequence.
ACCESSION   CF298908
VERSION     CF298908.1  GI:33670669
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="7LEAF--02-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 620
CF299133/c
LOCUS       CF299133                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-A06, mRNA
            sequence.
ACCESSION   CF299133
VERSION     CF299133.1  GI:33670894
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 621
CF299359/c
LOCUS       CF299359                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F15, mRNA
            sequence.
ACCESSION   CF299359
VERSION     CF299359.1  GI:33671120
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
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  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 622
CF299937/c
LOCUS       CF299937                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C12, mRNA
            sequence.
ACCESSION   CF299937
VERSION     CF299937.1  GI:33671698
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="7LEAF--04-C12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 623
CF300118/c
LOCUS       CF300118                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G10, mRNA
            sequence.
ACCESSION   CF300118
VERSION     CF300118.1  GI:33671879
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 624
CF300587/c
LOCUS       CF300587                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-C01, mRNA
            sequence.
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ACCESSION   CF300587
VERSION     CF300587.1  GI:33672348
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 625
CF300658/c
LOCUS       CF300658                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-D14, mRNA
            sequence.
ACCESSION   CF300658
VERSION     CF300658.1  GI:33672419
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 626
CF300929/c
LOCUS       CF300929                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J11, mRNA
            sequence.
ACCESSION   CF300929
VERSION     CF300929.1  GI:33672690
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 627
CF301247/c
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LOCUS       CF301247                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-A15, mRNA
            sequence.
ACCESSION   CF301247
VERSION     CF301247.1  GI:33673008
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
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Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 628
CF301286/c
LOCUS       CF301286                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-B15, mRNA
            sequence.
ACCESSION   CF301286
VERSION     CF301286.1  GI:33673047
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 629
CF302158/c
LOCUS       CF302158                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--07-G20, mRNA
            sequence.
ACCESSION   CF302158
VERSION     CF302158.1  GI:33673919
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1
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RESULT 630
CF302830/c
LOCUS       CF302830                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--08-L16, mRNA
            sequence.
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 631
CF302898/c
LOCUS       CF302898                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--08-N08, mRNA
            sequence.
ACCESSION   CF302898
VERSION     CF302898.1  GI:33674659
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 632
CF310516/c
LOCUS       CF310516                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-D09, mRNA sequence.
ACCESSION   CF310516
VERSION     CF310516.1  GI:33682277
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--05-D09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 633
CF310517
LOCUS       CF310517                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-D09, mRNA sequence.
ACCESSION   CF310517
VERSION     CF310517.1  GI:33682278
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /cultivar="Nackdong"
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                     /clone="ABF--05-D09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 634
CF312721/c
LOCUS       CF312721                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--08-J13, mRNA sequence.
ACCESSION   CF312721
VERSION     CF312721.1  GI:33684482
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 635
CF313171/c
LOCUS       CF313171                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-D10.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--01-D10, mRNA sequence.
ACCESSION   CF313171
VERSION     CF313171.1  GI:33684932
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /db_xref="taxon:39947"
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 636
CF314239/c
LOCUS       CF314239                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-L01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-L01, mRNA sequence.
ACCESSION   CF314239
VERSION     CF314239.1  GI:33686000
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--02-L01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 637
CF314874/c
LOCUS       CF314874                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-J07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--03-J07, mRNA sequence.
ACCESSION   CF314874
VERSION     CF314874.1  GI:33686635
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 638
CF315395/c
LOCUS       CF315395                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-E20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--04-E20, mRNA sequence.
ACCESSION   CF315395
VERSION     CF315395.1  GI:33687156
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
```

```
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="HD--04-E20"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 639
CF316439/c
LOCUS       CF316439                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-L17, mRNA sequence.
ACCESSION   CF316439
VERSION     CF316439.1  GI:33688200
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="HD--05-L17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 640
CF316440
LOCUS       CF316440                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--05-L17, mRNA sequence.
ACCESSION   CF316440
VERSION     CF316440.1  GI:33688201
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
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                     /clone="HD--05-L17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 641
CF316637/c
LOCUS       CF316637                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--06-A04.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
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            HD--06-A04, mRNA sequence.
ACCESSION   CF316637
VERSION     CF316637.1  GI:33688398
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--06-A04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 642
CF318290/c
LOCUS       CF318290                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-F19.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-F19, mRNA sequence.
ACCESSION   CF318290
VERSION     CF318290.1  GI:33690051
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 643
CF319066/c
LOCUS       CF319066                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H02.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
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            HD--09-H02, mRNA sequence.
ACCESSION   CF319066
VERSION     CF319066.1  GI:33690827
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db         13 AAAAAAAAAAAAA 1


RESULT 644
CF319531/c
LOCUS       CF319531                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-B03.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-B03, mRNA sequence.
ACCESSION   CF319531
VERSION     CF319531.1  GI:33691292
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Db         13 AAAAAAAAAAAAA 1


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LOCUS       CF319532                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-B03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-B03, mRNA sequence.
ACCESSION   CF319532
VERSION     CF319532.1  GI:33691293
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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RESULT 646
CF319919
LOCUS       CF319919                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-J17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--10-J17, mRNA sequence.
ACCESSION   CF319919
VERSION     CF319919.1  GI:33691680
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

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              ||||||| |||||
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ACCESSION CF320017
VERSION CF320017.1 GI:33691778
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 648
CF320018
LOCUS CF320018 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-L20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-L20, mRNA sequence.
ACCESSION CF320018
VERSION CF320018.1 GI:33691779
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
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Db          1 AAAAAAAAAAAAA 13
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RESULT 649
CF320143/c
LOCUS CF320143 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-O13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-O13, mRNA sequence.
ACCESSION CF320143
VERSION CF320143.1 GI:33691904
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     line."

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Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 650
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LOCUS       CF320938                13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-A06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--12-A06, mRNA sequence.
ACCESSION   CF320938
VERSION     CF320938.1  GI:33692699
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
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Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 651
CF326844/c
LOCUS       CF326844                13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-B12, mRNA
            sequence.
ACCESSION   CF326844
VERSION     CF326844.1  GI:33801943
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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FEATURES             Location/Qualifiers
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  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 652
CF327070/c
LOCUS       CF327070                13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
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            sequence.
ACCESSION   CF327070
VERSION     CF327070.1  GI:33802396
KEYWORDS    EST.
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--01-G09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 653
CF327339/c
LOCUS       CF327339                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA
            sequence.
ACCESSION   CF327339
VERSION     CF327339.1  GI:33802936
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--01-M15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 654
CF327340
LOCUS       CF327340                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA
            sequence.
ACCESSION   CF327340
VERSION     CF327340.1  GI:33802938
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--01-M15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 655
CF327576/c
LOCUS       CF327576                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-B22, mRNA
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          sequence.
ACCESSION   CF327576
VERSION     CF327576.1  GI:33803404
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-B22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 656
CF327888/c
LOCUS       CF327888                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-I22, mRNA
            sequence.
ACCESSION   CF327888
VERSION     CF327888.1  GI:33804024
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /cultivar="Nackdong"
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                     /clone="NACL--02-I22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 657
CF327939/c
LOCUS       CF327939                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-K02, mRNA
            sequence.
ACCESSION   CF327939
VERSION     CF327939.1  GI:33804127
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--02-K02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 658
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CF328153/c
LOCUS       CF328153                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-O19, mRNA
            sequence.
ACCESSION   CF328153
VERSION     CF328153.1  GI:33804556
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /clone="NACL--02-O19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 659
CF328228/c
LOCUS       CF328228                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-A13, mRNA
            sequence.
ACCESSION   CF328228
VERSION     CF328228.1  GI:33804702
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--03-A13"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 660
CF328807/c
LOCUS       CF328807                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-O07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-O07, mRNA
            sequence.
ACCESSION   CF328807
VERSION     CF328807.1  GI:33805856
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
                     /clone="NACL--03-O07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 661
CF329075/c
LOCUS       CF329075                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-E07, mRNA
            sequence.
ACCESSION   CF329075
VERSION     CF329075.1  GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 662
CF329076
LOCUS       CF329076                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-E07, mRNA
            sequence.
ACCESSION   CF329076
VERSION     CF329076.1  GI:33806395
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 663
CF329417/c
LOCUS       CF329417                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-L19, mRNA
            sequence.
ACCESSION   CF329417
VERSION     CF329417.1  GI:33807072
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
                     /clone="NACL--04-L19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 664
CF329460/c
LOCUS       CF329460                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-M18, mRNA
            sequence.
ACCESSION   CF329460
VERSION     CF329460.1  GI:33807156
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--04-M18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 665
CF329729
LOCUS       CF329729                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-C14, mRNA
            sequence.
ACCESSION   CF329729
VERSION     CF329729.1  GI:33807674
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--05-C14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13


RESULT 666
CF329800/c
LOCUS       CF329800                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-E04, mRNA
            sequence.
ACCESSION   CF329800
VERSION     CF329800.1  GI:33807817
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-E04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
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RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1
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RESULT 667
CF329801
LOCUS CF329801 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION CF329801
VERSION CF329801.1 GI:33807819
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 668
CF329869/c
LOCUS CF329869 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-F18, mRNA sequence.
ACCESSION CF329869
VERSION CF329869.1 GI:33807959
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--05-F18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1
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RESULT 669
CF329946/c
LOCUS CF329946 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION CF329946
VERSION CF329946.1 GI:33808114
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
||||||| |||||
Db 13 AAAAAAAAAAAAA 1

RESULT 670
CF329988/c
LOCUS CF329988 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-I10, mRNA sequence.
ACCESSION CF329988
VERSION CF329988.1 GI:33808198
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
||||||| |||||
Db 13 AAAAAAAAAAAAA 1

RESULT 671
CF330023/c
LOCUS CF330023 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-J05, mRNA sequence.
ACCESSION CF330023
VERSION CF330023.1 GI:33808268
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
||||||| |||||
Db 13 AAAAAAAAAAAAA 1

RESULT 672
CF330725
LOCUS CF330725 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-J01, mRNA sequence.
ACCESSION CF330725
VERSION CF330725.1 GI:33809672
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 673
CF331041/c
LOCUS       CF331041                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-A04, mRNA
            sequence.
ACCESSION   CF331041
VERSION     CF331041.1  GI:33810299
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--07-A04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 674
CF331266/c
LOCUS       CF331266                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-F06, mRNA
            sequence.
ACCESSION   CF331266
VERSION     CF331266.1  GI:33810744
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="NACL--07-F06"
                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 675
CF331273
LOCUS       CF331273                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
            sequence.
ACCESSION   CF331273
VERSION     CF331273.1  GI:33810757
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 676
CF331903/c
LOCUS       CF331903                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-D07, mRNA
            sequence.
ACCESSION   CF331903
VERSION     CF331903.1  GI:33812027
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 677
CF332079/c
LOCUS       CF332079                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-H04, mRNA
            sequence.
ACCESSION   CF332079
VERSION     CF332079.1  GI:33812379
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="NACL--08-H04"
                     /tissue_type="callus"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 678
CF332695/c
LOCUS       CF332695                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--01-E21, mRNA sequence.
ACCESSION   CF332695
VERSION     CF332695.1  GI:33813618
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
```

```
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 679
CF332696
LOCUS       CF332696                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--01-E21, mRNA sequence.
ACCESSION   CF332696
VERSION     CF332696.1  GI:33813620
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                      cDNA library (JMT)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                      methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 680
CF333486/c
LOCUS       CF333486                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-G11, mRNA sequence.
ACCESSION   CF333486
VERSION     CF333486.1  GI:33815268
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 681
CF333972/c
LOCUS       CF333972                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-B12, mRNA sequence.
ACCESSION   CF333972
VERSION     CF333972.1  GI:33816249
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         13 AAAAAAAAAAAAA 1


RESULT 682
CF333973
LOCUS       CF333973                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-B12, mRNA sequence.
ACCESSION   CF333973
VERSION     CF333973.1  GI:33816251
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 683
CF334347/c
LOCUS       CF334347                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-J19, mRNA sequence.
ACCESSION   CF334347
VERSION     CF334347.1  GI:33817022
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 684
CF337022/c
LOCUS       CF337022                  13 bp    mRNA    linear   EST 18-AUG-2003
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```
DEFINITION  JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--07-E22, mRNA sequence.
ACCESSION   CF337022
VERSION     CF337022.1  GI:33822426
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--07-E22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 685
CN546046/c
LOCUS       CN546046                 13 bp    mRNA    linear   EST 30-APR-2004
DEFINITION  EST 17998 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL007H03 3', mRNA sequence.
ACCESSION   CN546046
VERSION     CN546046.1  GI:46910671
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
  TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultivar="Cabernet Sauvignon"
                     /db_xref="taxon:29760"
                     /clone="B3CS00RL007H03"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 13;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         13 AAAAAAAAAAAAA 1


RESULT 686
CN752228
LOCUS       CN752228                 13 bp    mRNA    linear   EST 19-MAY-2004
DEFINITION  ApHL3SD-XXVIII-A5 ApHL3SD Acyrthosiphon pisum cDNA clone
            ApHL3SDXXVIIIA5 5', mRNA sequence.
ACCESSION   CN752228
VERSION     CN752228.1  GI:47517225
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
  ORGANISM  Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
  TITLE     An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
  JOURNAL   Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR PRimers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXVIII  row: A  column: 5.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Acyrthosiphon pisum"
                     /mol_type="mRNA"
                     /cultivar="yr2"
                     /db_xref="taxon:7029"
                     /clone="ApHL3SDXXVIIIA5"
                     /tissue_type="head"
                     /dev_stage="third instar nymph (L3)"
                     /lab_host="TOP10"
                     /clone_lib="ApHL3SD"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
                     Sample name: ApHL3SD ; Plant growth place: INRA-Rennes,
                     UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
                     conditions: peat ; Sowing date: 20/03/2003 ; Harvesting
                     date: 10/04/2003 ; Stress date: no stress ; Description:
                     aphids inoculated on one-week old Vicia faba germinations
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under non sterile conditions. ; experimental condition: short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 687
CN752875
LOCUS CN752875 13 bp mRNA linear EST 19-MAY-2004
DEFINITION ApHL3LD-VII-H10 ApHL3LD Acyrthosiphon pisum cDNA clone ApHL3LDVIIH10 5', mRNA sequence.
ACCESSION CN752875
VERSION CN752875.1 GI:47517872
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 13)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts.
PCR PRimers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: VII row: H column: 10.
FEATURES Location/Qualifiers
source 1. .13
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ApHL3LDVIIH10"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="ApHL3LD"
/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB; Sample name: ApHL3LD ; Plant growth place: INRA-Rennes, UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 18/01/2003 ; Harvesting date: 03/02/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 688
CN753196
LOCUS CN753196 13 bp mRNA linear EST 19-MAY-2004
DEFINITION ApHL3LD-XVI-A12 ApHL3LD Acyrthosiphon pisum cDNA clone ApHL3LDXVIA12 5', mRNA sequence.
ACCESSION CN753196
VERSION CN753196.1 GI:47518193
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 13)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts.
PCR PRimers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: XVI row: A column: 12.
FEATURES Location/Qualifiers
source 1. .13
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ApHL3LDXVIA12"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="ApHL3LD"
/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB; Sample name: ApHL3LD ; Plant growth place: INRA-Rennes, UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 18/01/2003 ; Harvesting date: 03/02/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 689
BQ586422/c
LOCUS BQ586422 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013307-024-013-O02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-013-O02 3-PRIME, mRNA sequence.
ACCESSION BQ586422
VERSION BQ586422.1 GI:26116004
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

```
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 13  row: O  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:186441"
                     /db_xref="taxon:161934"
                     /clone="024-013-O02"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 690
BQ587890/c
LOCUS       BQ587890                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013302-024-009-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-009-B02 3-PRIME, mRNA sequence.
ACCESSION   BQ587890
VERSION     BQ587890.1  GI:26117472
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 9  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184980"
                     /db_xref="taxon:161934"
                     /clone="024-009-B02"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 691
BQ589191/c
LOCUS       BQ589191                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014009-024-015-I20-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-I20 3-PRIME, mRNA sequence.
ACCESSION   BQ589191
VERSION     BQ589191.1  GI:26118774
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 15  row: I  column: 20
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187878"
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/db_xref="taxon:161934"
/clone="024-015-I20"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
||||||| |||||
Db 14 AAAAAAAAAAAAA 2

RESULT 692
BQ590242/c
LOCUS BQ590242 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-E16 5-PRIME, mRNA sequence.
ACCESSION BQ590242
VERSION BQ590242.1 GI:26119825
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 19 row: E column: 16
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189878"
/db_xref="taxon:161934"
/clone="024-019-E16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
||||||| |||||
Db 14 AAAAAAAAAAAAA 2

RESULT 693
BQ590261/c
LOCUS BQ590261 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-K14 3-PRIME, mRNA sequence.
ACCESSION BQ590261
VERSION BQ590261.1 GI:26119844
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         14 AAAAAAAAAAAAA 2


RESULT 694
BQ591168/c
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            cDNA clone 024-017-H18 3-PRIME, mRNA sequence.
ACCESSION   BQ591168
VERSION     BQ591168.1  GI:26120751
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
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FEATURES             Location/Qualifiers
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                     /lab_host="EMDH10B"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         14 AAAAAAAAAAAAA 2


RESULT 695
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LOCUS       BQ591176                  14 bp    mRNA    linear   EST 06-DEC-2002
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            cDNA clone 024-017-N20 3-PRIME, mRNA sequence.
ACCESSION   BQ591176
VERSION     BQ591176.1  GI:26120759
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /lab_host="EMDH10B"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
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Db         14 AAAAAAAAAAAAA 2


RESULT 696
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LOCUS       BQ591207                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-B04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION   BQ591207
VERSION     BQ591207.1  GI:26120790
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
```

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES Location/Qualifiers
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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
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Db 14 AAAAAAAAAAAAA 2

RESULT 697
BQ591380/c
LOCUS BQ591380 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012714-024-017-B15-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION BQ591380
VERSION BQ591380.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 15
Seq primer: T7; GTAATACGACTCACTATAGGGC.

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SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAA 2

RESULT 698
BQ591482/c
LOCUS BQ591482 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012713-024-017-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26121065
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGGC.

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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAA 2

RESULT 699
BQ593052/c
LOCUS BQ593052 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012375-024-028-C03-SP6 MPIZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-028-C03 5-PRIME, mRNA sequence.
ACCESSION BQ593052
VERSION BQ593052.1 GI:26122635
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 28 row: C column: 03
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
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Db 14 AAAAAAAAAAAAA 2

RESULT 700
CF277935/c
LOCUS CF277935 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-K11, mRNA sequence.
ACCESSION CF277935
VERSION CF277935.1 GI:33655321
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAA 3617
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Db 14 AAAAAAAAAAAAA 2

RESULT 701
CF278001/c
LOCUS CF278001 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

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           Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-L21,
           mRNA sequence.
ACCESSION  CF278001
VERSION    CF278001.1  GI:33655387
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
  ORGANISM Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 14)
  AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="14ETL--03-L21"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 702
CF278452/c
LOCUS      CF278452                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION 14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
           Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F22,
           mRNA sequence.
ACCESSION  CF278452
VERSION    CF278452.1  GI:33655838
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
  ORGANISM Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 14)
  AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="14ETL--04-F22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         14 AAAAAAAAAAAAA 2


RESULT 703
CF279473/c
LOCUS      CF279473                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION 14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
           Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-M14,
           mRNA sequence.
ACCESSION  CF279473
VERSION    CF279473.1  GI:33656859
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
  ORGANISM Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 14)
  AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="14ETL--05-M14"
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         14 AAAAAAAAAAAAA 2


RESULT 704
CF279992/c
LOCUS       CF279992                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--06-I01,
            mRNA sequence.
ACCESSION   CF279992
VERSION     CF279992.1  GI:33657378
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="14ETL--06-I01"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 705
CF281958/c
LOCUS       CF281958                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-D24,
            mRNA sequence.
ACCESSION   CF281958
VERSION     CF281958.1  GI:33659345
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 706
CF282350/c
LOCUS       CF282350                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,
            mRNA sequence.
ACCESSION   CF282350
VERSION     CF282350.1  GI:33659737
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 707
CF294449/c
LOCUS       CF294449                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--03-P15, mRNA
            sequence.
ACCESSION   CF294449
VERSION     CF294449.1  GI:33663482
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--03-P15"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 708
CF295570/c
LOCUS       CF295570                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--05-J06, mRNA
            sequence.
ACCESSION   CF295570
VERSION     CF295570.1  GI:33664603
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="30DGS--05-J06"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 709
CF296120/c
LOCUS       CF296120                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-F17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--06-F17, mRNA
            sequence.
ACCESSION   CF296120
VERSION     CF296120.1  GI:33665153
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /cultivar="Nackdong"
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                     /clone="30DGS--06-F17"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2
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RESULT 710
CF297969/c
LOCUS CF297969 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-C16, mRNA sequence.
ACCESSION CF297969
VERSION CF297969.1 GI:33669730
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2
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RESULT 711
CF298109/c
LOCUS CF298109 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-F19, mRNA sequence.
ACCESSION CF298109
VERSION CF298109.1 GI:33669870
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2
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RESULT 712
CF299368/c
LOCUS CF299368 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F21, mRNA sequence.
ACCESSION CF299368
VERSION CF299368.1 GI:33671129
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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                     /clone="7LEAF--03-F21"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 713
CF300542/c
LOCUS       CF300542                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-B01, mRNA
            sequence.
ACCESSION   CF300542
VERSION     CF300542.1  GI:33672303
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="7LEAF--05-B01"
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         14 AAAAAAAAAAAAA 2


RESULT 714
CF301020/c
LOCUS       CF301020                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-L10, mRNA
            sequence.
ACCESSION   CF301020
VERSION     CF301020.1  GI:33672781
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 715
CF301083/c
LOCUS       CF301083                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M19, mRNA
            sequence.
ACCESSION   CF301083
VERSION     CF301083.1  GI:33672844
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 716
CF301380/c
LOCUS       CF301380                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
            sequence.
ACCESSION   CF301380
VERSION     CF301380.1  GI:33673141
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 717
CF302675/c
LOCUS       CF302675                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--08-G18, mRNA
            sequence.
ACCESSION   CF302675
VERSION     CF302675.1  GI:33674436
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 718
CF302846/c
LOCUS       CF302846                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--08-M05, mRNA
            sequence.
ACCESSION   CF302846
VERSION     CF302846.1  GI:33674607
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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```
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 719
CF308006/c
LOCUS       CF308006                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--01-K10, mRNA sequence.
ACCESSION   CF308006
VERSION     CF308006.1  GI:33679767
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 720
CF308220/c
LOCUS       CF308220                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--01-P06, mRNA sequence.
ACCESSION   CF308220
VERSION     CF308220.1  GI:33679981
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="ABF--01-P06"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 721
CF308445/c
LOCUS       CF308445                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--02-E10, mRNA sequence.
ACCESSION   CF308445
VERSION     CF308445.1  GI:33680206
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 722
CF308918/c
LOCUS       CF308918                14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--02-O16, mRNA sequence.
ACCESSION   CF308918
VERSION     CF308918.1  GI:33680679
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /cultivar="Nackdong"
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                     /clone="ABF--02-O16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 723
CF310714/c
LOCUS       CF310714                14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-I11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--05-I11, mRNA sequence.
ACCESSION   CF310714
VERSION     CF310714.1  GI:33682475
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     line."

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RESULT 724
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            ABF--06-F09, mRNA sequence.
ACCESSION   CF311201
VERSION     CF311201.1  GI:33682962
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     element binding transcription factor 3 overexpression
                     line."

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Db         14 AAAAAAAAAAAAA 2


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LOCUS       CF311813                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--07-D22, mRNA sequence.
ACCESSION   CF311813
VERSION     CF311813.1  GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Db         14 AAAAAAAAAAAAA 2


RESULT 726
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DEFINITION  HD--08-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--08-G13, mRNA sequence.
ACCESSION   CF318323
VERSION     CF318323.1  GI:33690084
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     reverse transcribed and then used for PCR. mRNA was
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derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         14 AAAAAAAAAAAAA 2
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RESULT 727
CF318450/c
LOCUS CF318450 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-J08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-J08, mRNA sequence.
ACCESSION CF318450
VERSION CF318450.1 GI:33690211
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         14 AAAAAAAAAAAAA 2
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RESULT 728
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LOCUS CF319826 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-H16, mRNA sequence.
ACCESSION CF319826
VERSION CF319826.1 GI:33691587
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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RESULT 729
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LOCUS CF321246 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--12-G24.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--12-G24, mRNA sequence.
ACCESSION CF321246
VERSION CF321246.1 GI:33693007
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAA 2

RESULT 730
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LOCUS CF327097 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-H01, mRNA sequence.
ACCESSION CF327097
VERSION CF327097.1 GI:33802449
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
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REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Db 14 AAAAAAAAAAAAA 2

RESULT 731
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ACCESSION CF327119
VERSION CF327119.1 GI:33802493
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 92.3%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAA 2

RESULT 732
CF327203/c
LOCUS CF327203 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-J16, mRNA sequence.
ACCESSION CF327203
VERSION CF327203.1 GI:33802665
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Db         13 AAAAAAAAAAAAA 1


RESULT 733
CF327445/c
LOCUS       CF327445                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-O24, mRNA
            sequence.
ACCESSION   CF327445
VERSION     CF327445.1  GI:33803149
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
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REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 734
CF328490/c
LOCUS       CF328490                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-G21, mRNA
            sequence.
ACCESSION   CF328490
VERSION     CF328490.1  GI:33805226
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:39947"
                      /clone="NACL--03-G21"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 735
CF328540/c
LOCUS       CF328540                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-H24, mRNA
            sequence.
ACCESSION   CF328540
VERSION     CF328540.1  GI:33805324
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--03-H24"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 736
CF328669/c
LOCUS       CF328669                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--03-K23, mRNA
            sequence.
ACCESSION   CF328669
VERSION     CF328669.1  GI:33805587
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--03-K23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 737
CF328994/c
LOCUS       CF328994                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-C11, mRNA
            sequence.
ACCESSION   CF328994
VERSION     CF328994.1  GI:33806228
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--04-C11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 738
CF329217/c
LOCUS       CF329217                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--04-H10, mRNA
            sequence.
ACCESSION   CF329217
VERSION     CF329217.1  GI:33806672
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
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                      /clone="NACL--04-H10"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 739
CF329990
LOCUS       CF329990                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-I11, mRNA
            sequence.
ACCESSION   CF329990
VERSION     CF329990.1  GI:33808202
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa (japonica cultivar-group)"
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                      /clone="NACL--05-I11"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 740
CF330784/c
LOCUS       CF330784                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--06-K10, mRNA
            sequence.
ACCESSION   CF330784
VERSION     CF330784.1  GI:33809790
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Oryza sativa (japonica cultivar-group)"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
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                      /clone="NACL--06-K10"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 741
CF331272/c
LOCUS       CF331272                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
            sequence.
ACCESSION   CF331272
VERSION     CF331272.1  GI:33810755
KEYWORDS    EST.
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SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:39947"
                     /clone="NACL--07-F09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 742
CF331861/c
LOCUS       CF331861                14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--08-C10, mRNA
            sequence.
ACCESSION   CF331861
VERSION     CF331861.1  GI:33811945
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39947"
                     /clone="NACL--08-C10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 743
CF333214/c
LOCUS       CF333214                14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-A10, mRNA sequence.
ACCESSION   CF333214
VERSION     CF333214.1  GI:33814707
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT--02-A10"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 744
CF333215
LOCUS       CF333215                14 bp    mRNA    linear   EST 18-AUG-2003
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DEFINITION  JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-A10, mRNA sequence.
ACCESSION   CF333215
VERSION     CF333215.1  GI:33814709
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     cDNA library (JMT)"
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Qy       3605 AAAAAAACAAAAA 3617
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Db          1 AAAAAAAAAAAAA 13


RESULT 745
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LOCUS       CF333399                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-E12, mRNA sequence.
ACCESSION   CF333399
VERSION     CF333399.1  GI:33815074
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 746
CF334202/c
LOCUS       CF334202                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-G11, mRNA sequence.
ACCESSION   CF334202
VERSION     CF334202.1  GI:33816736
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     methyltransferase overexpression line."

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  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 747
CF334281/c
LOCUS       CF334281                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-I05, mRNA sequence.
ACCESSION   CF334281
VERSION     CF334281.1  GI:33816894
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 748
CF334290/c
LOCUS       CF334290                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--03-I11, mRNA sequence.
ACCESSION   CF334290
VERSION     CF334290.1  GI:33816914
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 749
CF335781/c
LOCUS       CF335781                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--05-J13, mRNA sequence.
ACCESSION   CF335781
VERSION     CF335781.1  GI:33819936
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 750
CF336094/c
LOCUS       CF336094                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-A10, mRNA sequence.
ACCESSION   CF336094
VERSION     CF336094.1  GI:33820566
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
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Db         14 AAAAAAAAAAAAA 2


RESULT 751
CF336106/c
LOCUS       CF336106                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-A17, mRNA sequence.
ACCESSION   CF336106
VERSION     CF336106.1  GI:33820590
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Qy       3605 AAAAAAACAAAAA 3617
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Db         14 AAAAAAAAAAAAA 2


RESULT 752
CF336287/c
LOCUS       CF336287                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-E15, mRNA sequence.
ACCESSION   CF336287
VERSION     CF336287.1  GI:33820962
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
             ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 753
CF336906/c
LOCUS       CF336906                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--07-C05, mRNA sequence.
ACCESSION   CF336906
VERSION     CF336906.1  GI:33822182
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
             ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 754
CF330198/c
LOCUS       CF330198                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--05-N04, mRNA
            sequence.
ACCESSION   CF330198
VERSION     CF330198.1  GI:33808624
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--05-N04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.1e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAAC 3618
             |||||| ||||||
Db         14 AAAAAAAAAAAAC 2


Search completed: October 24, 2005, 15:27:49
Job time : 22 secs
```

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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-403-888A-142

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTTGGGGTT 19


RESULT 10
US-09-788-338-3
; Sequence 3, Application US/09788338
; Patent No. 6485916
; GENERAL INFORMATION:
;  APPLICANT: MURAMATSU, TAKAMICHI
;  APPLICANT:  FUJITA, TAKESHI
;  APPLICANT:  KIYAMA, MASAHARU
;  APPLICANT:  IRIE, TAKASHI
;  TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
;  TITLE OF INVENTION:  EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
;  TITLE OF INVENTION:  NUCLEIC ACID SAMPLES THEREBY
;  FILE REFERENCE: NIT-129-02
;  CURRENT APPLICATION NUMBER: US/09/788,338
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: 09/313,637
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: JP 10-153651
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-788-338-3

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 11
US-09-300-958A-64
; Sequence 64, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-64

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 12
US-09-090-672B-106
; Sequence 106, Application US/09090672B
; Patent No. 6828428
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  106:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-106

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 13
US-09-120-853-4/c
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; Sequence 4, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
;  APPLICANT: Kamiya, Kinya
;  APPLICANT: Matsuda, Yoko
;  APPLICANT: Uchida, Kiyoshi
;  TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
;  FILE REFERENCE: 07898/030001
;  CURRENT APPLICATION NUMBER: US/09/120,853
;  CURRENT FILING DATE: 1998-07-21
;  EARLIER APPLICATION NUMBER: JP 213838/1997
;  EARLIER FILING DATE: 1997-07-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Artificial
;   OTHER INFORMATION: nucleic acid sequence
US-09-120-853-4

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGCT 2279
              |||||||||||||||||
Db         17 TCTTTCCTCTTTCTGCT 1


RESULT 14
US-09-228-942-7/c
; Sequence 7, Application US/09228942
; Patent No. 6203988
; GENERAL INFORMATION:
;  APPLICANT: Kambara, Hideki
;  APPLICANT: Uematsu, Chihiro
;  TITLE OF INVENTION: DNA FRAGMENT ANALYSIS METHOD AND REAGENT KIT
;  FILE REFERENCE: ASA-757
;  CURRENT APPLICATION NUMBER: US/09/228,942
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: oligonucleotide ligated to 3' end of DNA fragment
US-09-228-942-7

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         20 TTTTTTTTTTTTTTTGG 4


RESULT 15
US-08-482-918-32
; Sequence 32, Application US/08482918
; Patent No. 6207417
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,918
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/33005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-482-918-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 16
US-09-224-681-32
; Sequence 32, Application US/09224681
; Patent No. 6207454
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Method for Enhancing the Efficiency of Gene
;    TITLE OF INVENTION:  Transfer with Stem Cell Factor (SCF) Polypeptide
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/224,681
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/005,893
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;      FILING DATE:  12-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/449,653
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/35199
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-224-681-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 17
US-08-336-728A-32
; Sequence 32, Application US/08336728A
; Patent No. 6207802
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/336,728A
;      FILING DATE:  09-NOV-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/32956
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-336-728A-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 18
US-09-635-251-32
; Sequence 32, Application US/09635251
; Patent No. 6759215
;  GENERAL INFORMATION:
;       APPLICANT: Zsebo, Krisztina M.
;                  Bosselman, Robert A.
;                  Suggs, Sidney V.
;                  Martin, Francis H.
;       TITLE OF INVENTION: Stem Cell Factor
;       NUMBER OF SEQUENCES: 104
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;            STREET: 6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: United States of America
;            ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/635,251
;            FILING DATE: 07-Aug-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/449,182
;            FILING DATE: 24-MAY-1995
;            APPLICATION NUMBER: 08/172,329
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;             FILING DATE: 21-DEC-1993
;             APPLICATION NUMBER: 07/982,255
;             FILING DATE: 25-NOV-1992
;             APPLICATION NUMBER: 07/684,535
;             FILING DATE: 04-OCT-1991
;             APPLICATION NUMBER: 07/589,701
;             FILING DATE: 01-OCT-1990
;             APPLICATION NUMBER: 07/573,616
;             FILING DATE: 24-AUG-1990
;             APPLICATION NUMBER: 07/537,198
;             FILING DATE: 11-JUN-1990
;             APPLICATION NUMBER: 07/422,383
;             FILING DATE: 16-OCT-1989
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Clough, David W.
;             REGISTRATION NUMBER: 36,107
;             REFERENCE/DOCKET NUMBER: 01017/32957A
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 32:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-635-251-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 19
US-08-004-552-1
; Sequence 1, Application US/08004552
; Patent No. 5482836
;  GENERAL INFORMATION:
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Ito, Takashi
;    APPLICANT:  Smith, Cassandra L.
;    TITLE OF INVENTION:  DNA PURIFICATION BY TRIPLEX-AFFINITY
;    TITLE OF INVENTION:  CAPTURE AND AFFINITY CAPTURE ELECTROPHORESIS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Karen S. Smith
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  CA 94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/004,552
;      FILING DATE:  19930114
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, Karen S.
;      REGISTRATION NUMBER:  31,426
;      REFERENCE/DOCKET NUMBER:  A-57666/KSS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..20
;      OTHER INFORMATION:  /note= "BTC-20 Oligonucleotide,
;      OTHER INFORMATION:  biotinylated at 5'-end."
US-08-004-552-1

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 20
US-08-863-639A-72/c
; Sequence 72, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-72

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
```

```
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 21
US-08-863-639A-93
; Sequence 93, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-93

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db          1 CTCTCTCTCTCTCTCTCTCT 20


RESULT 22
US-09-725-265-31/c
; Sequence 31, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-31

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 23
US-09-909-595-56/c
; Sequence 56, Application US/09909595
; Patent No. 6586245
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Scott E. Davis
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
;  FILE REFERENCE: RTS-0223
;  CURRENT APPLICATION NUMBER: US/09/909,595
;  CURRENT FILING DATE:  2001-07-18
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-909-595-56

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4482 AATGTATTTGATTTATAAGT 4501
              |||| |||||||||||| |||
Db         20 AATGCATTTGATTTATCAGT 1


RESULT 24
US-09-081-385-40
; Sequence 40, Application US/09081385
; Patent No. 6593456
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
```

```
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/081,385
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-081-385-40

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20


RESULT 25
US-09-860-473-56
; Sequence 56, Application US/09860473
; Patent No. 6656732
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
;  FILE REFERENCE: RTS-0222
;  CURRENT APPLICATION NUMBER: US/09/860,473
;  CURRENT FILING DATE:  2001-05-18
;  NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-860-473-56

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3229 TGTTGAGCCAGTGGGCCAGC 3248
              || |||||  ||||||||||||
Db          1 TGCTGAGCGAGTGGGCCAGC 20


RESULT 26
US-09-556-127-31/c
; Sequence 31, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-31

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 49;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 27
US-09-581-822-2
; Sequence 2, Application US/09581822
; Patent No. 6737253
; GENERAL INFORMATION:
;  APPLICANT: Tillett, Daniel
;  TITLE OF INVENTION: Method of Amplification of Nucleic Acid
;  FILE REFERENCE: 400716/BSW
;  CURRENT APPLICATION NUMBER: US/09/581,822
;  CURRENT FILING DATE:  2000-05-01
;  PRIOR APPLICATION NUMBER: AU PQ 0087
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer Sequence
US-09-581-822-2

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1423 TTAACCCATTCCAGTACAGT 1442
              ||||||||| |||||||| |
Db          2 TTAACCCATACCAGTACAAT 21


RESULT 28
US-09-475-947A-104/c
; Sequence 104, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
```

```
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: human
US-09-475-947A-104

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 57;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATAC 2411
              ||||||||| ||||||||
Db         18 ATATATATATATATATAC 1


RESULT 29
US-09-725-265-16
; Sequence 16, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-16

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 57;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 30
US-09-556-127-16
; Sequence 16, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-16

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 57;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 31
US-09-696-791-924
; Sequence 924, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 924
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk8 ribozyme binding site
US-09-696-791-924

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 59;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1830 CACAAAGCTTCTAAAGCA 1847
              |||| ||||||||||||||
Db          1 CACAGAGCTTCTAAAGCA 18


RESULT 32
US-09-965-599-4
; Sequence 4, Application US/09965599
; Patent No. 6555670
; GENERAL INFORMATION:
;  APPLICANT: Aizawa, Akira
;  APPLICANT:  Kawakami, Akiko
;  APPLICANT:  Kondo, Toshihiko
;  TITLE OF INVENTION: Testis-Specific Gene
;  FILE REFERENCE: 6920/0J871
;  CURRENT APPLICATION NUMBER: US/09/965,599
;  CURRENT FILING DATE:  2001-09-26
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer HT15-C
US-09-965-599-4

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 62;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4515
              ||| |||||||||||||||
Db          1 AAGCTTTTTTTTTTTTTT 18


RESULT 33
US-09-129-603-4
; Sequence 4, Application US/09129603A
; Patent No. 6790944
; GENERAL INFORMATION:
;  APPLICANT: Ishiwata, Tetsuyoshi
;  APPLICANT: Sakurada, Mikiko
;  APPLICANT: Nishimura, Ayako
;  APPLICANT: Nakagawa, Satoshi
;  APPLICANT: Kuga, Tetsuro
;  APPLICANT: Nishi, Tatsunari
;  APPLICANT: No. 6790944ura, No. 6790944uo
;  APPLICANT: Sawada, Shigemasa
;  APPLICANT: Nagase, Takahiro
;  APPLICANT: Takei, Masami
;  TITLE OF INVENTION: No. 6790944el Protein
;  FILE REFERENCE: 766.25
;  CURRENT APPLICATION NUMBER: US/09/129,603A
;  CURRENT FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: PCT/JP97/04469
;  EARLIER FILING DATE: 1997-12-05
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: other nucleic acid from homo sapiens, synthesized
;   OTHER INFORMATION: DNA
US-09-129-603-4

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 34
US-09-090-672B-105
; Sequence 105, Application US/09090672B
; Patent No. 6828428
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-105

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 35
US-09-090-672B-107
; Sequence 107, Application US/09090672B
; Patent No. 6828428
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-107

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 36
US-09-437-076-2
; Sequence 2, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
;  APPLICANT: Barber-Guillem, Emilio
;  APPLICANT: Nelson, M. Bud
;  APPLICANT: Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  CURRENT APPLICATION NUMBER: US/09/437,076
;  CURRENT FILING DATE: 1999-11-09
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: Word for Windows
; SEQ ID NO 2
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: synthesized
US-09-437-076-2

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          3 GTTTTTTTTTTTTTTT 18


RESULT 37
US-09-637-751A-5
; Sequence 5, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
;  APPLICANT:  Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Binary Encoded Sequence Tags
; Patent No. 6383754
;  FILE REFERENCE:  AGL 100
;  CURRENT APPLICATION NUMBER: US/09/637,751A
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-5

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 38
US-09-637-751A-6
; Sequence 6, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
;  APPLICANT:  Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Binary Encoded Sequence Tags
; Patent No. 6383754
;  FILE REFERENCE:  AGL 100
;  CURRENT APPLICATION NUMBER: US/09/637,751A
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-6

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 39
US-09-994-311-5
; Sequence 5, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-5

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 72;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 2 TTTTTTTTTTTTTTTG 17

RESULT 40
US-09-994-311-6
; Sequence 6, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/994,311
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-6

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 72;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 2 TTTTTTTTTTTTTTTG 17

RESULT 41
US-09-142-108C-29
; Sequence 29, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Brugliera, Filippa
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142,108C
; CURRENT FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: PN8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-142-108C-29

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 72;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 3 TTTTTTTTTTTTTTTG 18

RESULT 42
US-09-904-744-2
; Sequence 2, Application US/09904744
; Patent No. 6828142
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; TITLE OF INVENTION: dendrimers in a signal amplification system
; FILE REFERENCE: B-73
; CURRENT APPLICATION NUMBER: US/09/904,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/437076
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/107828
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-904-744-2

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 72;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
         ||||||||||||||||
Db 3 GTTTTTTTTTTTTTTT 18

RESULT 43
US-09-487-445-55
; Sequence 55, Application US/09487445
; Patent No. 6258600
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: RTS-0107
; CURRENT APPLICATION NUMBER: US/09/487,445
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-445-55

  Query Match 0.4%; Score 16; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 79;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1772 GTTGATTATCTTCAGC 1787
         ||||||||||||||||
Db 3 GTTGATTATCTTCAGC 18

```
RESULT 44
US-09-112-580-161/c
; Sequence 161, Application US/09112580
; Patent No. 6610539
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT: YOUNG, Aiping
;  APPLICANT: DUGOURD, Dominique
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
;  TITLE OF INVENTION: MICROORGANISMS
;  FILE REFERENCE: 032396-016
;  CURRENT APPLICATION NUMBER: US/09/112,580
;  CURRENT FILING DATE: 1998-07-09
;  EARLIER APPLICATION NUMBER: US 60/052,160
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 265
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-112-580-161

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 79;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1284 GAACCGGAGATGGAAA 1299
              ||||||||||||||||
Db         18 GAACCGGAGATGGAAA 3


RESULT 45
US-08-850-880-10/c
; Sequence 10, Application US/08850880
; Patent No. 5925545
;  GENERAL INFORMATION:
;    APPLICANT:  Reznikoff, William S
;    APPLICANT:  Gorysin, Igor Y
;    APPLICANT:  Zhou, Hong
;    TITLE OF INVENTION:  System for In Vitro Transposition
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/850,880
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berson, Bennett J
;      REGISTRATION NUMBER:  37094
;      REFERENCE/DOCKET NUMBER:  960296.94142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608/251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Tn5 wild type inside end"
US-08-850-880-10

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 46
US-08-944-916-10/c
; Sequence 10, Application US/08944916
; Patent No. 5948622
;  GENERAL INFORMATION:
;    APPLICANT:  Reznikoff, William S
;    APPLICANT:  Goryshin, Igor Y
;    APPLICANT:  York, Dona L
;    APPLICANT:  Zhou, Hong
;    TITLE OF INVENTION:  System for In Vitro Transposition
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,916
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/814,877
;      FILING DATE:  09-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/850,880
;      FILING DATE:  02-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berson, Bennett J
;      REGISTRATION NUMBER:  37094
;      REFERENCE/DOCKET NUMBER:  960296.94916
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608/251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Tn5 wild type inside end"
US-08-944-916-10

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 47
```

```
US-09-159-363-2/c
; Sequence 2, Application US/09159363A
; Patent No. 6159736
; GENERAL INFORMATION:
;  APPLICANT: Reznikoff, William S
;  APPLICANT: Goryshin, Igor Y
;  TITLE OF INVENTION: Method for Making Insertional Mutations
;  FILE REFERENCE: 960296.95688
;  CURRENT APPLICATION NUMBER: US/09/159,363A
;  CURRENT FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-09-159-363-2

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 48
US-09-635-969-6/c
; Sequence 6, Application US/09635969
; Patent No. 6294385
; GENERAL INFORMATION:
;  APPLICANT: Goryshin, Igor Y
;  APPLICANT: Reznikoff, William S
;  TITLE OF INVENTION: METHOD FOR MAKING INSERTIONAL MUTATIONS
;  FILE REFERENCE: 960296.96854
;  CURRENT APPLICATION NUMBER: US/09/635,969
;  CURRENT FILING DATE: 2000-08-10
;  EARLIER APPLICATION NUMBER: 09/159,363
;  EARLIER FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-09-635-969-6

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 49
US-09-632-021-4/c
; Sequence 4, Application US/09632021
; Patent No. 6406896
; GENERAL INFORMATION:
;  APPLICANT:  Reznikoff, William S
;  APPLICANT:  Naumann, Todd A
;  TITLE OF INVENTION:  Transposase Enzyme and Method for Use
;  FILE REFERENCE:  960296.96471
;  CURRENT APPLICATION NUMBER: US/09/632,021
;  CURRENT FILING DATE:  2000-08-02
;  PRIOR APPLICATION NUMBER:  60/146686
;  PRIOR FILING DATE:  1999-08-02
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-09-632-021-4

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 50
US-09-272-432A-10/c
; Sequence 10, Application US/09272432A
; Patent No. 6437109
;  GENERAL INFORMATION:
;    APPLICANT:  Reznikoff, William S
;    APPLICANT:  Goryshin, Igor Y
;    APPLICANT:  Zhou, Hong
;    TITLE OF INVENTION:  System for In Vitro Transposition
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/272,432A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berson, Bennett J
;      REGISTRATION NUMBER:  37094
;      REFERENCE/DOCKET NUMBER:  960296.96277
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608/251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Tn5 wild type inside end"
US-09-272-432A-10

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 51
US-09-350-852A-3
; Sequence 3, Application US/09350852A
; Patent No. 6596509
; GENERAL INFORMATION:
;  APPLICANT:  Bauer, David W.
;  APPLICANT:  Beer, Steven V.
```

```
;  APPLICANT:  Bogdanove, Adam J.
;  APPLICANT:  Collmer, Alan
;  APPLICANT:  Ham, Jong Hyun
;  TITLE OF INVENTION:  RECOMBINANT CONSTRUCTS AND SYSTEMS FOR SECRETION OF
;  TITLE OF INVENTION:  PROTEINS VIA TYPE III SECRETION SYSTEMS
;  FILE REFERENCE:  19603/2061
;  CURRENT APPLICATION NUMBER: US/09/350,852A
;  CURRENT FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  60/092,357
;  PRIOR FILING DATE:  1998-07-10
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  primer
US-09-350-852A-3

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db          1 AGATCTGATCAAGAGACAG 19


RESULT 52
US-09-696-791-3907
; Sequence 3907, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3907
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3907

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1117 TGAGGGCTTCCACAACTAC 1135
              |||||||||| ||| ||||
Db          1 TGAGGGCTTCGACACCTAC 19


RESULT 53
5212080-3/c
;Patent No. 5212080
;    APPLICANT: NAG, DILIP K.;HUANG, HENRY V.;BERG, DOUGLAS E.
;    TITLE OF INVENTION: METHOD OF DNA SEQUENCOM=NG USING DNA
;TRANSPOSON TN5SEQL
;    NUMBER OF SEQUENCES: 6
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/508,379
;      FILING DATE: 12-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 105,422
;      FILING DATE: 05-OCT-1987
;SEQ ID NO:3:
;      LENGTH: 19
5212080-3

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 54
5212080-3/c
;Patent No. 5212080
;    APPLICANT: NAG, DILIP K.;HUANG, HENRY V.;BERG, DOUGLAS E.
;    TITLE OF INVENTION: METHOD OF DNA SEQUENCOM=NG USING DNA
;TRANSPOSON TN5SEQL
;    NUMBER OF SEQUENCES: 6
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/508,379
;      FILING DATE: 12-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 105,422
;      FILING DATE: 05-OCT-1987
;SEQ ID NO:3:
;      LENGTH: 19
5212080-3

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 85;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 55
US-08-937-067-17
; Sequence 17, Application US/08937067
; Patent No. 6433155
;  GENERAL INFORMATION:
;    APPLICANT:  Umansky, Samuil
;    APPLICANT:  Melkonyan, Hovsep
;    TITLE OF INVENTION:  A FAMILY OF GENES ENCODING
;    TITLE OF INVENTION:  APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
;    TITLE OF INVENTION:  METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,067
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lehnhardt, Susan K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  23647-20018.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
```

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;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-937-067-17

  Query Match             0.4%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 87;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||| :
Db          1 TTTTTTTTTTTTTTNS 17


RESULT 56
US-08-373-124A-2151/c
; Sequence 2151, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2151:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-2151

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 98;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAAA 3979
              ||||||||| ||||||||
Db         17 TATATAAAAAATAAAAA 1


RESULT 57
US-08-373-124A-2153/c
; Sequence 2153, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-2153

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 98;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAAA 3978
              ||||||||| |||||||
Db         17 ATATATAAAAAATAAAA 1


RESULT 58
```

```
US-08-435-628-2151/c
; Sequence 2151, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2151:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-2151

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 98;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAAA 3979
              ||||||| |||||||
Db         17 TATATAAAAAATAAAAA 1


RESULT 59
US-08-435-628-2153/c
; Sequence 2153, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-2153

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 98;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAAA 3978
              ||||||||| |||||||
Db         17 ATATATAAAAAATAAAA 1


RESULT 60
US-08-584-040-2549
; Sequence 2549, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
```

```
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2549:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2549

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 98;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ::::::::::::::::
Db          1 ACUUUUUUUUUUUUUUU 17


RESULT 61
US-09-371-772B-1073
; Sequence 1073, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1073

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 98;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ::::::::::::::::
Db          1 ACUUUUUUUUUUUUUUU 17


RESULT 62
US-09-685-664B-1073
; Sequence 1073, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1073

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 98;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ::::::::::::::::
Db          1 ACUUUUUUUUUUUUUUU 17


RESULT 63
US-08-974-565C-10/c
; Sequence 10, Application US/08974565C
; Patent No. 5932423
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Coleman, Roger
;    APPLICANT:  Seilhamer, Jeffrey J.
;    APPLICANT:  Fisher, Douglas A.
;    TITLE OF INVENTION:  CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
```

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,565C
;      FILING DATE:  Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/624,663
;      FILING DATE:  March 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murry, Lynn E.
;      REGISTRATION NUMBER:  42,918
;      REFERENCE/DOCKET NUMBER:  PF-0057-1 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-974-565C-10

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              | |||||||||||||||
Db         17 TTCTGCTGATGTGCTTC 1


RESULT 64
US-09-725-265-17
; Sequence 17, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 65
US-09-725-265-20
; Sequence 20, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 66
US-09-556-127-17
; Sequence 17, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 67
US-09-556-127-20
; Sequence 20, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-20

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 68
PCT-US91-03680-73
; Sequence 73, Application PC/TUS9103680
;  GENERAL INFORMATION:
;     APPLICANT:  Matteucci, Mark D.
;     APPLICANT:  Krawczyk, Steven
;     TITLE OF INVENTION:  SEQUENCE-SPECIFIC NONPHOTOACTIVATED
;     TITLE OF INVENTION:  CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
;     TITLE OF INVENTION:  DUPLEX DNA
;     NUMBER OF SEQUENCES:  158
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Morrison & Foerster
;       STREET:  545 Middlefield Road, Suite 200
;       CITY:  Menlo Park
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94025
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US91/03680
;       FILING DATE:  19910524
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murashige, Kate H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  4610-0011.40
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-327-7250
;       TELEFAX:  415-327-2951
;       TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  73:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  modified_base
;       LOCATION:  5
;       OTHER INFORMATION:  /mod_base= OTHER
;       OTHER INFORMATION:  /note= "5-methylcytosine"
;     FEATURE:
;       NAME/KEY:  modified_base
;       LOCATION:  18
;       OTHER INFORMATION:  /mod_base= OTHER
;       OTHER INFORMATION:  /note= "N4,N4-ethanocytosine"
PCT-US91-03680-73

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTT 2140
              ||||||||| |||||||
Db          1 TTTTCTTTTTTTTTTTT 17


RESULT 69
US-09-696-791-253
; Sequence 253, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 253
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk2 ribozyme binding site
US-09-696-791-253

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
              |||||| ||||||||||
Db          2 GGCCCTATTCCCTGGAG 18


RESULT 70
US-09-696-791-254
; Sequence 254, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
```

```
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 254
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk2 ribozyme binding site
US-09-696-791-254

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
                ||||||  ||||||||||
Db          1 GGCCCTATTCCCTGGAG 17


RESULT 71
US-09-696-791-925
; Sequence 925, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 925
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk8 ribozyme binding site
US-09-696-791-925

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1831 ACAAAGCTTCTAAAGCA 1847
                ||| |||||||||||||
Db          1 ACAGAGCTTCTAAAGCA 17


RESULT 72
US-09-390-324B-2
; Sequence 2, Application US/09390324B
; Patent No. 6342376
; GENERAL INFORMATION:
;  APPLICANT: Kozian, Detlef
;  APPLICANT:  Reuner, Birgit
;  TITLE OF INVENTION: Two-color differential display as a method for
;  TITLE OF INVENTION:  detecting regulated genes
;  FILE REFERENCE: 2481-1635
;  CURRENT APPLICATION NUMBER: US/09/390,324B
;  CURRENT FILING DATE:  1999-09-07
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-09-390-324B-2

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
                ||||||||||||||:
Db          1 TTTTTTTTTTTTTTTV 16


RESULT 73
US-10-015-593-2
; Sequence 2, Application US/10015593
; Patent No. 6645741
; GENERAL INFORMATION:
;  APPLICANT: Kozian, Detlef
;  APPLICANT:  Reuner, Birgit
;  TITLE OF INVENTION: Two-color differential display as a method for
;  TITLE OF INVENTION:  detecting regulated genes
;  FILE REFERENCE: 2481-1635
;  CURRENT APPLICATION NUMBER: US/10/015,593
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/390,324
;  PRIOR FILING DATE: 2001-05-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-10-015-593-2

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
                ||||||||||||||:
Db          1 TTTTTTTTTTTTTTTV 16


RESULT 74
US-09-130-079-1/c
; Sequence 1, Application US/09130079
; Patent No. 6270966
;  GENERAL INFORMATION:
;    APPLICANT:  The United States of America, as represented by the
;    APPLICANT:  Secretary, Department of Health and Human Services
;    TITLE OF INVENTION:  RESTRICTION DISPLAY (RD-PCR) OF DIFFERENTIALLY EXPRESS
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive, 16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/130,079
;      FILING DATE:
```

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/011/379
;      FILING DATE:  09-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick, Anita M
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH108.001VPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  mRNA
US-09-130-079-1

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db         17 TTTTTTTTTTTTTTV 2


RESULT 75
US-10-103-614A-4/c
; Sequence 4, Application US/10103614A
; Patent No. 6716585
; GENERAL INFORMATION:
;  APPLICANT: SALMAN AL-MAHMOOD
;  TITLE OF INVENTION: METHOD FOR IDENTIFYING NOVEL GENES INVOLVED IN THE
;  TITLE OF INVENTION:  REGULATION OF ANGIOGENESIS, STUDY OF SAID GENES AND USE
;  TITLE OF INVENTION:  THEREOF FOR THERAPEUTIC PURPOSES
;  FILE REFERENCE: 1071-02
;  CURRENT APPLICATION NUMBER: US/10/103,614A
;  CURRENT FILING DATE:  2002-08-22
;  PRIOR APPLICATION NUMBER: PCT/FR00/02607
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: FR 99/11790
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   NAME/KEY: modified_base
;   LOCATION: (1)
;   OTHER INFORMATION: a, t, c or g
;   NAME/KEY: modified_base
;   LOCATION: (19)
;   OTHER INFORMATION: a, t, c or g
US-10-103-614A-4

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db         17 TTTTTTTTTTTTTTB 2


RESULT 76
US-09-371-307-85
; Sequence 85, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
;  APPLICANT: Brown, Sherri M.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: Piller, Kenneth J.
;  APPLICANT: Kishore, Ganesh M.
;  APPLICANT: Elich, Tedd D.
;  APPLICANT: Logusch, Eugene W.
;  APPLICANT: Rao, Sudabathula
;  APPLICANT: Ream, Joel E.
;  APPLICANT: Logusch, Sherry J.
;  TITLE OF INVENTION: Methods for controlling gibberellin levels
;  FILE REFERENCE: MOBT:216
;  CURRENT APPLICATION NUMBER: US/09/371,307A
;  CURRENT FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-371-307-85

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 77
US-08-452-196A-6/c
; Sequence 6, Application US/08452196A
; Patent No. 5576427
;  GENERAL INFORMATION:
;    APPLICANT:  Cook, Philip D.
;    APPLICANT:  Delecki, Daniel J.
;    APPLICANT:  Guinosso, Charles
;    TITLE OF INVENTION:  ACYCLIC NUCLEOSIDE
;    TITLE OF INVENTION:  ANALOGS AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  SEQUENCES
;    TITLE OF INVENTION:  CONTAINING THEM
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Department
;      STREET:  9 Great Valley Parkway
;      CITY:  Malvern
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19355
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.4 MB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.0B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,196A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/040,326
;      FILING DATE:  30 March 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul E. Dupont
;      REGISTRATION NUMBER:  27,438
;      REFERENCE/DOCKET NUMBER:  2525
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215)889-6338
;      TELEFAX:  (215)889-8800
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Nucleic Acid
;      DESCRIPTION:
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:  synthesized
US-08-452-196A-6

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 78
US-07-971-978-1
; Sequence 1, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  6-aza-thymidine substitution
US-07-971-978-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 79
US-08-756-728A-2/c
; Sequence 2, Application US/08756728A
; Patent No. 5821354
;  GENERAL INFORMATION:
;    APPLICANT:  Leclerc, Guy
;    APPLICANT:  Martel, Remi
;    TITLE OF INVENTION:  RADIOLABELED DNA OLIGONUCLEOTIDE, METHOD
;    TITLE OF INVENTION:  OF PREPARATION AND THERAPEUTIC USES THEREOF
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,728A
;      FILING DATE:  26-NOV-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1398-1-001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "PRIMER"
;    HYPOTHETICAL:  NO
US-08-756-728A-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 80
US-08-663-918-3
; Sequence 3, Application US/08663918
; Patent No. 5824793
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeffe
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide N3 {symbol 174 \f "Sy
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/663,918
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-663-918-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         1 TTTTTTTTTTTTTTT 15


RESULT 81
US-08-663-918-4/c
; Sequence 4, Application US/08663918
; Patent No. 5824793
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeffe
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide N3 {symbol 174 \f "Sy
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/663,918
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-663-918-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 82
```

```
US-08-292-620A-361
; Sequence 361, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  361:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-361

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.1e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 83
US-08-292-620A-362
; Sequence 362, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  362:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-362

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.1e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 84
US-08-771-789-3
; Sequence 3, Application US/08771789
; Patent No. 5859233
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein
;    APPLICANT:  Karen Fearon
;    APPLICANT:  Sergei Gryaznov
;    APPLICANT:  Sarah McCurdy
;    APPLICANT:  Jeffery Nelson
;    APPLICANT:  Ronald G. Schultz
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide
;    TITLE OF INVENTION:  N3 {symbol 174 \f "Symbol" \s 12|}P5  Phosphoramidates
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,789
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/663,918
;      FILING DATE:  14-JUN-1996
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-771-789-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 85
US-08-771-789-4/c
; Sequence 4, Application US/08771789
; Patent No. 5859233
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein
;    APPLICANT:  Karen Fearon
;    APPLICANT:  Sergei Gryaznov
;    APPLICANT:  Sarah McCurdy
;    APPLICANT:  Jeffery Nelson
;    APPLICANT:  Ronald G. Schultz
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide
;    TITLE OF INVENTION:  N3 {symbol 174 \f "Symbol" \s 12|}P5  Phosphoramidates
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,789
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/663,918
;      FILING DATE:  14-JUN-1996
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-771-789-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          15 TTTTTTTTTTTTTTT 1


RESULT 86
US-08-358-556A-10
; Sequence 10, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..15
US-08-358-556A-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 87
US-08-358-556A-16/c
; Sequence 16, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..15
US-08-358-556A-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          15 TTTTTTTTTTTTTTT 1


RESULT 88
US-08-585-684B-638/c
; Sequence 638, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  638:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-638

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGAT 1418
              |||||||||||||||
Db         15 GATGCTAAAGATGAT 1


RESULT 89
US-08-922-170B-5
; Sequence 5, Application US/08922170B
; Patent No. 5968822
;  GENERAL INFORMATION:
;    APPLICANT:  Iris Pecker, Israel Vlodavsky and Elena
;    APPLICANT:  Feinstein
;    TITLE OF INVENTION:  POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
;    TITLE OF INVENTION:  HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
;    TITLE OF INVENTION:  SAME IN TRANSDUCED CELLS
```

```
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark M. Friedman c/o Robert Sheinbein
;      STREET:  2940 Birchtree lane
;      CITY:  Silver Spring
;      STATE:  Maryland
;      COUNTRY:  United States of America
;      ZIP:  20906
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 megabyte, 3.5" microdisk
;      COMPUTER:  Twinhead* Slimnote-890TX
;      OPERATING SYSTEM:  MS DOS version 6.2,
;      OPERATING SYSTEM:  Windows version 3.11
;      SOFTWARE:  Word for Windows version 2.0 converted to
;      SOFTWARE:  an ASCI file
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/922,170B
;      FILING DATE:  2 SEP 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Friedmam, Mark M.
;      REGISTRATION NUMBER:  33,883
;      REFERENCE/DOCKET NUMBER:  910/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  972-3-5625553
;      TELEFAX:  972-3-5625554
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-922-170B-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 90
US-08-863-639A-5/c
; Sequence 5, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          15 TTTTTTTTTTTTTTT 1


RESULT 91
US-08-863-639A-9
; Sequence 9, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 92
US-08-693-831-1
; Sequence 1, Application US/08693831
; Patent No. 6017700
; GENERAL INFORMATION:
;  APPLICANT: Horn, Thomas
;  APPLICANT: Letsinger, Robert L.
;  APPLICANT: Balasubramanian, Tanjore N.
;  TITLE OF INVENTION: CATIONIC OLIGONUCLEOTIDES, AND RELATED METHODS OF
;  TITLE OF INVENTION: SYNTHESIS AND USE
;  FILE REFERENCE: 1117.002
;  CURRENT APPLICATION NUMBER: US/08/693,831
;  CURRENT FILING DATE: 1996-07-31
;  EARLIER APPLICATION NUMBER: US 08/693,831
;  EARLIER FILING DATE: 1996-07-31
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Description of Artificial Sequence: poly-T
US-08-693-831-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 93
US-08-832-021-51
; Sequence 51, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-51

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGG 4518
             |||||||||||||||
Db          1 TTTTTTTTTTTTGGG 15


RESULT 94
US-09-183-619-4
; Sequence 4, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
;  APPLICANT: DELLINGER, DOUGLAS J.
;  APPLICANT: DAHM, SUEANN C.
;  APPLICANT: ILSLEY, DIANE D.
;  APPLICANT: ACH, ROBERT A.
;  APPLICANT: TROLL, MARK A.
;  TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
;  FILE REFERENCE: 10981619-1
;  CURRENT APPLICATION NUMBER: US/09/183,619
;  CURRENT FILING DATE: 1998-10-30
;  EARLIER APPLICATION NUMBER: 08/735,381
;  EARLIER FILING DATE: 1996-10-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Reporter probe
US-09-183-619-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.1e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 95
US-09-071-845-361
; Sequence 361, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
```

```
;       APPLICATION NUMBER:  07/989,849
;       FILING DATE:  December 7, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  208/149
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  361:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-071-845-361

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.1e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 96
US-09-071-845-362
; Sequence 362, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  362:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-362

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.1e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 97
US-09-038-073-638/c
; Sequence 638, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  638:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-638

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGAT 1418
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                ||||||||||||||||
Db         15 GATGCTAAAGATGAT 1


RESULT 98
US-09-167-375-1/c
; Sequence 1, Application US/09167375B
; Patent No. 6291438
; GENERAL INFORMATION:
;  APPLICANT: Jui H. Wang
;  TITLE OF INVENTION: Antiviral anticancer poly-substituted phenyl derivatized oligorib
;  TITLE OF INVENTION: methods for their use.
;  FILE REFERENCE: WNGJ 2002 (CIP-1)
;  CURRENT APPLICATION NUMBER: US/09/167,375B
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Retroviral reverse transcriptase inhibitor
US-09-167-375-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 99
US-08-150-156A-19
; Sequence 19, Application US/08150156A
; Patent No. 6357163
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;    TITLE OF INVENTION:  DIAGNOSTICS AND ANALYTICAL PROCEDURES
;    NUMBER OF SEQUENCES:  40
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/150,156A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0986/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0987/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0510/92
;      FILING DATE:  15-APR-1992
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      DOCUMENT NUMBER:  WO PCT/EP92/01220
;      FILING DATE:  22-MAY-1992
US-08-150-156A-19

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 100
US-08-150-156A-20/c
; Sequence 20, Application US/08150156A
; Patent No. 6357163
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;    TITLE OF INVENTION:  DIAGNOSTICS AND ANALYTICAL PROCEDURES
;    NUMBER OF SEQUENCES:  40
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/150,156A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0986/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0987/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0510/92
;      FILING DATE:  15-APR-1992
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      DOCUMENT NUMBER:  WO PCT/EP92/01220
;      FILING DATE:  22-MAY-1992
US-08-150-156A-20

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 101
US-08-108-591B-17
; Sequence 17, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/08/108,591B
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-17

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 102
US-08-108-591B-18/c
; Sequence 18, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/08/108,591B
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 103
US-09-619-103-21/c
; Sequence 21, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-21

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 104
US-09-300-958A-68
; Sequence 68, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-68

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 105
US-08-988-024C-9
; Sequence 9, Application US/08988024C
; Patent No. 6635452
; GENERAL INFORMATION:
;  APPLICANT: Monforte, Joseph A.
;  APPLICANT:  Becker, Christopher H.
;  APPLICANT:  Pollart, Daniel J.
;  APPLICANT:  Shaler, Thomas A.
;  TITLE OF INVENTION: Releasable No. 6635452volatile Mass-Label Molecules
;  FILE REFERENCE: 24736-2057
;  CURRENT APPLICATION NUMBER: US/08/988,024C
;  CURRENT FILING DATE:  1997-12-10
;  PRIOR APPLICATION NUMBER: US 60/033,037
;  PRIOR FILING DATE: 1996-12-10
;  PRIOR APPLICATION NUMBER: US 60/046,719
;  PRIOR FILING DATE: 1997-05-16
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-08-988-024C-9
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  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 106
US-09-435-739-5
; Sequence 5, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky, Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 00/20454
;  CURRENT APPLICATION NUMBER: US/09/435,739
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
US-09-435-739-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 107
US-10-091-231-2
; Sequence 2, Application US/10091231
; Patent No. 6664388
; GENERAL INFORMATION:
;  APPLICANT: NELSON, Jeffrey S.
;  TITLE OF INVENTION: REAGENTS FOR OLIGONUCLEOTIDE CLEAVAGE AND DEPROTECTION
;  FILE REFERENCE: 4688US
;  CURRENT APPLICATION NUMBER: US/10/091,231
;  CURRENT FILING DATE:  2002-03-04
;  PRIOR APPLICATION NUMBER: US 60/274,309
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-091-231-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 108
US-09-930-218-5
; Sequence 5, Application US/09930218
; Patent No. 6677137
; GENERAL INFORMATION:
;  APPLICANT: goldshmidt, orit
;  APPLICANT:  pecker, iris
;  APPLICANT:  vlodavsky, israel
;  APPLICANT:  israel, michal
;  TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H
;  TITLE OF INVENTION:  HEPARANASE ACTIVITY
;  FILE REFERENCE: 01/22335
;  CURRENT APPLICATION NUMBER: US/09/930,218
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/666,390
;  PRIOR FILING DATE: 2000-09-20
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide
US-09-930-218-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 109
US-08-468-719A-17
; Sequence 17, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf H.
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
;  FILE REFERENCE: ISPS-1999
;  CURRENT APPLICATION NUMBER: US/08/468,719A
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-17

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 110
US-08-468-719A-18/c
; Sequence 18, Application US/08468719A
; Patent No. 6710163
```

```
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf H.
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
;  FILE REFERENCE: ISPS-1999
;  CURRENT APPLICATION NUMBER: US/08/468,719A
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 111
US-08-462-977B-17
; Sequence 17, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS-1993
;  CURRENT APPLICATION NUMBER: US/08/462,977B
;  CURRENT FILING DATE:  1995-06-05
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-17

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 112
US-08-462-977B-18/c
; Sequence 18, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS-1993
;  CURRENT APPLICATION NUMBER: US/08/462,977B
;  CURRENT FILING DATE:  1995-06-05
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 113
US-09-988-113-5
; Sequence 5, Application US/09988113
; Patent No. 6790658
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 01/22781
;  CURRENT APPLICATION NUMBER: US/09/988,113
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: US 09/776,874
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US09/258,892
;  PRIOR FILING DATE: 1999-03-01
;  PRIOR APPLICATION NUMBER: PCT/US98/17954
;  PRIOR FILING DATE: 1998-08-31
;  PRIOR APPLICATION NUMBER: US 09/109,386
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 08/922,170
;  PRIOR FILING DATE: 1997-09-02
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 114
US-10-352-704-10
; Sequence 10, Application US/10352704
; Patent No. 6825339
```

```
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..15
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-352-704-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 115
US-10-352-704-16/c
; Sequence 16, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..15
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-352-704-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 116
US-07-971-978-36
; Sequence 36, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/971,978
;       FILING DATE:  February 18, 1993
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/558,806
;       FILING DATE:  July 27, 1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Joseph Lucci
;       REGISTRATION NUMBER:  33,307
;       REFERENCE/DOCKET NUMBER:  ISIS-0333
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-568-3100
;       TELEFAX:  215-568-3439
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  1
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  2
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  3
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  5
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  6
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  7
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  8
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  9
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  10
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  11
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  12
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  13
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  14
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  15
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
US-07-971-978-36

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 117
US-07-971-978-42
; Sequence 42, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
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;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  15
;      OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
US-07-971-978-42

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 118
US-07-971-978-60
; Sequence 60, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
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;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  15
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
US-07-971-978-60

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 119
US-08-415-370-2
; Sequence 2, Application US/08415370
; Patent No. 5801155
;  GENERAL INFORMATION:
;    APPLICANT:  Kutyavin, Igor V.
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Gamper, Howard B.
;    APPLICANT:  Meyer, Jr., Rich B.
;    TITLE OF INVENTION:  COVALENTLY LINKED OLIGONUCLEOTIDE MINOR
;    TITLE OF INVENTION:  GROOVE BINDER CONJUGATES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KLEIN & SZEKERES
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/415,370
;      FILING DATE:  03-APR-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-09-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-854-5502
;      TELEFAX:  714-854-4897
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-415-370-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 120
US-08-687-551-15
; Sequence 15, Application US/08687551
; Patent No. 5856435
;  GENERAL INFORMATION:
;    APPLICANT:  BAZILE, Didier
;    APPLICANT:  EMILE, Carole
;    APPLICANT:  HELENE, Claude
;    APPLICANT:  SPENLEHAUER, Gilles
;    TITLE OF INVENTION:  NUCLEIC ACID-CONTAINING COMPOSITION, ITS
;    TITLE OF INVENTION:  PREPARATION AND USE
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Rd. 3C43
;      CITY:  Collegeville
```

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;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19426
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/687,551
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  FR 94/01381
;       FILING DATE:  08-FEB-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/FR95/00098
;       FILING DATE:  27-JAN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith Ph.D., Julie K.
;       REGISTRATION NUMBER:  38,619
;       REFERENCE/DOCKET NUMBER:  ST94007-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (610)454-3839
;       TELEFAX:  (610)454-3808
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
US-08-687-551-15

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 121
US-09-141-764-2
; Sequence 2, Application US/09141764
; Patent No. 6084102
;  GENERAL INFORMATION:
;    APPLICANT:  Kutyavin, Igor V.
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Gamper, Howard B.
;    APPLICANT:  Meyer, Jr., Rich B.
;    TITLE OF INVENTION:  COVALENTLY LINKED OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  MINOR
;    TITLE OF INVENTION:  GROOVE BINDER CONJUGATES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KLEIN & SZEKERES
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/141,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/415,370
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-09-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-854-5502
;      TELEFAX:  714-854-4897
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-141-764-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 122
US-08-851-843A-131/c
; Sequence 131, Application US/08851843A
; Patent No. 6093809
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6093809el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/851,843A
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-851-843A-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 123
US-08-854-050-131/c
; Sequence 131, Application US/08854050
; Patent No. 6261836
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6261836el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/854,050
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/851,843
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-854-050-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 124
US-09-430-323-131/c
; Sequence 131, Application US/09430323
; Patent No. 6309867
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. 6309867el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/430,323
;             FILING DATE: 29-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002930US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-430-323-131
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  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 125
US-09-507-345A-2
; Sequence 2, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-507-345A-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 126
US-09-507-345A-3
; Sequence 3, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by 6-aminohexanoic acid
;             (-NH(CH-2)-6COOH)"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-507-345A-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 127
US-09-507-345A-4
; Sequence 4, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
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;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = one
;             4-amino-N-methylpyrrol-2-carboxylic acid residue"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-507-345A-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 128
US-09-507-345A-5
; Sequence 5, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = two
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-507-345A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 129
US-09-507-345A-6
; Sequence 6, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
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;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = three
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-507-345A-6

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 130
US-09-507-345A-7
; Sequence 7, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = four
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-507-345A-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 131
US-09-507-345A-8
; Sequence 8, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
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;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = five
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-507-345A-8

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 132
US-09-619-103-22/c
; Sequence 22, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-22

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 133
US-09-739-928-2
; Sequence 2, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 134
US-09-739-928-3
; Sequence 3, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
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;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by 6-aminohexanoic acid
;             (-NH(CH-2)-6COOH)"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-739-928-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 135
US-09-739-928-4
; Sequence 4, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = one
;             4-amino-N-methylpyrrol-2-carboxylic acid residue"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-739-928-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 136
US-09-739-928-5
; Sequence 5, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
```

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;            REGISTRATION NUMBER: 37,369
;            REFERENCE/DOCKET NUMBER: 17682A-003510US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  16
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = two
;            4-amino-N-methylpyrrol-2-carboxylic acid residues"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-739-928-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 137
US-09-739-928-6
; Sequence 6, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;       APPLICANT: Kutyavin, Igor V.
;                  Lukhtanov, Eugeny A.
;                  Gamper, Howard B.
;                  Meyer Jr., Rich B.
;       TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                           Groove Binder Conjugates
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/739,928
;            FILING DATE: 11-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/415,370
;            FILING DATE: 03-APR-1995
;            APPLICATION NUMBER: US 09/141,764
;            FILING DATE: 27-AUG-1998
;            APPLICATION NUMBER: US 09/507,345
;            FILING DATE: 18-FEB-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kezer, William B.
;            REGISTRATION NUMBER: 37,369
;            REFERENCE/DOCKET NUMBER: 17682A-003510US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  16
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = three
;            4-amino-N-methylpyrrol-2-carboxylic acid residues"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-739-928-6

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 138
US-09-739-928-7
; Sequence 7, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;       APPLICANT: Kutyavin, Igor V.
;                  Lukhtanov, Eugeny A.
;                  Gamper, Howard B.
;                  Meyer Jr., Rich B.
;       TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                           Groove Binder Conjugates
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/739,928
;            FILING DATE: 11-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/415,370
;            FILING DATE: 03-APR-1995
;            APPLICATION NUMBER: US 09/141,764
;            FILING DATE: 27-AUG-1998
;            APPLICATION NUMBER: US 09/507,345
;            FILING DATE: 18-FEB-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kezer, William B.
;            REGISTRATION NUMBER: 37,369
;            REFERENCE/DOCKET NUMBER: 17682A-003510US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
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;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  16
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = four
;            4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-739-928-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 139
US-09-739-928-8
; Sequence 8, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/739,928
;            FILING DATE: 11-May-2001
;            CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/415,370
;            FILING DATE: 03-APR-1995
;            APPLICATION NUMBER: US 09/141,764
;            FILING DATE: 27-AUG-1998
;            APPLICATION NUMBER: US 09/507,345
;            FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Kezer, William B.
;            REGISTRATION NUMBER: 37,369
;            REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  16
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = five
;            4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-739-928-8

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 140
US-09-958-610A-1/c
; Sequence 1, Application US/09958610A
; Patent No. 6756492
; GENERAL INFORMATION:
;  APPLICANT: Beier, Markus
;  APPLICANT:  Hoheisel, Jorg
;  TITLE OF INVENTION: Nucleoside Derivatives with Photolabile Protective Groups
;  FILE REFERENCE: 03528.0135.PCUS00
;  CURRENT APPLICATION NUMBER: US/09/958,610A
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: PCT/DE00/011448
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 100 03 631.7
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: DE 199 15. 867.3
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-958-610A-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 141
US-09-895-585-9
; Sequence 9, Application US/09895585
; Patent No. 6759039
; GENERAL INFORMATION:
;  APPLICANT: Tsang, Wen-Ghih
;  APPLICANT:  Zheng, Tianli
;  APPLICANT:  Huang, Chang Jiang
;  APPLICANT:  AmCyte, Inc.
;  TITLE OF INVENTION: Culturing Pancreatic Stem Cells Having a Specified,
;  TITLE OF INVENTION:  Intermediate Stage of Development
;  FILE REFERENCE: 021164-000100US
;  CURRENT APPLICATION NUMBER: US/09/895,585
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/215,634
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/246,306
;  PRIOR FILING DATE: 2000-11-06
;  PRIOR APPLICATION NUMBER: US 60/291,787
;  PRIOR FILING DATE: 2001-05-17
;  NUMBER OF SEQ ID NOS: 9
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo-(dT)-16
US-09-895-585-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 142
US-09-152-059-70
; Sequence 70, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-70

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 143
US-09-766-253-131/c
; Sequence 131, Application US/09766253
; Patent No. 6808880
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. 6808880el Telomerase
;        NUMBER OF SEQUENCES: 171
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,253
;             FILING DATE: 19-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/846,017
;             FILING DATE: 1997-04-25
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002920US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-766-253-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 144
US-08-851-843A-132
; Sequence 132, Application US/08851843A
; Patent No. 6093809
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6093809el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/851,843A
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-851-843A-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 145
US-09-250-075-5
; Sequence 5, Application US/09250075
; Patent No. 6207819
; GENERAL INFORMATION:
;  APPLICANT:  Manoharan, Muthiah
;  APPLICANT:  Maier, Martin A
;  TITLE OF INVENTION:  Compounds Processes And Intermediates For Synthesis Of
;  TITLE OF INVENTION:  Mixed Backbone Oligomeric Compounds
;  FILE REFERENCE:  ISIS3299
;  CURRENT APPLICATION NUMBER: US/09/250,075
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: 2'-methoxyethoxy (MOE); modified linkage
;   OTHER INFORMATION: Description of Artificial Sequence:  No. 6207819el
;   OTHER INFORMATION: Sequence
US-09-250-075-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 146
US-08-854-050-132
; Sequence 132, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6261836el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/854,050
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/851,843
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-854-050-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

```
RESULT 147
US-08-821-827C-30
; Sequence 30, Application US/08821827C
; Patent No. 6297425
; GENERAL INFORMATION:
;  APPLICANT: Scelonge, Christopher J.
;  APPLICANT:  Bidney, Dennis L.
;  TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
;  TITLE OF INVENTION:  ASPERGILLUS PHOENICES
;  FILE REFERENCE: 0561A
;  CURRENT APPLICATION NUMBER: US/08/821,827C
;  CURRENT FILING DATE:  1997-03-21
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(17)
;   OTHER INFORMATION: n = A,T,C or G
US-08-821-827C-30

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 148
US-09-290-202B-30
; Sequence 30, Application US/09290202B
; Patent No. 6303846
; GENERAL INFORMATION:
;  APPLICANT: Scelonge, Christopher J.
;  APPLICANT:  Bidney, Dennis L.
;  TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
;  TITLE OF INVENTION:  ASPERGILLUS PHOENICES
;  FILE REFERENCE: 0561D
;  CURRENT APPLICATION NUMBER: US/09/290,202B
;  CURRENT FILING DATE:  1999-04-12
;  PRIOR APPLICATION NUMBER: 08/821,827
;  PRIOR FILING DATE: 1997-03-21
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(17)
;   OTHER INFORMATION: n = A,T,C or G
US-09-290-202B-30

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 149
US-09-430-323-132
; Sequence 132, Application US/09430323
; Patent No. 6309867
;  GENERAL INFORMATION:
;       APPLICANT: Cech, Thomas R.
;                  Lingner, Joachim
;                  Nakamura, Toru
;                  Chapman, Karen B.
;                  Morin, Gregg B.
;                  Harley, Calvin
;                  Andrews, William H.
;       TITLE OF INVENTION: No. 6309867el Telomerase
;       NUMBER OF SEQUENCES: 225
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, 8th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/430,323
;            FILING DATE: 29-Oct-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/854,050
;            FILING DATE: 09-MAY-1997
;            APPLICATION NUMBER: US 08/851,843
;            FILING DATE: 06-MAY-1997
;            APPLICATION NUMBER: US 08/846,017
;            FILING DATE: 25-APR-1997
;            APPLICATION NUMBER: US 08/844,419
;            FILING DATE: 18-APR-1997
;            APPLICATION NUMBER: US 08/724,643
;            FILING DATE: 01-OCT-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Apple,  Randolph T.
;            REGISTRATION NUMBER: 36,429
;            REFERENCE/DOCKET NUMBER: 015389-002930US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 132:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 17 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-430-323-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 150
US-08-584-040-2550
; Sequence 2550, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
```

```
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2550:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2550

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 151
US-08-584-040-2551
; Sequence 2551, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2551:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2551

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 152
US-08-584-040-2552
; Sequence 2552, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
```

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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2552:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2552

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 153
US-08-584-040-5642/c
; Sequence 5642, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5642:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-5642

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 154
US-09-619-103-23/c
; Sequence 23, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-23

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         17 TTTTTTTTTTTTTTT 3


RESULT 155
US-09-726-096A-5
; Sequence 5, Application US/09726096A
; Patent No. 6462184
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT:  Maier, Martin A.
;  TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back
;  TITLE OF INVENTION:  Oligomeric Compounds
;  FILE REFERENCE: ISIS4528
;  CURRENT APPLICATION NUMBER: US/09/726,096A
;  CURRENT FILING DATE:  2000-11-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(19)
```

```
;   OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
;   OTHER INFORMATION: internucleoside linkage
US-09-726-096A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 156
US-09-475-947A-118
; Sequence 118, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: human
US-09-475-947A-118

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 157
US-09-300-958A-63
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 158
US-09-371-772B-1074
; Sequence 1074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1074

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 159
US-09-371-772B-1075
; Sequence 1075, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1075

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTT 4515
             :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 160
US-09-371-772B-1076
; Sequence 1076, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1076

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 161
US-09-371-772B-2532/c
; Sequence 2532, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2532
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-2532

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
             |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 162
US-09-766-253-132
; Sequence 132, Application US/09766253
; Patent No. 6808880
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. 6808880el Telomerase
;        NUMBER OF SEQUENCES: 171
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,253
;             FILING DATE: 19-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/846,017
;             FILING DATE: 1997-04-25
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002920US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 132:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-766-253-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 163
US-09-685-664B-1074
; Sequence 1074, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
```

```
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1074

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 164
US-09-685-664B-1075
; Sequence 1075, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1075

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 165
US-09-685-664B-1076
; Sequence 1076, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1076

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 166
US-09-685-664B-2532/c
; Sequence 2532, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2532
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-09-685-664B-2532

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 167
US-08-621-914A-16
```

```
; Sequence 16, Application US/08621914A
; Patent No. 5707807
;  GENERAL INFORMATION:
;    APPLICANT:  KATO, KIKUYA
;    TITLE OF INVENTION:  MOLECULAR INDEXING FOR EXPRESSED GENE
;    TITLE OF INVENTION:  ANALYSIS
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,914A
;      FILING DATE:  26-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LAWRENCE III, STANTON T.
;      REGISTRATION NUMBER:  25,736
;      REFERENCE/DOCKET NUMBER:  7005-107-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  other nucleic acid
US-08-621-914A-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 168
US-08-346-429-3/c
; Sequence 3, Application US/08346429
; Patent No. 5837820
;  GENERAL INFORMATION:
;    APPLICANT:  DeRose, Richard
;    APPLICANT:  Douce, Roland
;    APPLICANT:  Duval, Manuel
;    APPLICANT:  Job, Claudette
;    APPLICANT:  Job, Dominique
;    TITLE OF INVENTION:  PROTEIN CAPABLE OF BEING BIOTINYLATED WHICH CAN
;    TITLE OF INVENTION:  BE USED FOR DETERMINING THE GERMINATION STAGE OF
;    TITLE OF INVENTION:  A SEED
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY SCOTT MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/346,429
;      FILING DATE:  29-NOV-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9507
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-346-429-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 169
US-08-358-556A-12
; Sequence 12, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
```

```
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..18
US-08-358-556A-12

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 170
US-08-358-556A-18/c
; Sequence 18, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..18
US-08-358-556A-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          18 TTTTTTTTTTTTTTT 4


RESULT 171
US-08-469-852A-4
; Sequence 4, Application US/08469852A
; Patent No. 5874213
;  GENERAL INFORMATION:
;    APPLICANT:  Cummins, Lendell L.
;    APPLICANT:  Freier, Susan M.
;    APPLICANT:  Griffey, Richard
;    APPLICANT:  Srivatsa, Susan G.
;    TITLE OF INVENTION:  Capillary Electrophoretic Detection of
;    TITLE OF INVENTION:  Nucleic Acids
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5874213ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,852A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/295,509
;      FILING DATE:  24-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michael P. Straher
;      REGISTRATION NUMBER:  38,325
;      REFERENCE/DOCKET NUMBER:  ISIS-2015
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-469-852A-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 172
US-08-295-509B-4
; Sequence 4, Application US/08295509B
; Patent No. 6045995
;  GENERAL INFORMATION:
;    APPLICANT:  Cummins, Lendell L.
;    APPLICANT:  Freier, Susan M.
;    APPLICANT:  Griffey, Richard
;    APPLICANT:  Srivatsa, Susan G.
;    TITLE OF INVENTION:  Capillary Electrophoretic Detection of
```

```
;    TITLE OF INVENTION:  Nucleic Acids
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and No. 6045995ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/295,509B
;      FILING DATE:  24-AUG-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michael P. Straher
;      REGISTRATION NUMBER:  38,325
;      REFERENCE/DOCKET NUMBER:  ISIS-1395
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-295-509B-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 173
US-08-884-029-9
; Sequence 9, Application US/08884029
; Patent No. 6071745
;  GENERAL INFORMATION:
;    APPLICANT:  Lin, Ching-I Patsy
;    APPLICANT:  Wallace, Robert Bruce
;    APPLICANT:  Cossman, Jeffrey
;    APPLICANT:  French, Cynthia
;    TITLE OF INVENTION:  Lyophilization of Cultured Human Cells
;    TITLE OF INVENTION:  to Preserve RNA and DNA
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/884,029
;      FILING DATE:  27-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parent, Annette S.
;      REGISTRATION NUMBER:  42,058
;      REFERENCE/DOCKET NUMBER:  02558B-059100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  13..18
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "t at positions 13-18 may be
;      OTHER INFORMATION:  present or absent"
US-08-884-029-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 174
US-08-941-445A-30/c
; Sequence 30, Application US/08941445A
; Patent No. 6107060
;  GENERAL INFORMATION:
;    APPLICANT:  Keeling, Peter
;    APPLICANT:  Guan, Hanping
;    TITLE OF INVENTION:  Starch Encapsulation
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Greenlee, Winner and Sullivan, P.C.
;      STREET:  5370 Manhattan Circle
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/941,445A
;      FILING DATE:  30-SEP-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,855
;      FILING DATE:  30-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winner, Ellen P
;      REGISTRATION NUMBER:  28,547
;      REFERENCE/DOCKET NUMBER:  89-97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
US-08-941-445A-30
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  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 175
US-09-437-076-1/c
; Sequence 1, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
;  APPLICANT: Barber-Guillem, Emilio
;  APPLICANT: Nelson, M. Bud
;  APPLICANT: Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  CURRENT APPLICATION NUMBER: US/09/437,076
;  CURRENT FILING DATE: 1999-11-09
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: Word for Windows
; SEQ ID NO 1
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    NAME/KEY:
;    LOCATION:
;    OTHER INFORMATION: synthesized
US-09-437-076-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 176
US-09-637-751A-7
; Sequence 7, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
;  APPLICANT:  Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Binary Encoded Sequence Tags
; Patent No. 6383754
;  FILE REFERENCE:  AGL 100
;  CURRENT APPLICATION NUMBER: US/09/637,751A
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 177
US-09-545-225-9
; Sequence 9, Application US/09545225
; Patent No. 6410321
;  GENERAL INFORMATION:
;       APPLICANT: Lin, Ching-I Patsy
;                  Wallace, Robert Bruce
;                  Cossman, Jeffrey
;                  French, Cynthia
;       TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                           to Preserve RNA and DNA
;       NUMBER OF SEQUENCES: 9
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/545,225
;            FILING DATE: 07-Apr-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/884,029
;            FILING DATE: 27-JUN-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Parent, Annette S.
;            REGISTRATION NUMBER: 42,058
;            REFERENCE/DOCKET NUMBER: 02558B-059100US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  13..18
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "t at positions 13-18 may be
;            present or absent"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-225-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 178
US-09-619-103-24/c
; Sequence 24, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
```

```
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-24

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4

RESULT 179
US-09-370-541-14
; Sequence 14, Application US/09370541
; Patent No. 6639062
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT: Prakash, Thazha P
;  APPLICANT: Kawasaki, Andrew M
;  TITLE OF INVENTION: Aminoxxy-Modified Nucleosidic Compounds And Oligomeric
;  TITLE OF INVENTION: Compounds Prepared Therefrom
;  FILE REFERENCE: ISIS3993
;  CURRENT APPLICATION NUMBER: US/09/370,541
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: 09/130,973
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 09/016,520
;  EARLIER FILING DATE: 1998-01-30
;  EARLIER APPLICATION NUMBER: 60/037,143
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 09/344,260
;  EARLIER FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: antisense
;    OTHER INFORMATION: sequence
US-09-370-541-14

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15

RESULT 180
US-10-125-295-9
; Sequence 9, Application US/10125295
; Patent No. 6686460
;   GENERAL INFORMATION:
;        APPLICANT: Lin, Ching-I Patsy
;                   Wallace, Robert Bruce
;                   Cossman, Jeffrey
;                   French, Cynthia
;        TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                            to Preserve RNA and DNA
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/125,295
;             FILING DATE: 17-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/545,225
;             FILING DATE: 07-Apr-2000
;             APPLICATION NUMBER: US 08/884,029
;             FILING DATE: 27-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 02558B-059100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "t at positions 13-18 may be
;             present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-125-295-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15

RESULT 181
US-09-803-263-6/c
; Sequence 6, Application US/09803263
; Patent No. 6706476
; GENERAL INFORMATION:
;  APPLICANT: Thirstrup, Kenneth
;  TITLE OF INVENTION: A Process for Amplifying and Labeling Single Stranded cDNA by 5'
;  TITLE OF INVENTION:  Adapter Mediated Amplification
;  FILE REFERENCE: 674513-2003.1
;  CURRENT APPLICATION NUMBER: US/09/803,263
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 19
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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Poly-a tail
US-09-803-263-6

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4

RESULT 182
US-09-803-263-7
; Sequence 7, Application US/09803263
; Patent No. 6706476
; GENERAL INFORMATION:
;  APPLICANT: Thirstrup, Kenneth
;  TITLE OF INVENTION: A Process for Amplifying and Labeling Single Stranded cDNA by 5'
;  TITLE OF INVENTION:  Adapter Mediated Amplification
;  FILE REFERENCE: 674513-2003.1
;  CURRENT APPLICATION NUMBER: US/09/803,263
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Complement of poly-a tail
US-09-803-263-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15

RESULT 183
US-09-994-311-7
; Sequence 7, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15

RESULT 184
US-09-142-108C-27
; Sequence 27, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/09/142,108C
;  CURRENT FILING DATE:  1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-142-108C-27

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15

RESULT 185
US-09-142-108C-28
; Sequence 28, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/09/142,108C
;  CURRENT FILING DATE:  1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-142-108C-28

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 186
US-09-809-545A-84
; Sequence 84, Application US/09809545A
; Patent No. 6800455
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  White, R. Tyler
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.017A
;  CURRENT APPLICATION NUMBER: US/09/809,545A
;  CURRENT FILING DATE:  2001-03-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-09-809-545A-84

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 187
US-10-352-704-12
; Sequence 12, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-352-704-12

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 188
US-10-352-704-18/c
; Sequence 18, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
```

```
;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-352-704-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 189
US-09-904-744-1/c
; Sequence 1, Application US/09904744
; Patent No. 6828142
; GENERAL INFORMATION:
;  APPLICANT: Barbera-Guillem, Emilio
;  APPLICANT:  Nelson, M. Bud
;  APPLICANT:  Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  TITLE OF INVENTION:  dendrimers in a signal amplification system
;  FILE REFERENCE: B-73
;  CURRENT APPLICATION NUMBER: US/09/904,744
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/437076
;  PRIOR FILING DATE: 1999-11-09
;  PRIOR APPLICATION NUMBER: 60/107828
;  PRIOR FILING DATE: 1998-11-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthesized
US-09-904-744-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 190
PCT-US91-03680-74
; Sequence 74, Application PC/TUS9103680
;  GENERAL INFORMATION:
;    APPLICANT:  Matteucci, Mark D.
;    APPLICANT:  Krawczyk, Steven
;    TITLE OF INVENTION:  SEQUENCE-SPECIFIC NONPHOTOACTIVATED
;    TITLE OF INVENTION:  CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
;    TITLE OF INVENTION:  DUPLEX DNA
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/03680
;      FILING DATE:  19910524
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  4610-0011.40
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  5
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  18
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N4,N4-ethanocytosine"
PCT-US91-03680-74

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTT 2140
              ||||:|||| |||||||
Db          1 TTTTMTTTTTTTTTTTT 17


RESULT 191
PCT-US94-05407-4
; Sequence 4, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-4

  Query Match              0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   0.0%;  Pred. No. 1.3e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 192
US-08-384-324-4
; Sequence 4, Application US/08384324
; Patent No. 5844110
;  GENERAL INFORMATION:
;    APPLICANT:  Gold, Barry I.
;    TITLE OF INVENTION:  Synthetic Triple Helix-Forming Compounds
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dann, Dorfman, Herrell and Skillman
;      STREET:  1601 Market Street, Suite 720
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/384,324
;      FILING DATE:  31-JAN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Janet E.
;      REGISTRATION NUMBER:  36,252
;      REFERENCE/DOCKET NUMBER:  63076
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-4100
;      TELEFAX:  (215) 563-4044
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-384-324-4

  Query Match              0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTTT 2144
              |||||  ||||||||||||
Db          1 TCTTTCTTTTTTTTCTTT 18


RESULT 193
US-08-885-126-12
; Sequence 12, Application US/08885126A
; Patent No. 5955597
; GENERAL INFORMATION:
;  APPLICANT: Arnold, Lyle J.
;  APPLICANT: Riley, Timothy A.
;  APPLICANT: Reynolds, Mark A.
;  APPLICANT: Schwartz, David A.
;  TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE
;  TITLE OF INVENTION: OLIGOMERS
;  FILE REFERENCE: GENTA.020FW2
;  CURRENT APPLICATION NUMBER: US/08/885,126A
;  CURRENT FILING DATE: 1997-06-30
;  EARLIER APPLICATION NUMBER: 08/343,018
;  EARLIER FILING DATE: 1994-11-21
;  EARLIER APPLICATION NUMBER: 08/154,013
;  EARLIER FILING DATE: 1993-11-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;    LENGTH: 18
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Chemically synthesized oligomer
US-08-885-126-12

  Query Match              0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              |:|:|:|:| |:| |:|:
Db          1 CUCUCUCUCUCUCUCUCU 18


RESULT 194
US-08-944-483-13
; Sequence 13, Application US/08944483
; Patent No. 6232456
;  GENERAL INFORMATION:
;    APPLICANT:  COHEN, MAURICE
;    APPLICANT:  COLPITTS, TRACEY L.
;    APPLICANT:  FRIEDMAN, PAULA N.
;    APPLICANT:  GRANADOS, EDWARD N.
;    APPLICANT:  KLASS, MICHAEL R.
;    APPLICANT:  RUSSELL, JOHN C.
;    APPLICANT:  STEWART, KENT D.
;    APPLICANT:  STROUPE, STEVEN D.
;    TITLE OF INVENTION:  NOVEL SERINE PROTEASE REAGENTS
;    TITLE OF INVENTION:  AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
;    TITLE OF INVENTION:  OF THE PROSTATE
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,483
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Becker, Cheryl L.
;      REGISTRATION NUMBER:  35,441
;      REFERENCE/DOCKET NUMBER:  6183.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847/935-1729
;      TELEFAX:  847/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-944-483-13

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1960 TCAAGCCCCACCACATAG 1977
              |||||||||  | ||||||
Db          1 TCAAGCCCCGCTACATAG 18


RESULT 195
US-08-700-530-3/c
; Sequence 3, Application US/08700530
; Patent No. 6316186
; GENERAL INFORMATION:
;  APPLICANT: EKINS, Roger P
;  TITLE OF INVENTION: Binding assay using binding agents with tail groups
;  FILE REFERENCE: 0380-P01180US0
;  CURRENT APPLICATION NUMBER: US/08/700,530
;  CURRENT FILING DATE:  1996-10-23
;  PRIOR APPLICATION NUMBER: PCT/GB95/00521
;  PRIOR FILING DATE: 1995-03-10
;  PRIOR APPLICATION NUMBER: GB 9404709.9
;  PRIOR FILING DATE: 1994-03-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:
;    OTHER INFORMATION: Oligonucleotide
US-08-700-530-3

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTC 3199
              ||||||||  ||| |||||
Db         18 TCTCTCTCTCTCTCTCTC 1


RESULT 196
US-08-700-530-4
; Sequence 4, Application US/08700530
; Patent No. 6316186
; GENERAL INFORMATION:
;  APPLICANT: EKINS, Roger P
;  TITLE OF INVENTION: Binding assay using binding agents with tail groups
;  FILE REFERENCE: 0380-P01180US0
;  CURRENT APPLICATION NUMBER: US/08/700,530
;  CURRENT FILING DATE:  1996-10-23
;  PRIOR APPLICATION NUMBER: PCT/GB95/00521
;  PRIOR FILING DATE: 1995-03-10
;  PRIOR APPLICATION NUMBER: GB 9404709.9
;  PRIOR FILING DATE: 1994-03-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:
;    OTHER INFORMATION: Oligonucleotide
US-08-700-530-4

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              |||||||||  ||| ||||
Db          1 CTCTCTCTCTCTCTCTCT 18


RESULT 197
PCT-US96-01473-4
; Sequence 4, Application PC/TUS9601473
;  GENERAL INFORMATION:
;    APPLICANT:  University of Nebraska, Board of Regents
;    APPLICANT:  Gold, Barry I.
;    TITLE OF INVENTION:  Synthetic Triple Helix-Forming Compounds
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dann, Dorfman, Herrell and Skillman
;      STREET:  1601 Market Street    Suite 720
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-2307
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01473
;      FILING DATE:  29-JAN-1996
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/384,324
;      FILING DATE:  01-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Janet E.
;      REGISTRATION NUMBER:  36,252
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-4100
;      TELEFAX:  (215) 563-4044
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
PCT-US96-01473-4

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTTT 2144
              |||||  ||||||||||||
Db          1 TCTTTCTTTTTTTTCTTT 18


RESULT 198
US-08-087-387-6
; Sequence 6, Application US/08087387
; Patent No. 5473060
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Oligonucleotide clamps having diagnostic andtherapeutic applic
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics
;      STREET:  465 Lincoln Centre Drive
;      CITY:  Foster City
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/087,387
;      FILING DATE:  19930702
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
;      TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-087-387-6

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTTT 16


RESULT 199
US-08-455-627-6
; Sequence 6, Application US/08455627
; Patent No. 5571677
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Convergent Synthesis of Branched and Multiply
;    TITLE OF INVENTION:  Connected Macromolecular Structures
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward LLP
;      STREET:  Five Palo Alto Square, 3000 El Camino Real
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,627
;      FILING DATE:  31-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Jackie N.
;      REGISTRATION NUMBER:  35,966
;      REFERENCE/DOCKET NUMBER:  LYNX-003/01 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5000
;      TELEFAX:  415-857-0663
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-455-627-6

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTTT 16


RESULT 200
US-07-971-978-2
; Sequence 2, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
```

```
;      LOCATION:  6
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  6-aza-thymidine substitution
US-07-971-978-2

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATAT 2409
              ||||||||| ||||||
Db          1 ATATATATATATATAT 16


RESULT 201
US-07-971-978-2/c
; Sequence 2, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  6-aza-thymidine substitution
US-07-971-978-2

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATAT 2409
              ||||||||| ||||||
Db         16 ATATATATATATATAT 1


RESULT 202
US-08-461-271-6
; Sequence 6, Application US/08461271
; Patent No. 5741643
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Oligonucleotide clamps having diagnostic
;    TITLE OF INVENTION:  and therapeutic applications
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics
;      STREET:  465 Lincoln Centre Drive
;      CITY:  Foster City
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,271
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/087,387
;      FILING DATE:  2-Jul-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
```

```
;       TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-461-271-6

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTTT 16


RESULT 203
US-08-713-685A-6
; Sequence 6, Application US/08713685A
; Patent No. 5817795
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Oligonucleotide clamps having diagnostic
;    TITLE OF INVENTION:  and therapeutic applications
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics
;      STREET:  465 Lincoln Centre Drive
;      CITY:  Foster City
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/713,685A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/461,271
;      FILING DATE:
;      APPLICATION NUMBER:  08/087,387
;      FILING DATE:  2-Jul-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
;      TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-713-685A-6

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTTT 16


RESULT 204
US-08-689-856-6
; Sequence 6, Application US/08689856
; Patent No. 5830658
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Convergent Synthesis of Branched and Multiply
;    TITLE OF INVENTION:  Connected Macromolecular Structures
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward LLP
;      STREET:  Five Palo Alto Square, 3000 El Camino Real
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/689,856
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,627
;      FILING DATE:  31-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Jackie N.
;      REGISTRATION NUMBER:  35,966
;      REFERENCE/DOCKET NUMBER:  LYNX-003/01 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5000
;      TELEFAX:  415-857-0663
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-689-856-6

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTTT 16


RESULT 205
US-09-070-477-6
; Sequence 6, Application US/09070477
; Patent No. 6048974
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Oligonucleotide clamps having diagnostic
;    TITLE OF INVENTION:  and therapeutic applications
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics
;      STREET:  465 Lincoln Centre Drive
;      CITY:  Foster City
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/070,477
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/713,685
;      FILING DATE:
;      APPLICATION NUMBER:  08/461,271
;      FILING DATE:
;      APPLICATION NUMBER:  08/087,387
;      FILING DATE:  2-Jul-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
;      TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-070-477-6

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTT 4514
              | ||||||||||||||
Db          1 ACTTTTTTTTTTTTT 16


RESULT 206
US-08-882-649A-8
; Sequence 8, Application US/08882649A
; Patent No. 6344316
;   GENERAL INFORMATION:
;        APPLICANT: Lockhart, David J.
;                   Chee, Mark
;                   Gunderson, Kevin
;                   Chaoqiang, Lai
;                   Wodicka, Lisa
;                   Cronin, Maureen T.
;                   Lee, Danny
;                   Tran, Huu M.
;                   Matsuzaki, Hajime
;                   McGall, Glenn H.
;        TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Joe Liebeschuetz
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/882,649A
;             FILING DATE: 25-Jun-1997
;             CLASSIFICATION: 435-006.000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/010,471
;             FILING DATE: 23-JAN-1996
;             APPLICATION NUMBER: US 60/035,170
;             FILING DATE: 09-JAN-1997
;             APPLICATION NUMBER: PCT/US97/01603
;             FILING DATE: 22-JAN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-019410US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: YES
;                        (ix)  Features:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-882-649A-8

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              | |||||||||||||||
Db          1 GVTTTTTTTTTTTTT 16


RESULT 207
US-09-371-772B-5823/c
; Sequence 5823, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5823
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-5823

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3653 TAGCTCAGTCATCAAA 3668
              |||||||||||||| |
Db         16 TAGCTCAGTCATCAGA 1


RESULT 208
US-08-373-124A-1060
; Sequence 1060, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
```

```
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1060:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-1060

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              :|:| |:|:|:|||::
Db          2 UAUAUAUAUAUACAUU 17


RESULT 209
US-08-373-124A-2149/c
; Sequence 2149, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2149:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-2149

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3964 ATATAAACAATAAAAA 3979
              ||||||| ||||||||
Db         17 ATATAAAAAATAAAAA 2


RESULT 210
US-08-373-124A-2155/c
; Sequence 2155, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
```

```
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2155:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-2155

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAA 3977
                ||||||||| ||||||
Db         16 ATATATAAAAAATAAA 1


RESULT 211
US-08-435-628-1060
; Sequence 1060, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1060:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-1060

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+02;
  Matches    8;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
                :|:| |:|:|:|||::
Db          2 UAUAUAUAUAUACAUU 17


RESULT 212
US-08-435-628-2149/c
; Sequence 2149, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
```

```
;       APPLICATION NUMBER:  07/936,422
;       FILING DATE:  August 26, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  209/035
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  2149:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  17 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-435-628-2149

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3964 ATATAAACAATAAAAA 3979
              ||||||| ||||||||
Db         17 ATATAAAAAATAAAAA 2


RESULT 213
US-08-435-628-2155/c
; Sequence 2155, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2155:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-2155

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3962 ATATATAAACAATAAA 3977
              ||||||||| ||||||
Db         16 ATATATAAAAAATAAA 1


RESULT 214
US-08-584-040-2548
; Sequence 2548, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2548:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2548
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```
  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   6.2%;  Pred. No. 1.8e+02;
  Matches    1;  Conservative   14;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ::::::::::::::
Db          2 ACUUUUUUUUUUUUUU 17


RESULT 215
US-08-584-040-2553/c
; Sequence 2553, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2553:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2553

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         17 TGGAAAAAAAAAAAAA 2


RESULT 216
US-08-584-040-2554/c
; Sequence 2554, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2554:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2554

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         16 TGGAAAAAAAAAAAAA 1


RESULT 217
US-08-584-040-5915/c
; Sequence 5915, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5915:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-5915

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCA 3486
              ||||| ||||||||||
Db         17 GTCAGCGTGAACTGCA 2


RESULT 218
US-09-371-772B-1072
; Sequence 1072, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1072
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1072

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   6.2%;  Pred. No. 1.8e+02;
  Matches    1;  Conservative   14;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ::::::::::::::
Db          2 ACUUUUUUUUUUUUUU 17


RESULT 219
US-09-371-772B-1077/c
; Sequence 1077, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1077
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1077

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         17 TGGAAAAAAAAAAAAA 2


RESULT 220
US-09-371-772B-1078/c
; Sequence 1078, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1078

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
```

Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3602 TGGAAAAAAACAAAAA 3617
              ||||||||||  |||||
Db         16 TGGAAAAAAAAAAAAA 1
```

RESULT 221
US-09-371-772B-2754/c
; Sequence 2754, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2754

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3471 GTCAGGGTGAACTGCA 3486
              |||||  ||||||||||
Db         17 GTCAGCGTGAACTGCA 2
```

RESULT 222
US-09-371-772B-4739/c
; Sequence 4739, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4739

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3651 TGTAGCTCAGTCATCA 3666
              | ||||||||||||||
Db         17 TTTAGCTCAGTCATCA 2
```

RESULT 223
US-09-827-998-744
; Sequence 744, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 744
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-744

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3057 GCTAGCTGCCACTTTC 3072
              ||||||||||  |||||
Db          2 GCTAGCTGCCTCTTTC 17
```

RESULT 224
US-09-827-998-745
; Sequence 745, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 745
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-745

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3057 GCTAGCTGCCACTTTC 3072
              ||||||||||  |||||
Db          1 GCTAGCTGCCTCTTTC 16
```

```
RESULT 225
US-09-685-664B-1072
; Sequence 1072, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1072
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1072

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   6.2%;  Pred. No. 1.8e+02;
  Matches    1;  Conservative   14;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              | ::::::::::::::
Db          2 ACUUUUUUUUUUUUUU 17


RESULT 226
US-09-685-664B-1077/c
; Sequence 1077, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1077
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1077

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         17 TGGAAAAAAAAAAAA 2


RESULT 227
US-09-685-664B-1078/c
; Sequence 1078, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1078

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         16 TGGAAAAAAAAAAAA 1


RESULT 228
US-09-685-664B-2754/c
; Sequence 2754, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2754
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-09-685-664B-2754

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3471 GTCAGGGTGAACTGCA 3486
              ||||| ||||||||||
Db         17 GTCAGCGTGAACTGCA 2


RESULT 229
US-09-475-947A-104
; Sequence 104, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: human
US-09-475-947A-104

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              |||||||| |||||||
Db          2 TATATATATATATATA 17


RESULT 230
US-08-330-000-1
; Sequence 1, Application US/08330000
; Patent No. 5686242
;  GENERAL INFORMATION:
;    APPLICANT:  Bruice, Thomas W.
;    APPLICANT:  Lima, Walter F.
;    TITLE OF INVENTION:  DETERMINATION OF OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  FOR THERAPEUTICS, DIAGNOSTICS   AND RESEARCH REAGENTS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5686242ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,000
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  755,485
;      FILING DATE:  September 5, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07489
;      FILING DATE:  September 4, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ralph, Rebecca Lynne
;      REGISTRATION NUMBER:  35,152
;      REFERENCE/DOCKET NUMBER:  ISIS-1723
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-330-000-1

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4513
              | ||||||||||||||
Db          3 ATGTTTTTTTTTTTT 18


RESULT 231
US-08-965-908-1
; Sequence 1, Application US/08965908
; Patent No. 6022691
;  GENERAL INFORMATION:
;    APPLICANT:  Bruice, Thomas W.
;    APPLICANT:  Lima, Walter F.
;    TITLE OF INVENTION:  DETERMINATION OF OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  FOR THERAPEUTICS, DIAGNOSTICS   AND RESEARCH REAGENTS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 6022691ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,908
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330,000
;      FILING DATE:
;      APPLICATION NUMBER:  755,485
;      FILING DATE:  September 5, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07489
;      FILING DATE:  September 4, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ralph, Rebecca Lynne
;      REGISTRATION NUMBER:  35,152
;      REFERENCE/DOCKET NUMBER:  ISIS-1723
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-965-908-1

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4513
              | ||||||||||||||
Db          3 ATGTTTTTTTTTTTTT 18


RESULT 232
US-09-256-492-14
; Sequence 14, Application US/09256492
; Patent No. 6040178
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD5 EXPRESSION
;  FILE REFERENCE: RTS-0057
;  CURRENT APPLICATION NUMBER: US/09/256,492
;  CURRENT FILING DATE: 1999-02-23
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 14
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-492-14

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1825 TTTGACACAAAGCTTC 1840
              |||||||||||  ||||
Db          1 TTTGACACAAATCTTC 16


RESULT 233
US-09-143-212-64/c
; Sequence 64, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia and Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
;  FILE REFERENCE: RTS-0005
;  CURRENT APPLICATION NUMBER: US/09/143,212B
;  CURRENT FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-64

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1348 ACCAGCCAGGCAGAGG 1363
              ||||||| ||||||||
Db         17 ACCAGCCTGGCAGAGG 2


RESULT 234
US-09-012-097A-58/c
; Sequence 58, Application US/09012097A
; Patent No. 6187757
;  GENERAL INFORMATION:
;    APPLICANT:  Clackson, Timothy
;    APPLICANT:  Gilman, Michael
;    APPLICANT:  Holt, Dennis
;    APPLICANT:  Keenan, Terence
;    APPLICANT:  Rozamus, Leonard
;    APPLICANT:  Yang, Wu
;    TITLE OF INVENTION:  Regulation of Biological Events Using
;    TITLE OF INVENTION:  No. 6187757el Compounds
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARIAD Pharmaceuticals, Inc.
;      STREET:  26 Landsdowne Street
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02139
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/012,097A
;      FILING DATE:  22-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berstein Esq., David L.
;      REGISTRATION NUMBER:  31,235
;      REFERENCE/DOCKET NUMBER:  374 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-494-0400
;      TELEFAX:  617-494-0208
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "SYNTHETIC OLIGONUCLEOTIDE"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-09-012-097A-58

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              |||||||||||  ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 235
US-08-584-040-3020/c
; Sequence 3020, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  3020:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-3020

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGC 3670
                ||||||||||| |||
Db         18 GCTCAGTCATCAGAGC 3


RESULT 236
US-09-725-265-15
; Sequence 15, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
                ||||  ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 237
US-09-725-265-19
; Sequence 19, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-19

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
                ||||  ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 238
US-09-481-620A-91/c
; Sequence 91, Application US/09481620A
; Patent No. 6506379
; GENERAL INFORMATION:
;  APPLICANT: ARIAD Gene Therapeutics, Inc.
;  TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
;  FILE REFERENCE: 345B PCT
;  CURRENT APPLICATION NUMBER: US/09/481,620A
;  CURRENT FILING DATE:  2000-01-12
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligo sequence
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(18)
US-09-481-620A-91

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       1313 TGAGTTTGGGGTCCCT 1328
              ||||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2
```

```
RESULT 239
US-09-422-978-4138
; Sequence 4138, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4138
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-13525 for SEQ 204,
US-09-422-978-4138

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3998 ATTGTAATCGTGTGCC 4013
              ||||||||||| ||||
Db          2 ATTGTAATCGTATGCC 17
```

```
RESULT 240
US-09-853-533A-17/c
; Sequence 17, Application US/09853533A
; Patent No. 6541448
; GENERAL INFORMATION:
;  APPLICANT: Monsanto Company
;  APPLICANT:  Isaac, Barbara
;  APPLICANT:  Krieger, Elysia
;  APPLICANT:  Mettus, Anne-Marie
;  APPLICANT:  Moshiri, Farhad
;  APPLICANT:  Sivasupramaniam, Sakuntala
;  TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO ANTHONOMUS INSECTS, AND METHODS
;  FILE REFERENCE: 38-21(51932)B
;  CURRENT APPLICATION NUMBER: US/09/853,533A
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 60/204,367
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: synthetic
;   FEATURE:
;   NAME/KEY: synthetic oligonucleotide
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: completely synthesized
US-09-853-533A-17

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              ||||||||||||| |||
Db         17 TATTTCTAATTCAACA 2
```

```
RESULT 241
US-09-853-533A-18
; Sequence 18, Application US/09853533A
; Patent No. 6541448
; GENERAL INFORMATION:
;  APPLICANT: Monsanto Company
;  APPLICANT:  Isaac, Barbara
;  APPLICANT:  Krieger, Elysia
;  APPLICANT:  Mettus, Anne-Marie
;  APPLICANT:  Moshiri, Farhad
;  APPLICANT:  Sivasupramaniam, Sakuntala
;  TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO ANTHONOMUS INSECTS, AND METHODS
;  FILE REFERENCE: 38-21(51932)B
;  CURRENT APPLICATION NUMBER: US/09/853,533A
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 60/204,367
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: synthetic
;   FEATURE:
;   NAME/KEY: synthetic oligonucleotide
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: completely synthesized
US-09-853-533A-18

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              ||||||||||||| |||
Db          2 TATTTCTAATTCAACA 17
```

```
RESULT 242
US-09-371-772B-1448/c
; Sequence 1448, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1448
```

```
  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGC 3670
              ||||||||||||  |||
Db         18 GCTCAGTCATCAGAGC 3


RESULT 243
US-09-781-804-58/c
; Sequence 58, Application US/09781804
; Patent No. 6649595
; GENERAL INFORMATION:
;  APPLICANT: ARIAD Gene Therapeutics, Inc.
;  TITLE OF INVENTION: Regulation of Biological Events Using No. 6649595el Compounds
;  FILE REFERENCE: 374 USD1
;  CURRENT APPLICATION NUMBER: US/09/781,804
;  CURRENT FILING DATE:  2001-08-31
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: oligonucleotide
US-09-781-804-58

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              ||||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 244
US-09-747-391-19/c
; Sequence 19, Application US/09747391
; Patent No. 6670124
; GENERAL INFORMATION:
;  APPLICANT: Chow, Robert
;  APPLICANT:  Tonai, Richard
;  APPLICANT:  StemCyte, Inc.
;  TITLE OF INVENTION: High Throughput Methods of HLA Typing
;  FILE REFERENCE: 020035-000210US
;  CURRENT APPLICATION NUMBER: US/09/747,391
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/172,768
;  PRIOR FILING DATE: 1999-12-20
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-747-391-19

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3492 TTGGCTGAGACCTGGG 3507
              |||||||  ||||||||
Db         18 TTGGCTGCGACCTGGG 3


RESULT 245
US-09-556-127-15
; Sequence 15, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-15

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              ||||  ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 246
US-09-556-127-19
; Sequence 19, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-19

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
```

```
                    |||| ||||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 247
US-09-685-664B-1448/c
; Sequence 1448, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1448

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGC 3670
              |||||||||||||  |||
Db         18 GCTCAGTCATCAGAGC 3


RESULT 248
US-08-882-649A-7/c
; Sequence 7, Application US/08882649A
; Patent No. 6344316
;   GENERAL INFORMATION:
;        APPLICANT: Lockhart, David J.
;                   Chee, Mark
;                   Gunderson, Kevin
;                   Chaoqiang, Lai
;                   Wodicka, Lisa
;                   Cronin, Maureen T.
;                   Lee, Danny
;                   Tran, Huu M.
;                   Matsuzaki, Hajime
;                   McGall, Glenn H.
;        TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Joe Liebeschuetz
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/882,649A
;             FILING DATE: 25-Jun-1997
;             CLASSIFICATION: 435-006.000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/010,471
;             FILING DATE: 23-JAN-1996
;             APPLICATION NUMBER: US 60/035,170
;             FILING DATE: 09-JAN-1997
;             APPLICATION NUMBER: PCT/US97/01603
;             FILING DATE: 22-JAN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-019410US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: YES
;                   (ix)  Features:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-882-649A-7

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.8e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              |||||||||||||:|
Db         15 TTTTTTTTTTTTTBG 1


RESULT 249
US-09-725-265-31
; Sequence 31, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-31

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 250
US-09-556-127-31
; Sequence 31, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-31

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.2e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 251
US-08-173-489C-75/c
; Sequence 75, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  double stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;      DESCRIPTION:  esterase D gene (Accession # M13450)
;      DESCRIPTION:  nucleotides 962 to 975
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  chromosome 13
;      MAP POSITION:  13q14.1-q14.2
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lee, E Y H P,  Lee, W H.
;      TITLE:  Molecular cloning of the
;      TITLE:  human esterase D gene, a genetic marker of
;      TITLE:  retinoblastoma
;      JOURNAL:  Proceedings of the National Academy of
;      JOURNAL:  Sciences, USA
;      VOLUME:  83
;      PAGES:  6337-6341
;      DATE:  1986
;      RELEVANT RESIDUES IN SEQ ID NO:  75 :FROM 1 TO 14
US-08-173-489C-75

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 252
US-08-173-489C-76
; Sequence 76, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
```

```
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 bases
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  third strand derived from esterase D
;      DESCRIPTION:  sequence region in Seq ID No. 586124475
;    HYPOTHETICAL:  Yes
;    ANTI-SENSE:  No
;    PUBLICATION INFORMATION:
;      RELEVANT RESIDUES IN SEQ ID NO:  76 :FROM 1 TO 14
US-08-173-489C-76

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 253
US-08-832-021-15
; Sequence 15, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-15

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 254
US-08-724-466B-12
; Sequence 12, Application US/08724466B
; Patent No. 6063606
;  GENERAL INFORMATION:
;    APPLICANT:  Petkovich, P. Martin, White, Jay A.,
;    APPLICANT:  Beckett, Barbara R., Jones, Glenville
;    TITLE OF INVENTION:  Retinoid Metabolizing Protein
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Blake, Cassels & Graydon
;      STREET:  Box 25, Commerce Court West
;      CITY:  Toronto
;      ZIP:  M5L 1A9
;      COUNTRY:  Canada
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 inch, 1.4 Mb storage
;      COMPUTER:  COMPAQ, IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS 5.1
;      SOFTWARE:  WORD PERFECT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,466B
;      FILING DATE:  October 1, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/667,546
;      FILING DATE:  June 21, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunt, John C.
;      REGISTRATION NUMBER:  36,424
;      REFERENCE/DOCKET NUMBER:  50767/00004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 863-4344
;      TELEFAX:  (416) 863-2653
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-724-466B-12

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 255
US-08-882-164D-12
; Sequence 12, Application US/08882164D
; Patent No. 6306624
;  GENERAL INFORMATION:
;    APPLICANT:  Petkovich, P. Martin, White, Jay A.,
;    APPLICANT:  Beckett, Barbara R., Jones, Glenville
;    TITLE OF INVENTION:  Retinoid Metabolizing Protein
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Blake, Cassels & Graydon
;      STREET:  Box 25, Commerce Court West
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5L 1A9
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 inch, 1.4 Mb storage
;      COMPUTER:  COMPAQ, IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS 5.1
;      SOFTWARE:  WORD PERFECT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/882,164D
;      FILING DATE:  June 25, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/667,546
;      FILING DATE:  June 21, 1996
;      APPLICATION NUMBER:  08/724,466
;      FILING DATE:  October 1, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunt, John C.
```

```
;      REGISTRATION NUMBER:  36,424
;      REFERENCE/DOCKET NUMBER:  50767/00010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 863-4344
;      TELEFAX:  (416) 863-2653
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-882-164D-12

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 256
US-09-462-569B-1
; Sequence 1, Application US/09462569B
; Patent No. 6392124
; GENERAL INFORMATION:
;  APPLICANT: PONZ ASCASO, Fernando
;  APPLICANT:  TORRES PASCUAL, Vicente
;  APPLICANT:  SANCHEZ SANCHEZ, Florentina
;  APPLICANT:  MARTINEZ HERRERA, David
;  TITLE OF INVENTION: INFECTIOUS VECTORS AND CLONES OF PLANTS DERIVED FROM
;  TITLE OF INVENTION:  THE TURNIP MOSAIC VIRUS (TuMV)
;  FILE REFERENCE: P/613-110
;  CURRENT APPLICATION NUMBER: US/09/462,569B
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER: PCT/ES98/00200
;  PRIOR FILING DATE: 1998-07-09
;  PRIOR APPLICATION NUMBER: ES P 9701522
;  PRIOR FILING DATE: 1997-07-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: construct
US-09-462-569B-1

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 257
US-09-619-103-20/c
; Sequence 20, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-20

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 258
US-10-103-614A-1
; Sequence 1, Application US/10103614A
; Patent No. 6716585
; GENERAL INFORMATION:
;  APPLICANT: SALMAN AL-MAHMOOD
;  TITLE OF INVENTION: METHOD FOR IDENTIFYING NOVEL GENES INVOLVED IN THE
;  TITLE OF INVENTION:  REGULATION OF ANGIOGENESIS, STUDY OF SAID GENES AND USE
;  TITLE OF INVENTION:  THEREOF FOR THERAPEUTIC PURPOSES
;  FILE REFERENCE: 1071-02
;  CURRENT APPLICATION NUMBER: US/10/103,614A
;  CURRENT FILING DATE:  2002-08-22
;  PRIOR APPLICATION NUMBER: PCT/FR00/02607
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: FR 99/11790
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-103-614A-1

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 259
US-09-152-059-65
; Sequence 65, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
```

```
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-65

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 260
US-09-152-059-66
; Sequence 66, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-66

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 261
US-09-152-059-67
; Sequence 67, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-67

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 262
US-09-152-059-68
; Sequence 68, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
```

```
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (11)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-68

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 263
US-09-152-059-80
; Sequence 80, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-80

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 264
US-09-152-059-81/c
; Sequence 81, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-81

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 265
US-09-152-059-82/c
; Sequence 82, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
```

```
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-82

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 266
US-09-152-059-83
; Sequence 83, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-83

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 267
US-09-152-059-84/c
; Sequence 84, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-84

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 268
US-09-152-059-85/c
; Sequence 85, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 85
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-85

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 269
US-09-152-059-86
; Sequence 86, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-86

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 270
US-09-152-059-87/c
; Sequence 87, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-87

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 271
US-09-152-059-88/c
; Sequence 88, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-88
```

```
  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 272
US-09-152-059-89
; Sequence 89, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-89

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 273
US-09-152-059-90/c
; Sequence 90, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-90

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 274
US-09-152-059-91/c
; Sequence 91, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-91

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1
```

```
RESULT 275
US-09-152-059-92
; Sequence 92, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (11)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-92

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 276
US-09-152-059-93/c
; Sequence 93, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-93

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 277
US-09-152-059-94/c
; Sequence 94, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-94

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
```

```
Db         14 TTTTTTTTTTTTTT 1


RESULT 278
US-09-152-059-96/c
; Sequence 96, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-96

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
             ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 279
US-09-152-059-97/c
; Sequence 97, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-97

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
             ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 280
US-09-152-059-98
; Sequence 98, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-98

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
             ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 281
US-09-152-059-99/c
; Sequence 99, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
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;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-99

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 282
US-09-152-059-100/c
; Sequence 100, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-100

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 283
US-09-152-059-101
; Sequence 101, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-101

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 284
US-09-152-059-102/c
; Sequence 102, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
```

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;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-102

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 285
US-09-152-059-103/c
; Sequence 103, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-103

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 286
US-09-152-059-104
; Sequence 104, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: modified_base
;    LOCATION: (7)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (9)
;    OTHER INFORMATION: LNA monomer
;    OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-104

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 287
US-09-152-059-105/c
; Sequence 105, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
```

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;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-105

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 288
US-09-152-059-106/c
; Sequence 106, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-106

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 289
US-09-152-059-107
; Sequence 107, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-107

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 290
US-09-152-059-108/c
; Sequence 108, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-108

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 291
US-09-152-059-109/c
; Sequence 109, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-109

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 292
US-09-152-059-110
; Sequence 110, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: modified_base
;    LOCATION: (5)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (7)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (9)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (11)
;    OTHER INFORMATION: LNA monomer
;    OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-110

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 293
US-09-152-059-111/c
; Sequence 111, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
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;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-111

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 294
US-09-152-059-112/c
; Sequence 112, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-112

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 295
US-09-152-059-113
; Sequence 113, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(13)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-113

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 296
US-09-152-059-114/c
; Sequence 114, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-114

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 297
US-09-152-059-115/c
; Sequence 115, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-115

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 298
US-09-152-059-117
; Sequence 117, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-117

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 299
US-09-152-059-118/c
; Sequence 118, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-118

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
```

```
                ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 300
US-09-152-059-119/c
; Sequence 119, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-119

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
                ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 301
US-09-152-059-120
; Sequence 120, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-120

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
                ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 302
US-09-152-059-121/c
; Sequence 121, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-121

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
                ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 303
US-09-152-059-122/c
; Sequence 122, Application US/09152059
; Patent No. 6794499
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; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-122

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 304
US-09-152-059-123
; Sequence 123, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-123

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 305
US-09-152-059-124/c
; Sequence 124, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-124

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 306
US-09-152-059-125/c
; Sequence 125, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
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;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-125

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 307
US-09-152-059-126
; Sequence 126, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-126

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 308
US-09-152-059-127/c
; Sequence 127, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-127

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 309
US-09-152-059-128/c
; Sequence 128, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
```

```
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-128

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 310
US-09-152-059-129
; Sequence 129, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-129

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         1 TTTTTTTTTTTTTT 14


RESULT 311
US-09-152-059-130/c
; Sequence 130, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-130

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 312
US-09-152-059-131/c
; Sequence 131, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
```

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;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-131

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 313
US-09-152-059-132
; Sequence 132, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-132

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 314
US-09-152-059-133/c
; Sequence 133, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-133

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 315
US-09-152-059-134/c
; Sequence 134, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-134

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 316
US-09-152-059-135
; Sequence 135, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-135

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 317
US-09-152-059-136/c
; Sequence 136, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-136

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 318
US-09-152-059-137/c
; Sequence 137, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-137

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
```

```
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 319
US-09-152-059-138
; Sequence 138, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-138

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 320
US-09-152-059-139/c
; Sequence 139, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-139

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 321
US-09-152-059-140/c
; Sequence 140, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-140

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 322
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US-09-152-059-141
; Sequence 141, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (11)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-141

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 323
US-09-152-059-142/c
; Sequence 142, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-142

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 324
US-09-152-059-143/c
; Sequence 143, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-143

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1
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```
RESULT 325
US-09-152-059-144
; Sequence 144, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(13)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-144

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 326
US-09-152-059-145/c
; Sequence 145, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-145

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 327
US-09-152-059-146/c
; Sequence 146, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-146

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 328
US-09-859-736-7
; Sequence 7, Application US/09859736
; Patent No. 6838244
; GENERAL INFORMATION:
;  APPLICANT: LI, WAN-LIANG ROBERT
;  APPLICANT:  ZHOU, JIAN S.
;  TITLE OF INVENTION: FLUORESCENT OLIGONUCLEOTIDES AND USES THEREOF
```

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;  FILE REFERENCE: 16517.248
;  CURRENT APPLICATION NUMBER: US/09/859,736
;  CURRENT FILING DATE:  2001-05-18
;  PRIOR APPLICATION NUMBER: 60/205,452
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: dT oligonucleotide
US-09-859-736-7

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 329
5453496-4
;Patent No. 5453496
;    APPLICANT: CARUTHERS, MARVIN H.;MARSHALL, WILLIAM S.;BRILL,
;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
;SEQ ID NO:4:
;      LENGTH: 14
5453496-4

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 330
5453496-4
;Patent No. 5453496
;    APPLICANT: CARUTHERS, MARVIN H.;MARSHALL, WILLIAM S.;BRILL,
;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
;SEQ ID NO:4:
;      LENGTH: 14
5453496-4

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 331
5453496-5/c
;Patent No. 5453496
;    APPLICANT: CARUTHERS, MARVIN H.;MARSHALL, WILLIAM S.;BRILL,
;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
;SEQ ID NO:5:
;      LENGTH: 14
5453496-5

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 332
5453496-5/c
;Patent No. 5453496
;    APPLICANT: CARUTHERS, MARVIN H.;MARSHALL, WILLIAM S.;BRILL,
;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
;SEQ ID NO:5:
;      LENGTH: 14
5453496-5

  Query Match             0.3%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 333
US-08-452-196A-3/c
; Sequence 3, Application US/08452196A
; Patent No. 5576427
;  GENERAL INFORMATION:
;    APPLICANT:  Cook, Philip D.
;    APPLICANT:  Delecki, Daniel J.
;    APPLICANT:  Guinosso, Charles
;    TITLE OF INVENTION:  ACYCLIC NUCLEOSIDE
;    TITLE OF INVENTION:  ANALOGS AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  SEQUENCES
;    TITLE OF INVENTION:  CONTAINING THEM
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Department
;      STREET:  9 Great Valley Parkway
;      CITY:  Malvern
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19355
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.4 MB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.0B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,196A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/040,326
;      FILING DATE:  30 March 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul E. Dupont
;      REGISTRATION NUMBER:  27,438
;      REFERENCE/DOCKET NUMBER:  2525
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215)889-6338
;      TELEFAX:  (215)889-8800
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Nucleic Acid
;      DESCRIPTION:
;    ANTI-SENSE:  yes
;    ORIGINAL SOURCE:  synthesized
;    FEATURE:
;      LOCATION:  14
;      OTHER INFORMATION:  8-[2,2-bis
;      OTHER INFORMATION:  (methoxymethyl)
;      OTHER INFORMATION:  propoxy]-9-
;      OTHER INFORMATION:  methyladenosine
US-08-452-196A-3

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              | ||||||||||||||
Db         15 TNTTTTTTTTTTTT 1


RESULT 334
US-08-452-196A-4/c
; Sequence 4, Application US/08452196A
; Patent No. 5576427
;  GENERAL INFORMATION:
;    APPLICANT:  Cook, Philip D.
;    APPLICANT:  Delecki, Daniel J.
;    APPLICANT:  Guinosso, Charles
;    TITLE OF INVENTION:  ACYCLIC NUCLEOSIDE
;    TITLE OF INVENTION:  ANALOGS AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  SEQUENCES
;    TITLE OF INVENTION:  CONTAINING THEM
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Department
;      STREET:  9 Great Valley Parkway
;      CITY:  Malvern
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19355
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.4 MB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.0B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,196A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/040,326
;      FILING DATE:  30 March 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul E. Dupont
;      REGISTRATION NUMBER:  27,438
;      REFERENCE/DOCKET NUMBER:  2525
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215)889-6338
;      TELEFAX:  (215)889-8800
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Nucleic Acid
;      DESCRIPTION:
;    ANTI-SENSE:  yes
;    ORIGINAL SOURCE:  synthesized
;    FEATURE:
;      LOCATION:  13
;      OTHER INFORMATION:  8-[2,2-bis
;      OTHER INFORMATION:  (methoxymethyl)
;      OTHER INFORMATION:  propoxy]-9-
;      OTHER INFORMATION:  methyladenosine
US-08-452-196A-4

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              || ||||||||||||
Db         15 TTNTTTTTTTTTTT 1


RESULT 335
US-08-292-620A-360
; Sequence 360, Application US/08292620A
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```
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  360:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-360

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 2e+02;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          2 UUUUUUUUUUUUUU 15


RESULT 336
US-08-292-620A-363
; Sequence 363, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  363:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-363

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 2e+02;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 14


RESULT 337
US-08-585-684B-639/c
; Sequence 639, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
```

```
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  639:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-639

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGA 1417
              ||||||||||||||
Db         14 GATGCTAAAGATGA 1


RESULT 338
US-08-585-684B-640/c
; Sequence 640, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  640:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-640

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGA 1417
              ||||||||||||||
Db         14 GATGCTAAAGATGA 1


RESULT 339
US-08-863-639A-7/c
; Sequence 7, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-7

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTG 4516
              ||||||||||||||
```

```
Db         15 TTTTTTTTTTTTTG 2


RESULT 340
US-08-832-021-49
; Sequence 49, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-49

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
             ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 341
US-08-832-021-50
; Sequence 50, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-50

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
             ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 342
US-08-832-021-52
; Sequence 52, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-52

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
             ||||||||||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 343
US-09-071-845-360
; Sequence 360, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
```

```
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  360:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-360

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 2e+02;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          2 UUUUUUUUUUUUUU 15


RESULT 344
US-09-071-845-363
; Sequence 363, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  363:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-363

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 2e+02;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 14


RESULT 345
US-09-038-073-639/c
; Sequence 639, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  639:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-639

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGA 1417
              ||||||||||||||
Db         14 GATGCTAAAGATGA 1


RESULT 346
```

```
US-09-038-073-640/c
; Sequence 640, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  640:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-640

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGA 1417
              ||||||||||||||
Db         14 GATGCTAAAGATGA 1


RESULT 347
US-09-475-947A-158
; Sequence 158, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: human
;    FEATURE:
;    OTHER INFORMATION: n signifies a, t, c or g.
US-09-475-947A-158

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||| |||
Db          1 TTTTTTTTTTTNTTT 15


RESULT 348
US-09-344-624-28
; Sequence 28, Application US/09344624
; Patent No. 6753154
; GENERAL INFORMATION:
;  APPLICANT: Chen, Huei-Mei
;  APPLICANT: Bissell, Mina
;  TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: 2960.44(HV)
;  CURRENT APPLICATION NUMBER: US/09/344,624
;  CURRENT FILING DATE: 1999-06-25
;  EARLIER APPLICATION NUMBER: 60/090,747
;  EARLIER FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-344-624-28

  Query Match             0.3%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTT 4511
              ||||||||||||||
Db          1 AAGTTTTTTTTTTT 14


RESULT 349
US-08-284-484A-4/c
; Sequence 4, Application US/08284484A
; Patent No. 5639873
;  GENERAL INFORMATION:
;    APPLICANT:  Barascut, et al.
;    TITLE OF INVENTION:  Oligothionucleotides
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and No. 5639873ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 720 Kb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,484A
;      FILING DATE:  04-AUG-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul K. Legaard
;
```

```
;      REGISTRATION NUMBER:  38,534
;      REFERENCE/DOCKET NUMBER:  MSWA-0001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-284-484A-4

  Query Match             0.3%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||||
Db         14 TTTTTTTTTTTTGG 1


RESULT 350
US-08-584-040-2553
; Sequence 2553, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2553:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2553

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 2.2e+02;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 14


RESULT 351
US-09-371-772B-1077
; Sequence 1077, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1077
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1077

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 2.2e+02;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 14


RESULT 352
US-09-685-664B-1077
; Sequence 1077, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1077
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
```

```
US-09-685-664B-1077

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 2.2e+02;
  Matches    0;  Conservative    14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4514
              :::::::::::::
Db          1 UUUUUUUUUUUUU 14


RESULT 353
US-09-434-131A-12/c
; Sequence 12, Application US/09434131A
; Patent No. 6344345
; GENERAL INFORMATION:
;  APPLICANT:  HAYASHIZAKI, Yoshihide
;  TITLE OF INVENTION:  METHOD FOR PRODUCING DOUBLE-STRANDED DNA WHOSE TERMINAL
;  TITLE OF INVENTION:  HOMOPOLYMER PART IS ELIMINATED AND METHOD FOR
;  TITLE OF INVENTION:  DETERMINING NUCLEOTIDE SEQUENCE
;  FILE REFERENCE:  024705-093
;  CURRENT APPLICATION NUMBER: US/09/434,131A
;  CURRENT FILING DATE:  1999-11-05
;  PRIOR APPLICATION NUMBER:  JP 316102/1998
;  PRIOR FILING DATE:  1998-11-06
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:hemimethylated
;   OTHER INFORMATION: cDNA
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(4)
;   OTHER INFORMATION: Nucleotides 2-4 are n wherein n = any nucleotide.
US-09-434-131A-12

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||   |
Db         17 GTTTTTTTTTTTTNNNG 1


RESULT 354
US-08-584-040-2552/c
; Sequence 2552, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2552:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2552

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 355
US-09-475-947A-118/c
; Sequence 118, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: human
US-09-475-947A-118

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 356
US-09-371-772B-1076/c
; Sequence 1076, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
```

```
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1076

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 357
US-09-685-664B-1076/c
; Sequence 1076, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1076

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 358
US-08-242-664-34/c
; Sequence 34, Application US/08242664
; Patent No. 5571937
;  GENERAL INFORMATION:
;    APPLICANT:  Watanabe, Kyoichi A.
;    APPLICANT:  Ren, Wu-Yun
;    APPLICANT:  Weil, Roger
;    TITLE OF INVENTION:  Complementary DNA and Toxins
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 1.44Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/242,664
;      FILING DATE:  May 12, 1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44683
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-977-9550
;      TELEFAX:  212-664-0525
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-242-664-34

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTT 2143
              ||||| ||||| |||||
Db         17 TCTTTGCTTTTCTTCTT 1


RESULT 359
US-08-233-130A-10/c
; Sequence 10, Application US/08233130A
; Patent No. 5587300
;  GENERAL INFORMATION:
;    APPLICANT:  Malter, James S.
;    TITLE OF INVENTION:  Method to Increase Regulatory Molecule
;    TITLE OF INVENTION:  Production
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  203 Textile Buildling, 119 No. 5587300th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,130A
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  119.00010101
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1220
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-233-130A-10

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACAT 2413
              || ||||||| ||||||
Db         17 TACATACATACATACAT 1


RESULT 360
US-08-233-130A-11
; Sequence 11, Application US/08233130A
; Patent No. 5587300
;  GENERAL INFORMATION:
;    APPLICANT:  Malter, James S.
;    TITLE OF INVENTION:  Method to Increase Regulatory Molecule
;    TITLE OF INVENTION:  Production
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  203 Textile Buildling, 119 No. 5587300th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,130A
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  119.00010101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1220
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-233-130A-11

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACAT 2413
              || ||||||| ||||||
Db          1 TACATACATACATACAT 17


RESULT 361
US-08-390-850-496
; Sequence 496, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
;   APPLICANT:  Draper, Kenneth G.
;   APPLICANT:  Pavco, Pamela
;   APPLICANT:  McSwiggen, James
;   APPLICANT:  Gustofson, John
;   APPLICANT:  Stinchcomb, Dan T.
;   TITLE OF INVENTION:  METHOD AND REAGENT FOR TREATMENT
;   TITLE OF INVENTION:  OF ARTHRITIC CONDITIONS
;   NUMBER OF SEQUENCES:  1151
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Lyon & Lyon
;     STREET:  633 West Fifth Street
;     STREET:  Suite 4700
;     CITY:  Los Angeles
;     STATE:  California
;     COUNTRY:  U.S.A.
;     ZIP:  90071
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;     MEDIUM TYPE:  storage
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  IBM P.C. DOS 5.0
;     SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/390,850
;     FILING DATE:  February 17, 1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/354,920
;     FILING DATE:  December 13, 1994
;     APPLICATION NUMBER:  08/152,487
;     FILING DATE:  No. 5612215ember 12, 1993
;     APPLICATION NUMBER:  07/989,848
;     FILING DATE:  December 7, 1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Warburg, Richard
;     REGISTRATION NUMBER:  32,327
;     REFERENCE/DOCKET NUMBER:  211/084
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (213) 489-1600
;     TELEFAX:  (213) 955-0440
;     TELEX:  67-3510
; INFORMATION FOR SEQ ID NO:  496:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  17 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US-08-390-850-496

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   47.1%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        899 TTGCTGCTGATGTGCTT 915
              ::||:||: |:| ||::
Db          1 UUGCUGCUCAUGAGCUU 17


RESULT 362
US-08-373-124A-172/c
; Sequence 172, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  172:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-172

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3387 AGTAGGAGGAAACAGTT 3403
              || |||||||||||| |
Db         17 AGGAGGAGGAAACAGGT 1


RESULT 363
US-08-373-124A-174/c
; Sequence 174, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  174:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-174

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACA 3400
              || || ||||||||||
Db         17 AGGAGGAGGAGGAAACA 1


RESULT 364
US-08-373-124A-1062/c
; Sequence 1062, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
```

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;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1062:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-1062

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATAT 2407
                ||||| |||||| ||||
Db         17 AAAATGTATATATATAT 1


RESULT 365
US-08-484-138-34/c
; Sequence 34, Application US/08484138
; Patent No. 5652350
;  GENERAL INFORMATION:
;    APPLICANT:  Watanabe, Kyoichi A.
;    APPLICANT:  Ren, Wu-Yun
;    APPLICANT:  Weil, Roger
;    TITLE OF INVENTION:  Complementary DNA and Toxins
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 1.44Mb
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,138
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44683-Z/JPW/MJG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-977-9550
;      TELEFAX:  212-664-0525
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-484-138-34

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTT 2143
                ||||| ||||| |||||
Db         17 TCTTTGCTTTTCTTCTT 1


RESULT 366
US-08-435-634-496
; Sequence 496, Application US/08435634
; Patent No. 5731295
;  GENERAL INFORMATION:
;    APPLICANT:  Draper, Kenneth G.
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Gustofson, John
;    APPLICANT:  Stinchcomb, Dan T.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR TREATMENT
;    TITLE OF INVENTION:  OF ARTHRITIC CONDITIONS
;    NUMBER OF SEQUENCES:  1151
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,634
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/390,850
;      FILING DATE:  February 17, 1995
;      APPLICATION NUMBER:  08/354,920
;      FILING DATE:  December 13, 1994
;      APPLICATION NUMBER:  08/152,487
;      FILING DATE:  No. 5731295ember 12, 1993
;      APPLICATION NUMBER:  07/989,848
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  211/084
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  496:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-634-496

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   47.1%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        899 TTGCTGCTGATGTGCTT 915
              ::||:||: |:| ||::
```

```
Db          1 UUGCUGCUCAUGAGCUU 17


RESULT 367
US-08-758-306-271
; Sequence 271, Application US/08758306
; Patent No. 5807743
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  McSwiggen, James A.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH
;    TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
;    TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
;    NUMBER OF SEQUENCES:  1379
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSeq Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/758,306
;      FILING DATE:  December 3, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  271:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-758-306-271

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   52.9%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2946 AGCCTCCTTTGTGTGTA 2962
              |||| |: :|:|:|:|
Db          1 AGCCUUCUCUGUGUGUA 17


RESULT 368
US-08-758-306-1015
; Sequence 1015, Application US/08758306
; Patent No. 5807743
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  McSwiggen, James A.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES
;    TITLE OF INVENTION:  ASSOCIATED WITH
;    TITLE OF INVENTION:  INTERLEUKIN-2 RECEPTOR
;    TITLE OF INVENTION:  GAMMA-CHAIN EXPRESSION
;    NUMBER OF SEQUENCES:  1379
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSeq Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/758,306
;      FILING DATE:  December 3, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1015:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-758-306-1015

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   64.7%;  Pred. No. 2.4e+02;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2102 AGTGGTCTCTGCTGGGG 2118
              ||  |:|:|:||:||||
Db          1 AGCUGUCUCUGCUGGGG 17


RESULT 369
US-08-435-628-172/c
; Sequence 172, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
```

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;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  172:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-172

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3387 AGTAGGAGGAAACAGTT 3403
              || |||||||||||| |
Db         17 AGGAGGAGGAAACAGGT 1


RESULT 370
US-08-435-628-174/c
; Sequence 174, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  174:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-174

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACA 3400
              || || ||||||||||||
Db         17 AGGAGGAGGAGGAAACA 1


RESULT 371
US-08-435-628-1062/c
; Sequence 1062, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
```

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;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1062:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-1062

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATAT 2407
              ||||| |||||| ||||
Db         17 AAAATGTATATATATAT 1


RESULT 372
US-08-173-489C-2
; Sequence 2, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  third strand derived from c-myc
;      DESCRIPTION:  sequence region in Seq ID No. 58612442
;    HYPOTHETICAL:  Yes
;    ANTI-SENSE:  No
;    PUBLICATION INFORMATION:
;      RELEVANT RESIDUES IN SEQ ID NO:  2 :FROM 1 TO 17
US-08-173-489C-2

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1509 TTTCTTCTCTTATCCTC 1525
              ||||||||| | |||||
Db          1 TTTCTTCTCCTCTCCTC 17


RESULT 373
US-08-849-021-3/c
; Sequence 3, Application US/08849021
; Patent No. 5955276
;  GENERAL INFORMATION:
;    APPLICANT:  MORGANTE, MICHELE
;    APPLICANT:  VOGEL, JULIE M.
;    TITLE OF INVENTION:  COMPOUND MICROSATELLITE
;    TITLE OF INVENTION:  PRIMERS FOR THE
;    TITLE OF INVENTION:  DETECTION OF GENETIC
;    TITLE OF INVENTION:  POLYMORPHISMS
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS AND
;      ADDRESSEE:  COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  U.S.A.
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PATENT IN RELEASE #1.0, VERSION 1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/849,021
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/346,456
;      FILING DATE:  28 NOVEMBER 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLOYD, LINDA AXAMETHY
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1064-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-892-8112
;      TELEFAX:  302-992-7949
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-849-021-3

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCT 3198
              ||||||| ||| ||||
Db         17 TCTCTCTCTCTCTCTCT 1
```

```
RESULT 374
US-08-849-021-4/c
; Sequence 4, Application US/08849021
; Patent No. 5955276
;  GENERAL INFORMATION:
;    APPLICANT:  MORGANTE, MICHELE
;    APPLICANT:  VOGEL, JULIE M.
;    TITLE OF INVENTION:  COMPOUND MICROSATELLITE
;    TITLE OF INVENTION:  PRIMERS FOR THE
;    TITLE OF INVENTION:  DETECTION OF GENETIC
;    TITLE OF INVENTION:  POLYMORPHISMS
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS AND
;      ADDRESSEE:  COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  U.S.A.
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PATENT IN RELEASE #1.0, VERSION 1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/849,021
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/346,456
;      FILING DATE:  28 NOVEMBER 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLOYD, LINDA AXAMETHY
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1064-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-892-8112
;      TELEFAX:  302-992-7949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-849-021-4

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3185 CTCTCCCTCCCTCTCTC 3201
              ||||| ||| |||||||
Db         17 CTCTCTCTCTCTCTCTC 1


RESULT 375
US-08-849-021-5
; Sequence 5, Application US/08849021
; Patent No. 5955276
;  GENERAL INFORMATION:
;    APPLICANT:  MORGANTE, MICHELE
;    APPLICANT:  VOGEL, JULIE M.
;    TITLE OF INVENTION:  COMPOUND MICROSATELLITE
;    TITLE OF INVENTION:  PRIMERS FOR THE
;    TITLE OF INVENTION:  DETECTION OF GENETIC
;    TITLE OF INVENTION:  POLYMORPHISMS
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS AND
;      ADDRESSEE:  COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  U.S.A.
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PATENT IN RELEASE #1.0, VERSION 1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/849,021
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/346,456
;      FILING DATE:  28 NOVEMBER 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLOYD, LINDA AXAMETHY
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1064-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-892-8112
;      TELEFAX:  302-992-7949
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-849-021-5

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCT 3198
              ||||||||| ||| ||||
Db          1 TCTCTCTCTCTCTCTCT 17


RESULT 376
US-08-849-021-6
; Sequence 6, Application US/08849021
; Patent No. 5955276
;  GENERAL INFORMATION:
;    APPLICANT:  MORGANTE, MICHELE
;    APPLICANT:  VOGEL, JULIE M.
;    TITLE OF INVENTION:  COMPOUND MICROSATELLITE
;    TITLE OF INVENTION:  PRIMERS FOR THE
;    TITLE OF INVENTION:  DETECTION OF GENETIC
;    TITLE OF INVENTION:  POLYMORPHISMS
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS AND
;      ADDRESSEE:  COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  U.S.A.
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PATENT IN RELEASE #1.0, VERSION 1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/849,021
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/346,456
```

```
;      FILING DATE:  28 NOVEMBER 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLOYD, LINDA AXAMETHY
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1064-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-892-8112
;      TELEFAX:  302-992-7949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-849-021-6

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3185 CTCTCCCTCCCTCTCTC 3201
              ||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTC 17


RESULT 377
US-08-985-162-813
; Sequence 813, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  813:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-813

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   41.2%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4481 GAATGTATTTGATTTAT 4497
              ||| |:|:::||::: :
Db          1 GAAAGUAUUUGAUUUUU 17


RESULT 378
US-08-998-099-68
; Sequence 68, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
;  APPLICANT: JARVIS, THALE
;  APPLICANT: MCSWIGGEN, JAMES A.
;  APPLICANT: STINCHCOMB, DAN T.
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
;  TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
;  FILE REFERENCE: 231/175
;  CURRENT APPLICATION NUMBER: US/08/998,099A
;  CURRENT FILING DATE: 1997-12-24
;  EARLIER APPLICATION NUMBER: 60/037,658
;  EARLIER FILING DATE: 1997-01-23
;  EARLIER APPLICATION NUMBER: 08/373,124
;  EARLIER FILING DATE: 1995-01-13
;  EARLIER APPLICATION NUMBER: 08/245,466
;  EARLIER FILING DATE: 1994-05-18
;  NUMBER OF SEQ ID NOS: 375
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-08-998-099-68

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 2.4e+02;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2312 ATAGTAATAAGATGGCT 2328
              | || ||:||||:|||:
Db          1 AAAGGAAUAAGAUGGCU 17


RESULT 379
US-08-584-040-2022
; Sequence 2022, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
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;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2022:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2022

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   47.1%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4545 TGGAAAATTTTCTCCTT 4561
              :|| |||: ::|:||:: 
Db          1 UGGGAAAUCUUCUCCUU 17


RESULT 380
US-08-584-040-2555/c
; Sequence 2555, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2555:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2555

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAA 3616
              | |||||||||| ||||
Db         17 TTTGGAAAAAAAAAAAA 1


RESULT 381
US-08-584-040-3981
; Sequence 3981, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  3981:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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```
;      TOPOLOGY:  linear
US-08-584-040-3981

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 2.4e+02;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAA 5203
              ||:|||| :||||: ||
Db          1 AAUAAAAUUGAAGUUAA 17


RESULT 382
US-08-584-040-6075
; Sequence 6075, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  6075:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-6075

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   52.9%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4854 CAAGACCTGAGTATTTT 4870
              |||| ||: ||:|:::: 
Db          1 CAAGUCCUCAGUAUUUU 17


RESULT 383
US-08-679-645-882/c
; Sequence 882, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
;    APPLICANT:  Zwick, Michael G.
;    APPLICANT:  Edington, Brent E.
;    APPLICANT:  McSwiggen, James A.
;    APPLICANT:  Merlo, Patricia Ann Owens
;    APPLICANT:  Guo, Lining
;    APPLICANT:  Skokut, Thomas A.
;    APPLICANT:  Young, Scott A.
;    APPLICANT:  Folkerts, Otto
;    APPLICANT:  Merlo, Donald J.
;    TITLE OF INVENTION:  COMPOSITION AND METHODS FOR
;    TITLE OF INVENTION:  MODULATION OF GENE EXPRESSION
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  1263
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/679,645
;      FILING DATE:  July 12, 1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/001,135
;      FILING DATE:  July 13, 1995
;      APPLICATION NUMBER:  08/300,726
;      FILING DATE:  September 2, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  219/247
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  882:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-679-645-882

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAA 3982
              ||| | ||||||||||| 
Db         17 ATACAAAATAAAAACAA 1


RESULT 384
US-09-474-432B-724
; Sequence 724, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
```

```
;  APPLICANT:  Burgin, Alex
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka
;  APPLICANT:  Sweedler, David
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
;  FILE REFERENCE: MBHB00-831-B (247/276)
;  CURRENT APPLICATION NUMBER: US/09/474,432B
;  CURRENT FILING DATE:  1999-12-19
;  PRIOR APPLICATION NUMBER: US 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/084,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: US 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: US 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 1526
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 724
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-474-432B-724

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   58.8%;  Pred. No. 2.4e+02;
  Matches   10;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2016 CTGCGGTGTTTGGCAAT 2032
              |:||||:| ::|||| :
Db          1 CUGCGGUGGUUGGCAUU 17


RESULT 385
US-09-371-772B-567
; Sequence 567, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 567
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-567

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   47.1%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4545 TGGAAAATTTTCTCCTT 4561
              :|| |||: ::|:||::
Db          1 UGGGAAAUCUUCUCCUU 17


RESULT 386
US-09-371-772B-1079/c
; Sequence 1079, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1079

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAA 3616
              | |||||||||| ||||
Db         17 TTTGGAAAAAAAAAAAA 1


RESULT 387
US-09-371-772B-1748
; Sequence 1748, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1748
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1748

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 2.4e+02;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAA 5203
              ||:|||| :||||: ||
Db          1 AAUAAAAUUGAAGUUAA 17


RESULT 388
US-09-371-772B-2912
; Sequence 2912, Application US/09371772B
```

```
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2912
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-2912

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   52.9%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4854 CAAGACCTGAGTATTTT 4870
              |||| ||: ||:|:::: 
Db          1 CAAGUCCUCAGUAUUUU 17


RESULT 389
US-09-476-387-723
; Sequence 723, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
;  FILE REFERENCE: MBHB00-831-C (249/073)
;  CURRENT APPLICATION NUMBER: US/09/476,387
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-476-387-723

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   58.8%;  Pred. No. 2.4e+02;
  Matches   10;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2016 CTGCGGTGTTTGGCAAT 2032
              |:||||:| ::|||| :
Db          1 CUGCGGUGGUUGGCAUU 17


RESULT 390
US-09-401-063-813
; Sequence 813, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  813:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-813

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   41.2%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4481 GAATGTATTTGATTTAT 4497
              ||| |:|:::||::: :
Db          1 GAAAGUAUUUGAUUUUU 17


RESULT 391
US-09-827-998-193/c
; Sequence 193, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
```

```
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 193
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-193

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1448 TTTAAAATTCAAAAGTA 1464
              ||||||||  |||||  ||
Db         17 TTTAAAATGCAAAAATA 1


RESULT 392
US-09-827-998-194/c
; Sequence 194, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 194
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-194

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1447 TTTTAAAATTCAAAAGT 1463
              |||||||||  |||||  |
Db         17 TTTTAAAATGCAAAAAT 1


RESULT 393
US-09-827-998-196/c
; Sequence 196, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 196
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-196

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1445 TCTTTTAAAATTCAAAA 1461
              | |||||||||  |||||
Db         17 TATTTTAAAATGCAAAA 1


RESULT 394
US-09-827-998-197/c
; Sequence 197, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 197
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-197

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1444 TTCTTTTAAAATTCAAA 1460
              || |||||||||  ||||
Db         17 TTATTTTAAAATGCAAA 1


RESULT 395
US-09-827-998-746
; Sequence 746, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 746
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-746
```

```
  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3058 CTAGCTGCCACTTTCAC 3074
              ||||||||| ||||| |
Db          1 CTAGCTGCCTCTTTCTC 17


RESULT 396
US-09-827-998-747
; Sequence 747, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 747
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-747

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3059 TAGCTGCCACTTTCACG 3075
              ||||||| ||||| ||
Db          1 TAGCTGCCTCTTTCTCG 17


RESULT 397
US-09-827-998-748
; Sequence 748, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 748
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-748

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3060 AGCTGCCACTTTCACGT 3076
              ||||||| ||||| |||

Db          1 AGCTGCCTCTTTCTCGT 17


RESULT 398
US-09-827-998-753
; Sequence 753, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 753
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-753

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2268 CCTCTTTCTGCTCTGCC 2284
              ||||||||| ||||||
Db          1 CCTCTTTCTCGTCTGCC 17


RESULT 399
US-09-866-108A-73/c
; Sequence 73, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
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```
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 73
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-73

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2521 GCTGGACATGAGATGGA 2537
              || | ||||||||||||
Db         17 GCAGCACATGAGATGGA 1


RESULT 400
US-09-866-108A-774
; Sequence 774, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 774
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-774

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1588 TGCCTCCCAGGCAAGCA 1604
              || ||||||||| ||||
Db          1 TGGCTCCCAGGCCAGCA 17


RESULT 401
US-09-866-108A-1009/c
; Sequence 1009, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1009
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-1009

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2923 TTTTCTTCTTTCCCTGG 2939
              || ||| ||||||||||
Db         17 TTCTCTGCTTTCCCTGG 1


RESULT 402
US-09-866-108A-7934/c
; Sequence 7934, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
```

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;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7934
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-7934

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1627 TCCAGCTTCCAAAGCCT 1643
              |||| |||||| |||||
Db         17 TCCAACTTCCAGAGCCT 1

RESULT 403
US-09-404-912-169
; Sequence 169, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
;  APPLICANT: John Landers
;  APPLICANT:  David Houseman
;  APPLICANT:  Barbara Jordan
;  APPLICANT:  Alain Charest
;  TITLE OF INVENTION: Methods and Products Related to
;  TITLE OF INVENTION:  Genotyping and DNA Analysis
;  FILE REFERENCE: M0656/7045(HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/404,912
;  CURRENT FILING DATE:  1999-09-24
;  PRIOR APPLICATION NUMBER: US 60/101,757
;  PRIOR FILING DATE: 1998-09-25
;  PRIOR APPLICATION NUMBER: PCT/US99/22283
;  PRIOR FILING DATE: 1999-09-24
;  NUMBER OF SEQ ID NOS: 691
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 169
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-404-912-169

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGGTT 4520
              |||||| ||||||| ||
Db          1 TTTTTTATTTTTGGATT 17

RESULT 404
US-09-685-664B-567
; Sequence 567, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 567
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-567

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   47.1%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4545 TGGAAAATTTTCTCCTT 4561
              :|| |||: ::|:||::
Db          1 UGGGAAAUCUUCUCCUU 17

RESULT 405
US-09-685-664B-1079/c
; Sequence 1079, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1079

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAA 3616
              | |||||||||| ||||
Db         17 TTTGGAAAAAAAAAAAA 1
```

```
RESULT 406
US-09-685-664B-1748
; Sequence 1748, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1748
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1748

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 2.4e+02;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAA 5203
              ||:|||| :||||: ||
Db          1 AAUAAAAUUGAAGUUAA 17


RESULT 407
US-09-685-664B-2912
; Sequence 2912, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2912
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-09-685-664B-2912

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   52.9%;  Pred. No. 2.4e+02;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4854 CAAGACCTGAGTATTTT 4870
              |||| ||: ||:|:::: 
Db          1 CAAGUCCUCAGUAUUUU 17


RESULT 408
US-09-596-141C-34
; Sequence 34, Application US/09596141C
; Patent No. 6821774
; GENERAL INFORMATION:
;  APPLICANT: Lawn, Richard M.
;  APPLICANT:  Wade, David
;  APPLICANT:  Oram, John F.
;  APPLICANT:  Garvin, Michael
;  TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol
;  TITLE OF INVENTION:  Efflux and Raising HDL using ATP Binding Cassette
;  TITLE OF INVENTION:  Transporter Protein ABC1
;  FILE REFERENCE: 99,395-B
;  CURRENT APPLICATION NUMBER: US/09/596,141C
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: US 60/140,264
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: US 60/153,872
;  PRIOR FILING DATE: 1999-09-14
;  PRIOR APPLICATION NUMBER: US 60/166,573
;  PRIOR FILING DATE: 1999-11-19
;  NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 34
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ABC1
;   OTHER INFORMATION: sequencing primer
US-09-596-141C-34

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1623 AGTGTCCAGCTTCCAAA 1639
              |||||||||| || |||
Db          1 AGTGTCCAGCATCTAAA 17


RESULT 409
US-09-595-526C-34
; Sequence 34, Application US/09595526C
; Patent No. 6835563
; GENERAL INFORMATION:
;  APPLICANT: Lawn, Richard M.
;  APPLICANT:  Wade, David
;  APPLICANT:  Oram, John F.
;  APPLICANT:  Garvin, Michael
;  TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol
;  TITLE OF INVENTION:  Efflux and Raising HDL using ATP Binding Cassette
;  TITLE OF INVENTION:  Transporter Protein ABC1
;  FILE REFERENCE: 99,395-A
;  CURRENT APPLICATION NUMBER: US/09/595,526C
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: US 60/140,264
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: US 60/153,872
;  PRIOR FILING DATE: 1999-09-14
;  PRIOR APPLICATION NUMBER: US 60/166,573
;  PRIOR FILING DATE: 1999-11-19
;  NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 34
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ABC1
```

```
;   OTHER INFORMATION: sequencing primer
US-09-595-526C-34

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1623 AGTGTCCAGCTTCCAAA 1639
              ||||||||||  || |||
Db          1 AGTGTCCAGCATCTAAA 17


RESULT 410
PCT-US92-01015-7
; Sequence 7, Application PC/TUS9201015
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, Geneva R
;    APPLICANT:  Provow, Sally P
;    TITLE OF INVENTION:  Production of Human Serum Albumin in
;    TITLE OF INVENTION:  Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 South LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/01015
;      FILING DATE:  19920204
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,040
;      FILING DATE:  04-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  50857PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)552-1311
;      TELEFAX:  (619)552-0095
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US92-01015-7

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3482 CTGCAAAGCTTTGGCTG 3498
              || |||||||| |||||
Db          1 CTTCAAAGCTTGGGCTG 17


RESULT 411
PCT-US95-06379-34/c
; Sequence 34, Application PC/TUS9506379
;  GENERAL INFORMATION:
;    APPLICANT:  Watanabe, Kyoichi A.
;    APPLICANT:  Ren, Wu-Yun
;    APPLICANT:  Weil, Roger
;    TITLE OF INVENTION:  Complementary DNA and Toxins
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch 1.44Mb
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06379
;      FILING DATE:  May 13, 1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44683-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0526
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-06379-34

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTT 2143
              ||||| ||||| |||||
Db         17 TCTTTGCTTTTCTTCTT 1


RESULT 412
US-09-725-265-17/c
; Sequence 17, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17
```

Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4495 TATAAGTTTTTTTTTTT 4511
|||| ||||||||||
Db 17 TATATATTTTTTTTTT 1

RESULT 413
US-09-556-127-17/c
; Sequence 17, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-17

Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4495 TATAAGTTTTTTTTTTT 4511
|||| ||||||||||
Db 17 TATATATTTTTTTTTT 1

RESULT 414
US-09-437-076-1
; Sequence 1, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
; APPLICANT: Barber-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; CURRENT APPLICATION NUMBER: US/09/437,076
; CURRENT FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Word for Windows
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-437-076-1

Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACA 3619
||||||||| ||||| |
Db 2 GGAAAAAAAAAAAAAAA 18

RESULT 415
US-09-904-744-1
; Sequence 1, Application US/09904744
; Patent No. 6828142
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; TITLE OF INVENTION: dendrimers in a signal amplification system
; FILE REFERENCE: B-73
; CURRENT APPLICATION NUMBER: US/09/904,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/437076
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/107828
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-904-744-1

Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACA 3619
||||||||| ||||| |
Db 2 GGAAAAAAAAAAAAAAA 18

RESULT 416
US-09-965-599-4/c
; Sequence 4, Application US/09965599
; Patent No. 6555670
; GENERAL INFORMATION:
; APPLICANT: Aizawa, Akira
; APPLICANT: Kawakami, Akiko
; APPLICANT: Kondo, Toshihiko
; TITLE OF INVENTION: Testis-Specific Gene
; FILE REFERENCE: 6920/0J871
; CURRENT APPLICATION NUMBER: US/09/965,599
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer HT15-C
US-09-965-599-4

Query Match 0.3%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAG 3620

```
                ||||||||  |||||  ||
Db         20 GAAAAAAAAAAAAAAAG 4


RESULT 417
US-09-780-045-110
; Sequence 110, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT E
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0130
;  CURRENT APPLICATION NUMBER: US/09/780,045
;  CURRENT FILING DATE:  2001-02-09
;  NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-045-110

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATACATT 2414
                ||||||| |||||||  ||
Db          1 TATATATGTATATATATTTT 20


RESULT 418
US-09-228-942-7
; Sequence 7, Application US/09228942
; Patent No. 6203988
; GENERAL INFORMATION:
;  APPLICANT: Kambara, Hideki
;  APPLICANT: Uematsu, Chihiro
;  TITLE OF INVENTION: DNA FRAGMENT ANALYSIS METHOD AND REAGENT KIT
;  FILE REFERENCE: ASA-757
;  CURRENT APPLICATION NUMBER: US/09/228,942
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: oligonucleotide ligated to 3' end of DNA fragment
US-09-228-942-7

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAACA 3619
                |||  ||||||| ||||| |
Db          1 TCTCCAAAAAAAAAAAAAAA 20


RESULT 419
US-08-479-248-6/c
; Sequence 6, Application US/08479248
; Patent No. 5594121
;  GENERAL INFORMATION:
;    APPLICANT:  FROEHLER, BRIAN
;    APPLICANT:  MATTEUCCI, MARK
;    TITLE OF INVENTION:  ENHANCED TRIPLE-HELIX AND DOUBLE-HELIX
;    TITLE OF INVENTION:  FORMATION WITH OLIGOMERS CONTAINING MODIFIED PURINES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GILEAD SCIENCES INC.
;      STREET:  353 Lakeside Drive
;      CITY:  Foster City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,248
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MUENCHAU, DARYL
;      REGISTRATION NUMBER:  36,616
;      REFERENCE/DOCKET NUMBER:  160.1C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 574-3000
;      TELEFAX:  (415) 573-4899
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  misc_difference
;      LOCATION:  one-of(1, 3, 5, 7, 10)
;      OTHER INFORMATION:  /note= "These positions are
;      OTHER INFORMATION:  2'-deoxyadenosine."
US-08-479-248-6

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATAT 2399
                ||||||||  ||||||
Db         15 AAAAATAATATATAT 1


RESULT 420
US-08-479-248-12
; Sequence 12, Application US/08479248
; Patent No. 5594121
;  GENERAL INFORMATION:
;    APPLICANT:  FROEHLER, BRIAN
;    APPLICANT:  MATTEUCCI, MARK
;    TITLE OF INVENTION:  ENHANCED TRIPLE-HELIX AND DOUBLE-HELIX
;    TITLE OF INVENTION:  FORMATION WITH OLIGOMERS CONTAINING MODIFIED PURINES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GILEAD SCIENCES INC.
;      STREET:  353 Lakeside Drive
;      CITY:  Foster City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,248
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
```

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MUENCHAU, DARYL
;      REGISTRATION NUMBER:  36,616
;      REFERENCE/DOCKET NUMBER:  160.1C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 574-3000
;      TELEFAX:  (415) 573-4899
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  misc_difference
;      LOCATION:  one-of(6, 9, 11, 13, 15)
;      OTHER INFORMATION:  /note= "This position is T,
;      OTHER INFORMATION:  5-(1-propynyl)-2'-deoxyruidine (pdU), or other suitable
;      OTHER INFORMATION:  pyrimidines."
;    FEATURE:
;      NAME/KEY:  misc_difference
;      LOCATION:  one-of(1, 2, 3, 4, 5, 7, 8, 10, 12, 14)
;      OTHER INFORMATION:  /note= "These positions are
;      OTHER INFORMATION:  2'-deoxyadenosine."
US-08-479-248-12

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+02;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATAT 2399
              |||||:|| |:|:|:
Db          1 AAAAAUAAAUAUAUAU 15


RESULT 421
US-08-334-847-57
; Sequence 57, Application US/08334847
; Patent No. 5693532
;  GENERAL INFORMATION:
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  Pavco, Pam
;    APPLICANT:  Woolf, Tod
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING RESPIRATORY
;    TITLE OF INVENTION:  SYNCYTIAL VIRUS
;    NUMBER OF SEQUENCES:  909
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/334,847
;      FILING DATE:  No. 5693532ember 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-334-847-57

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.8e+02;
  Matches    6;  Conservative    8;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5172 ATTGTGTTTGTTCAT 5186
              |::|:|:::|: ||:
Db          1 AUUGUGUUUGUGCAU 15


RESULT 422
US-08-334-847-516/c
; Sequence 516, Application US/08334847
; Patent No. 5693532
;  GENERAL INFORMATION:
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  Pavco, Pam
;    APPLICANT:  Woolf, Tod
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING RESPIRATORY
;    TITLE OF INVENTION:  SYNCYTIAL VIRUS
;    NUMBER OF SEQUENCES:  909
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/334,847
;      FILING DATE:  No. 5693532ember 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  516:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-334-847-516

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       4131 GATTTTCAAGATTCT 4145
              ||||||| |||||||
Db         15 GATTTTCTAGATTCT 1


RESULT 423
US-08-311-486C-33/c
; Sequence 33, Application US/08311486C
; Patent No. 5811300
;  GENERAL INFORMATION:
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth Draper
;    APPLICANT:  Kevin Kisich
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  TNF-'
;    NUMBER OF SEQUENCES:  1157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,486C
;      FILING DATE:  September 23, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/166
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-311-486C-33

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2537 AGAGGCTGAGGGACA 2551
              ||||||||||| |||
Db         15 AGAGGCTGAGGAACA 1


RESULT 424
US-08-311-486C-674/c
; Sequence 674, Application US/08311486C
; Patent No. 5811300
;  GENERAL INFORMATION:
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth Draper
;    APPLICANT:  Kevin Kisich
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  TNF-'
;    NUMBER OF SEQUENCES:  1157
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,486C
;      FILING DATE:  September 23, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/166
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  674:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-311-486C-674

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3749 AAGGGAGGAAGGCCT 3763
              |||| ||||||||||
Db         15 AAGGTAGGAAGGCCT 1


RESULT 425
US-08-292-620A-359
; Sequence 359, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
```

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;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  359:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-359

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   6.7%;  Pred. No. 2.8e+02;
  Matches    1;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              | ::::::::::::::
Db          1 GAUUUUUUUUUUUUU 15


RESULT 426
US-08-585-684B-666
; Sequence 666, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  666:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-666

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   53.3%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2858 TCTTGATTCCTGGCT 2872
              :|: ||::||:|||:
Db          1 UCUAGAUUCCUGGCU 15


RESULT 427
US-08-893-204C-2
; Sequence 2, Application US/08893204C
; Patent No. 6043044
;  GENERAL INFORMATION:
;    APPLICANT:  Hudson, Perry B.
;    APPLICANT:  Hakky, Said I.
;    APPLICANT:  Meyer-Siegler, Katherine
;    APPLICANT:  Hakki, A-Hamid
;    TITLE OF INVENTION:  DIAGNOSTIC AND PROGNOSTIC MARKER
;    TITLE OF INVENTION:  FOR METASTATIC ADEMOCARCINOMA
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rosenberg, Klein & Bilker
;      STREET:  3444 Ellicott Center Drive, Suite 105
;      CITY:  Ellicott City
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  21043
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inches,
;      MEDIUM TYPE:  1.44Mb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/893,204C
;      FILING DATE:  7/15/97
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rosenberg, Morton
;      REGISTRATION NUMBER:  26,049
;      REFERENCE/DOCKET NUMBER:  MR2493-5
;    TELECOMMUNICATION INFORMATION:
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```
;      TELEPHONE:  (410) 465-6678
;      TELEFAX:  (410) 461-3067
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  yes
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:  synthetic
;    PUBLICATION INFORMATION:
;      AUTHORS:  Katherine Meyer-Siegler
;      AUTHORS:  Perry Hudson
;      TITLE:  Enhanced Expression of Macrophage Migration
;      TITLE:  Inhibitory Factor in Prostatic Adenocarcinoma Metastases
;      JOURNAL:  Urology
;      VOLUME:  48
;      ISSUE:  3
;      PAGES:  448-452
;      DATE:  1996
;      RELEVANT RESIDUES IN SEQ ID NO:  2: FROM 1 TO 15
US-08-893-204C-2

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4515
              ||||||||||||| |
Db          1 TTTTTTTTTTTTCT 15


RESULT 428
US-08-832-021-27
; Sequence 27, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-27

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGG 4518
              ||||||||||||| |
Db          1 TTTTTTTTTTTTGAG 15


RESULT 429
US-08-832-021-33/c
; Sequence 33, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-33

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAA 3616
              |||||||||| ||||
Db         15 TGGAAAAAAAAAAAA 1


RESULT 430
US-08-832-021-39
; Sequence 39, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-39

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGG 4518
              ||||||||||||| |
Db          1 TTTTTTTTTTTTGCG 15


RESULT 431
US-08-832-021-43
; Sequence 43, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
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;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-43

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGG 4517
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTAGG 15


RESULT 432
US-08-832-021-47
; Sequence 47, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-47

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGG 4517
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCGG 15


RESULT 433
US-08-832-021-55
; Sequence 55, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-55

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTATG 15


RESULT 434
US-08-832-021-56
; Sequence 56, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-56

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTATT 15


RESULT 435
US-08-832-021-59
; Sequence 59, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-59

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       4502 TTTTTTTTTTTTTTG 4516
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCTG 15


RESULT 436
US-08-832-021-60
; Sequence 60, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-60

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2129 TTTTCTTTTTTTCTT 2143
              |||| ||||||||||
Db          1 TTTTTTTTTTTTCTT 15


RESULT 437
US-08-832-021-63
; Sequence 63, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-63

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTGTG 15


RESULT 438
US-08-832-021-64
; Sequence 64, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-64

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTGTT 15


RESULT 439
US-09-071-845-359
; Sequence 359, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  359:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-359

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   6.7%;  Pred. No. 2.8e+02;
  Matches    1;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              | ::::::::::::::
Db          1 GAUUUUUUUUUUUUU 15


RESULT 440
US-09-038-073-666
; Sequence 666, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  666:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-666

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   53.3%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2858 TCTTGATTCCTGGCT 2872
              :|: ||::||:|||:
Db          1 UCUAGAUUCCUGGCU 15


RESULT 441
US-09-475-947A-164
; Sequence 164, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: human
US-09-475-947A-164

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||  ||||||
Db          1 TTTTTTTTATTTTTT 15


RESULT 442
US-09-234-245-17/c
; Sequence 17, Application US/09234245
; Patent No. 6509457
; GENERAL INFORMATION:
;  APPLICANT: Thomas Jefferson University
;  APPLICANT: Raphael Rubin
;  APPLICANT: Manorama Tewari
;  TITLE OF INVENTION: Compositions And Methods For Modulating
;  TITLE OF INVENTION: Apoptosis
;  FILE REFERENCE: TJU-002
;  CURRENT APPLICATION NUMBER: US/09/234,245
;  CURRENT FILING DATE: 1999-01-20
;  EARLIER APPLICATION NUMBER: US 60/071,878
;  EARLIER FILING DATE: 1998-01-20
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: PCR primer
US-09-234-245-17

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 CTGGTGAACAGTGCT 1036
              |||||||||| ||||
Db         15 CTGGTGAACAATGCT 1
```

```
RESULT 443
US-09-124-238A-4
; Sequence 4, Application US/09124238A
; Patent No. 6300127
; GENERAL INFORMATION:
;  APPLICANT: Hair, Gregory A.
;  APPLICANT:  Boden, Scott D.
;  TITLE OF INVENTION: No. 6300127el Bone Mineralization Proteins, DNA, Vectors,
;  TITLE OF INVENTION:  Expression Systems
;  FILE REFERENCE: 06148.0115
;  CURRENT APPLICATION NUMBER: US/09/124,238A
;  CURRENT FILING DATE:  1998-07-29
;  PRIOR APPLICATION NUMBER: 60/054,219
;  PRIOR FILING DATE: 1997-07-30
;  PRIOR APPLICATION NUMBER: 60/080,407
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: MS Word
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Differential Display PCR Primer
US-09-124-238A-4

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 444
US-09-411-628-1
; Sequence 1, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
;  APPLICANT: University of Southern California
;  TITLE OF INVENTION: cDNA, GENOMIC, AND PREDICTED PROTEIN
;  TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
;  FILE REFERENCE: 13761-707
;  CURRENT APPLICATION NUMBER: US/09/411,628
;  CURRENT FILING DATE: 1999-10-01
;  EARLIER APPLICATION NUMBER: US 60/102,906
;  EARLIER FILING DATE: 1998-10-02
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Anchored primer
US-09-411-628-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 445
US-09-331-930A-4
; Sequence 4, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
;  APPLICANT: ZIMMET, PAUL Z.
;  APPLICANT:  COLLIER, GREGORY
;  TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
;  FILE REFERENCE: 22975-20007.00
;  CURRENT APPLICATION NUMBER: US/09/331,930A
;  CURRENT FILING DATE:  1999-06-30
;  PRIOR APPLICATION NUMBER: PCT/AU98/00902
;  PRIOR FILING DATE: 1998-10-30
;  PRIOR APPLICATION NUMBER: AU PP0117/97
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: AU PP0323/97
;  PRIOR FILING DATE: 1997-11-11
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-331-930A-4

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 446
US-09-721-975-4
; Sequence 4, Application US/09721975
; Patent No. 6444803
; GENERAL INFORMATION:
;  APPLICANT: Hair, Gregory A.
;  APPLICANT:  Boden, Scott D.
;  TITLE OF INVENTION: No. 6444803el Bone Mineralization Proteins, DNA, Vectors,
;  TITLE OF INVENTION:  Expression Systems
;  FILE REFERENCE: 06148.0115
;  CURRENT APPLICATION NUMBER: US/09/721,975
;  CURRENT FILING DATE:  2000-11-27
;  PRIOR APPLICATION NUMBER: US 09/124,238
;  PRIOR FILING DATE: 1998-07-29
;  PRIOR APPLICATION NUMBER: 60/054,219
;  PRIOR FILING DATE: 1997-07-30
;  PRIOR APPLICATION NUMBER: 60/080,407
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: MS Word
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Differential Display PCR Primer
US-09-721-975-4

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 447
US-08-894-251A-5
; Sequence 5, Application US/08894251A
; Patent No. 6455305
; GENERAL INFORMATION:
```

```
;  APPLICANT: Shlomo Melmed (Inventor)
;  APPLICANT:  Lin Pei (Inventor)
;  TITLE OF INVENTION: Pituitary-Tumor-Transforming Genes, and
;  TITLE OF INVENTION:  Related Products
;  FILE REFERENCE: P07 39556 (80392)
;  CURRENT APPLICATION NUMBER: US/08/894,251A
;  CURRENT FILING DATE:  1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-894-251A-5

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 448
US-08-894-251A-7
; Sequence 7, Application US/08894251A
; Patent No. 6455305
; GENERAL INFORMATION:
;  APPLICANT: Shlomo Melmed (Inventor)
;  APPLICANT:  Lin Pei (Inventor)
;  TITLE OF INVENTION: Pituitary-Tumor-Transforming Genes, and
;  TITLE OF INVENTION:  Related Products
;  FILE REFERENCE: P07 39556 (80392)
;  CURRENT APPLICATION NUMBER: US/08/894,251A
;  CURRENT FILING DATE:  1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: n = a, g, or c
US-08-894-251A-7

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 449
US-09-300-958A-56
; Sequence 56, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 56
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-56

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 450
US-09-300-958A-57
; Sequence 57, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 57
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-57

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 451
US-09-300-958A-58
; Sequence 58, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
```

```
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 58
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-58

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 452
US-09-300-958A-83
; Sequence 83, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 83
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-83

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 453
US-09-300-958A-84
; Sequence 84, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 84
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-84

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 454
US-09-300-958A-85
; Sequence 85, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-85

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 455
```

```
US-09-986-621-4
; Sequence 4, Application US/09986621
; Patent No. 6521750
; GENERAL INFORMATION:
;  APPLICANT: Hair, Gregory A.
;  APPLICANT:  Boden, Scott D.
;  TITLE OF INVENTION: No. 6521750el Bone Mineralization Proteins, DNA, Vectors,
;  TITLE OF INVENTION:  Expression Systems
;  FILE REFERENCE: 06148.0115
;  CURRENT APPLICATION NUMBER: US/09/986,621
;  CURRENT FILING DATE:  2001-11-09
;  PRIOR APPLICATION NUMBER: 09/124,238
;  PRIOR FILING DATE: 1998-07-29
;  PRIOR APPLICATION NUMBER: 60/080,407
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: MS Word
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Differential Display PCR Primer
US-09-986-621-4

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 456
US-09-371-772B-6072
; Sequence 6072, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6072
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-6072

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   53.3%;  Pred. No. 2.9e+02;
  Matches    8;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGT 4096
              :|:|:|| :|:|||:
Db          2 UGUGUGGGUGUGGGU 16


RESULT 457
US-09-527-972-15
; Sequence 15, Application US/09527972
; Patent No. 6642438
; GENERAL INFORMATION:
;  APPLICANT: Clendennen, Stephanie K.
;  APPLICANT: Kellogg, Jill A.
;  APPLICANT: Phan, Chau B.
;  APPLICANT: Mathews, Helena V.
;  APPLICANT: Webb, Nancy M.
;  TITLE OF INVENTION: Banana and Melon Promoters for
;  TITLE OF INVENTION: Expression of Transgenes in Plants
;  FILE REFERENCE: 4257-0019.30
;  CURRENT APPLICATION NUMBER: US/09/527,972
;  CURRENT FILING DATE: 2000-03-17
;  EARLIER APPLICATION NUMBER: US 60/125,310
;  EARLIER FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide primer
US-09-527-972-15

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 458
US-09-527-972-16
; Sequence 16, Application US/09527972
; Patent No. 6642438
; GENERAL INFORMATION:
;  APPLICANT: Clendennen, Stephanie K.
;  APPLICANT: Kellogg, Jill A.
;  APPLICANT: Phan, Chau B.
;  APPLICANT: Mathews, Helena V.
;  APPLICANT: Webb, Nancy M.
;  TITLE OF INVENTION: Banana and Melon Promoters for
;  TITLE OF INVENTION: Expression of Transgenes in Plants
;  FILE REFERENCE: 4257-0019.30
;  CURRENT APPLICATION NUMBER: US/09/527,972
;  CURRENT FILING DATE: 2000-03-17
;  EARLIER APPLICATION NUMBER: US 60/125,310
;  EARLIER FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide primer
US-09-527-972-16

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 459
US-09-527-972-17
; Sequence 17, Application US/09527972
; Patent No. 6642438
```

```
; GENERAL INFORMATION:
;  APPLICANT: Clendennen, Stephanie K.
;  APPLICANT: Kellogg, Jill A.
;  APPLICANT: Phan, Chau B.
;  APPLICANT: Mathews, Helena V.
;  APPLICANT: Webb, Nancy M.
;  TITLE OF INVENTION: Banana and Melon Promoters for
;  TITLE OF INVENTION: Expression of Transgenes in Plants
;  FILE REFERENCE: 4257-0019.30
;  CURRENT APPLICATION NUMBER: US/09/527,972
;  CURRENT FILING DATE: 2000-03-17
;  EARLIER APPLICATION NUMBER: US 60/125,310
;  EARLIER FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide primer
US-09-527-972-17

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 460
US-09-479-005A-437/c
; Sequence 437, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-C
;  CURRENT APPLICATION NUMBER: US/09/479,005A
;  CURRENT FILING DATE:  2000-01-07
;  PRIOR APPLICATION NUMBER: US 09/444,209
;  PRIOR FILING DATE: 1999-11-19
;  PRIOR APPLICATION NUMBER: US 09/159,274
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: US 60/059,473
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 437
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-479-005A-437

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1452 AAATTCAAAAGTATT 1466
              |||| ||||||||||
Db         16 AAATGCAAAAGTATT 2


RESULT 461
US-09-479-005A-508
; Sequence 508, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
;  FILE REFERENCE: MBHB00-884-C
;  CURRENT APPLICATION NUMBER: US/09/479,005A
;  CURRENT FILING DATE:  2000-01-07
;  PRIOR APPLICATION NUMBER: US 09/444,209
;  PRIOR FILING DATE: 1999-11-19
;  PRIOR APPLICATION NUMBER: US 09/159,274
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: US 60/059,473
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 508
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-479-005A-508

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+02;
  Matches    9;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1474 AACAACTCTGCCTTT 1488
              ||||| :|:|||:::
Db          2 AACAAAUCUGCCUUU 16


RESULT 462
US-10-174-794-1
; Sequence 1, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
;  APPLICANT: University of Southern California
;  TITLE OF INVENTION: cDNA, GENOMIC, AND PREDICTED PROTEIN
;  TITLE OF INVENTION:  SEQUENCES OF LEARNING-INDUCED KINASES
;  FILE REFERENCE: 13761-707
;  CURRENT APPLICATION NUMBER: US/10/174,794
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: US/09/411,628
;  PRIOR FILING DATE: 1999-10-01
;  PRIOR APPLICATION NUMBER: US 60/102,906
;  PRIOR FILING DATE: 1998-10-02
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Anchored primer
US-10-174-794-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 463
US-09-949-271A-5
; Sequence 5, Application US/09949271A
; Patent No. 6723519
; GENERAL INFORMATION:
;  APPLICANT: Shlomo Melmed (Inventor)
;  APPLICANT:  Lin Pei (Inventor)
;  TITLE OF INVENTION: Compositions and Method for Determining
;  TITLE OF INVENTION:  The Presence of Rat PRRG Peptide In A Sample
;  FILE REFERENCE: 18810-81108
;  CURRENT APPLICATION NUMBER: US/09/949,271A
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: US 08/894,251
;  PRIOR FILING DATE: 1999-07-23
```

```
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-949-271A-5

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 464
US-09-949-271A-7
; Sequence 7, Application US/09949271A
; Patent No. 6723519
; GENERAL INFORMATION:
;  APPLICANT: Shlomo Melmed (Inventor)
;  APPLICANT:  Lin Pei (Inventor)
;  TITLE OF INVENTION: Compositions and Method for Determining
;  TITLE OF INVENTION:  The Presence of Rat PRRG Peptide In A Sample
;  FILE REFERENCE: 18810-81108
;  CURRENT APPLICATION NUMBER: US/09/949,271A
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: US 08/894,251
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: n = a, g, or c
US-09-949-271A-7

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 465
US-09-949-476A-5
; Sequence 5, Application US/09949476A
; Patent No. 6750327
; GENERAL INFORMATION:
;  APPLICANT: Shlomo Melmed (Inventor)
;  APPLICANT:  Lin Pei (Inventor)
;  TITLE OF INVENTION: Compositions and Method for Determining
;  TITLE OF INVENTION:  The Presence of Human PRRG Peptide In A Sample
;  FILE REFERENCE: 18810-81107
;  CURRENT APPLICATION NUMBER: US/09/949,476A
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: US 08/894,251
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-949-476A-5

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 466
US-09-949-476A-7
; Sequence 7, Application US/09949476A
; Patent No. 6750327
; GENERAL INFORMATION:
;  APPLICANT: Shlomo Melmed (Inventor)
;  APPLICANT:  Lin Pei (Inventor)
;  TITLE OF INVENTION: Compositions and Method for Determining
;  TITLE OF INVENTION:  The Presence of Human PRRG Peptide In A Sample
;  FILE REFERENCE: 18810-81107
;  CURRENT APPLICATION NUMBER: US/09/949,476A
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: US 08/894,251
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: n = a, g, or c
US-09-949-476A-7

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 467
US-09-563-794B-137/c
; Sequence 137, Application US/09563794B
; Patent No. 6808876
; GENERAL INFORMATION:
;  APPLICANT: KRUGER, MARTIN
;  APPLICANT:  WELCH, PETER J.
;  APPLICANT:  BARBER, JACK R.
;  TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 039316-0801
;  CURRENT APPLICATION NUMBER: US/09/563,794B
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS: 144
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
```

```
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Combined DNA/RNA Molecule: DNA or
;   OTHER INFORMATION: RNA where u can be u for RNA or t for DNA
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-563-794B-137

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2073 AAGAAAAGACATTTT 2087
              ||| ||||||||||||
Db         15 AAGCAAAGACATTTT 1


RESULT 468
US-10-124-038-42/c
; Sequence 42, Application US/10124038
; Patent No. 6825010
; GENERAL INFORMATION:
;  APPLICANT: Spier, Eugene
;  APPLICANT:  Boyd, Victoria L
;  TITLE OF INVENTION: Methods and Compositions for Nucleotide Analysis
;  FILE REFERENCE: 7414.0045
;  CURRENT APPLICATION NUMBER: US/10/124,038
;  CURRENT FILING DATE:  2002-07-25
;  PRIOR APPLICATION NUMBER: US 60/284,409
;  PRIOR FILING DATE: 2001-04-16
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description: synthesized oligonucleotide primer
US-10-124-038-42

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4096 TGTGGGTGGGAGTGT 4110
              ||| ||||||||||||
Db         16 TGTTGGTGGGAGTGT 2


RESULT 469
US-10-261-821-11
; Sequence 11, Application US/10261821
; Patent No. 6835380
; GENERAL INFORMATION:
;  APPLICANT: Cedars-Sinai Medical Center (Assignee);
;  APPLICANT:  Gregory A. Horwitz (Inventor);
;  APPLICANT:  Xun Zhang (Inventor);
;  APPLICANT:  Shlomo Melmed (Inventor)
;  TITLE OF INVENTION: Pituitary Tumor Transforming Gene (PTTG)
;  TITLE OF INVENTION:  Carboxy-Terminal Peptides and Methods of Use Thereof to
;  TITLE OF INVENTION:  Inhibit Neoplastic Cellular Proliferation and/or
;  TITLE OF INVENTION:  Transformation
;  FILE REFERENCE: CEDAR-044527
;  CURRENT APPLICATION NUMBER: US/10/261,821
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: US/09/569,956
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: US 08/894,251
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Anchored primer sequence.
US-10-261-821-11

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 470
US-10-261-821-13
; Sequence 13, Application US/10261821
; Patent No. 6835380
; GENERAL INFORMATION:
;  APPLICANT: Cedars-Sinai Medical Center (Assignee);
;  APPLICANT:  Gregory A. Horwitz (Inventor);
;  APPLICANT:  Xun Zhang (Inventor);
;  APPLICANT:  Shlomo Melmed (Inventor)
;  TITLE OF INVENTION: Pituitary Tumor Transforming Gene (PTTG)
;  TITLE OF INVENTION:  Carboxy-Terminal Peptides and Methods of Use Thereof to
;  TITLE OF INVENTION:  Inhibit Neoplastic Cellular Proliferation and/or
;  TITLE OF INVENTION:  Transformation
;  FILE REFERENCE: CEDAR-044527
;  CURRENT APPLICATION NUMBER: US/10/261,821
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: US/09/569,956
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: US 08/894,251
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: PCT/US97/21463
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: US 60/031,338
;  PRIOR FILING DATE: 1996-11-21
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: n  = a, g, or c; Anchored primer sequence.
US-10-261-821-13

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 471
US-08-373-124A-1062
; Sequence 1062, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
```

```
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1062:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-1062

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   53.3%;  Pred. No. 3e+02;
  Matches    8;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2400 ATACATATATACATT 2414
                |:| |:|:|:|||::
Db          1 AUAUAUAUAUACAUU 15


RESULT 472
US-08-435-628-1062
; Sequence 1062, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1062:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-1062

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   53.3%;  Pred. No. 3e+02;
  Matches    8;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2400 ATACATATATACATT 2414
                |:| |:|:|:|||::
Db          1 AUAUAUAUAUACAUU 15


RESULT 473
US-08-330-000-1/c
; Sequence 1, Application US/08330000
; Patent No. 5686242
;  GENERAL INFORMATION:
;    APPLICANT:  Bruice, Thomas W.
;    APPLICANT:  Lima, Walter F.
;    TITLE OF INVENTION:  DETERMINATION OF OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  FOR THERAPEUTICS, DIAGNOSTICS   AND RESEARCH REAGENTS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5686242ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/08/330,000
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  755,485
;      FILING DATE:  September 5, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07489
;      FILING DATE:  September 4, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ralph, Rebecca Lynne
;      REGISTRATION NUMBER:  35,152
;      REFERENCE/DOCKET NUMBER:  ISIS-1723
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-330-000-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         18 AAAAAAAAAAAAACA 4


RESULT 474
US-08-965-908-1/c
; Sequence 1, Application US/08965908
; Patent No. 6022691
;  GENERAL INFORMATION:
;    APPLICANT:  Bruice, Thomas W.
;    APPLICANT:  Lima, Walter F.
;    TITLE OF INVENTION:  DETERMINATION OF OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  FOR THERAPEUTICS, DIAGNOSTICS   AND RESEARCH REAGENTS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 6022691ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,908
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330,000
;      FILING DATE:
;      APPLICATION NUMBER:  755,485
;      FILING DATE:  September 5, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/07489
;      FILING DATE:  September 4, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ralph, Rebecca Lynne
;      REGISTRATION NUMBER:  35,152
;      REFERENCE/DOCKET NUMBER:  ISIS-1723
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-965-908-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         18 AAAAAAAAAAAAACA 4


RESULT 475
US-09-371-307-85/c
; Sequence 85, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
;  APPLICANT: Brown, Sherri M.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: Piller, Kenneth J.
;  APPLICANT: Kishore, Ganesh M.
;  APPLICANT: Elich, Tedd D.
;  APPLICANT: Logusch, Eugene W.
;  APPLICANT: Rao, Sudabathula
;  APPLICANT: Ream, Joel E.
;  APPLICANT: Logusch, Sherry J.
;  TITLE OF INVENTION: Methods for controlling gibberellin levels
;  FILE REFERENCE: MOBT:216
;  CURRENT APPLICATION NUMBER: US/09/371,307A
;  CURRENT FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-371-307-85

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.2e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 476
US-08-494-577-10
; Sequence 10, Application US/08494577
; Patent No. 5786171
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  Hsieh, Chung-Ming
;    TITLE OF INVENTION:  AORTIC PREFERENTIALLY EXPRESSED GENE AND
;    TITLE OF INVENTION:  USES THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
```

```
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/494,577
;      FILING DATE:  22-JUN-1995
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  05433/012001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-494-577-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||:|
Db          1 TTTTTTTTTTTTVG 14


RESULT 477
US-08-795-868-10
; Sequence 10, Application US/08795868
; Patent No. 5846773
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Mu-En
;    APPLICANT:  Hsieh, Chung-Ming
;    TITLE OF INVENTION:  A SINGLE GENE ENCODING AORTIC-SPECIFIC
;    TITLE OF INVENTION:  AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,868
;      FILING DATE:  06-FEB-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/494,577
;      FILING DATE:  22-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  05433/032001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-795-868-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||:|
Db          1 TTTTTTTTTTTTVG 14


RESULT 478
US-09-303-069-10
; Sequence 10, Application US/09303069A
; Patent No. 6350592
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT: Hsieh, Chung-Ming
;  TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
;  TITLE OF INVENTION: MUSCLE CELL ISOFORMS AND USES THEREOF
;  FILE REFERENCE: 05433/039001
;  CURRENT APPLICATION NUMBER: US/09/303,069A
;  CURRENT FILING DATE: 1999-04-30
;  EARLIER APPLICATION NUMBER: US 09/134,250
;  EARLIER FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic poly T anchoring primer
US-09-303-069-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||:|
Db          1 TTTTTTTTTTTTVG 14


RESULT 479
US-09-134-250-10
; Sequence 10, Application US/09134250B
; Patent No. 6399753
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT: Hsieh, Chung-Ming
;  TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
;  TITLE OF INVENTION: MUSCLE CELL ISOFORMS AND USES THEREOF
;  FILE REFERENCE: 05433/038001
;  CURRENT APPLICATION NUMBER: US/09/134,250B
;  CURRENT FILING DATE: 1998-08-14
;  EARLIER APPLICATION NUMBER: US 08/795,868
;  EARLIER FILING DATE: 1997-02-06
;  EARLIER APPLICATION NUMBER: US 08/494,577
;  EARLIER FILING DATE: 1995-06-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: synthetic poly T anchoring primer
US-09-134-250-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGG 4517
              ||||||||||||:|
Db          1 TTTTTTTTTTTTVG 14


RESULT 480
US-09-300-958A-65
; Sequence 65, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 65
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-65

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTV 14


RESULT 481
US-08-621-914A-16/c
; Sequence 16, Application US/08621914A
; Patent No. 5707807
;  GENERAL INFORMATION:
;    APPLICANT:  KATO, KIKUYA
;    TITLE OF INVENTION:  MOLECULAR INDEXING FOR EXPRESSED GENE
;    TITLE OF INVENTION:  ANALYSIS
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,914A
;      FILING DATE:  26-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LAWRENCE III, STANTON T.
;      REGISTRATION NUMBER:  25,736
;      REFERENCE/DOCKET NUMBER:  7005-107-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  other nucleic acid
US-08-621-914A-16

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 482
US-08-346-429-3
; Sequence 3, Application US/08346429
; Patent No. 5837820
;  GENERAL INFORMATION:
;    APPLICANT:  DeRose, Richard
;    APPLICANT:  Douce, Roland
;    APPLICANT:  Duval, Manuel
;    APPLICANT:  Job, Claudette
;    APPLICANT:  Job, Dominique
;    TITLE OF INVENTION:  PROTEIN CAPABLE OF BEING BIOTINYLATED WHICH CAN
;    TITLE OF INVENTION:  BE USED FOR DETERMINING THE GERMINATION STAGE OF
;    TITLE OF INVENTION:  A SEED
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY SCOTT MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/346,429
;      FILING DATE:  29-NOV-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9507
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  cDNA
US-08-346-429-3

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 483
US-08-358-556A-12/c
; Sequence 12, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..18
US-08-358-556A-12

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 484
US-08-358-556A-18
; Sequence 18, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..18
US-08-358-556A-18

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 485
US-08-469-852A-4/c
; Sequence 4, Application US/08469852A
; Patent No. 5874213
;  GENERAL INFORMATION:
;    APPLICANT:  Cummins, Lendell L.
;    APPLICANT:  Freier, Susan M.
;    APPLICANT:  Griffey, Richard
;    APPLICANT:  Srivatsa, Susan G.
;    TITLE OF INVENTION:  Capillary Electrophoretic Detection of
;    TITLE OF INVENTION:  Nucleic Acids
;    NUMBER OF SEQUENCES:  4
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5874213ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,852A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/295,509
;      FILING DATE:  24-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michael P. Straher
;      REGISTRATION NUMBER:  38,325
;      REFERENCE/DOCKET NUMBER:  ISIS-2015
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-469-852A-4

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 486
US-08-295-509B-4/c
; Sequence 4, Application US/08295509B
; Patent No. 6045995
;  GENERAL INFORMATION:
;    APPLICANT:  Cummins, Lendell L.
;    APPLICANT:  Freier, Susan M.
;    APPLICANT:  Griffey, Richard
;    APPLICANT:  Srivatsa, Susan G.
;    TITLE OF INVENTION:  Capillary Electrophoretic Detection of
;    TITLE OF INVENTION:  Nucleic Acids
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and No. 6045995ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/295,509B
;      FILING DATE:  24-AUG-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michael P. Straher
;      REGISTRATION NUMBER:  38,325
;      REFERENCE/DOCKET NUMBER:  ISIS-1395
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-295-509B-4

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 487
US-08-884-029-9/c
; Sequence 9, Application US/08884029
; Patent No. 6071745
;  GENERAL INFORMATION:
;    APPLICANT:  Lin, Ching-I Patsy
;    APPLICANT:  Wallace, Robert Bruce
;    APPLICANT:  Cossman, Jeffrey
;    APPLICANT:  French, Cynthia
;    TITLE OF INVENTION:  Lyophilization of Cultured Human Cells
;    TITLE OF INVENTION:  to Preserve RNA and DNA
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/884,029
;      FILING DATE:  27-JUN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parent, Annette S.
;      REGISTRATION NUMBER:  42,058
;      REFERENCE/DOCKET NUMBER:  02558B-059100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  13..18
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "t at positions 13-18 may be
;      OTHER INFORMATION:  present or absent"
US-08-884-029-9

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
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```
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 488
US-08-941-445A-30
; Sequence 30, Application US/08941445A
; Patent No. 6107060
;  GENERAL INFORMATION:
;    APPLICANT:  Keeling, Peter
;    APPLICANT:  Guan, Hanping
;    TITLE OF INVENTION:  Starch Encapsulation
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Greenlee, Winner and Sullivan, P.C.
;      STREET:  5370 Manhattan Circle
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/941,445A
;      FILING DATE:  30-SEP-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,855
;      FILING DATE:  30-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winner, Ellen P
;      REGISTRATION NUMBER:  28,547
;      REFERENCE/DOCKET NUMBER:  89-97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
US-08-941-445A-30

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 489
US-09-637-751A-7/c
; Sequence 7, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
;  APPLICANT:  Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Binary Encoded Sequence Tags
; Patent No. 6383754
;  FILE REFERENCE:  AGL 100
;  CURRENT APPLICATION NUMBER: US/09/637,751A
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
              || ||||||| ||||| |
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 490
US-09-545-225-9/c
; Sequence 9, Application US/09545225
; Patent No. 6410321
;   GENERAL INFORMATION:
;        APPLICANT: Lin, Ching-I Patsy
;                   Wallace, Robert Bruce
;                   Cossman, Jeffrey
;                   French, Cynthia
;        TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                            to Preserve RNA and DNA
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/545,225
;             FILING DATE: 07-Apr-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/884,029
;             FILING DATE: 27-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 02558B-059100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "t at positions 13-18 may be
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;            present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-225-9

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 491
US-09-619-103-24
; Sequence 24, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-24

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 492
US-09-370-541-14/c
; Sequence 14, Application US/09370541
; Patent No. 6639062
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT: Prakash, Thazha P
;  APPLICANT: Kawasaki, Andrew M
;  TITLE OF INVENTION: Aminoxxy-Modified Nucleosidic Compounds And Oligomeric
;  TITLE OF INVENTION: Compounds Prepared Therefrom
;  FILE REFERENCE: ISIS3993
;  CURRENT APPLICATION NUMBER: US/09/370,541
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: 09/130,973
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 09/016,520
;  EARLIER FILING DATE: 1998-01-30
;  EARLIER APPLICATION NUMBER: 60/037,143
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 09/344,260
;  EARLIER FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-370-541-14

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 493
US-10-125-295-9/c
; Sequence 9, Application US/10125295
; Patent No. 6686460
;  GENERAL INFORMATION:
;       APPLICANT: Lin, Ching-I Patsy
;                  Wallace, Robert Bruce
;                  Cossman, Jeffrey
;                  French, Cynthia
;       TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                           to Preserve RNA and DNA
;       NUMBER OF SEQUENCES: 9
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/125,295
;            FILING DATE: 17-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/545,225
;            FILING DATE: 07-Apr-2000
;            APPLICATION NUMBER: US 08/884,029
;            FILING DATE: 27-JUN-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Parent, Annette S.
;            REGISTRATION NUMBER: 42,058
;            REFERENCE/DOCKET NUMBER: 02558B-059100US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  13..18
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "t at positions 13-18 may be
;            present or absent"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-125-295-9

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 494
US-09-803-263-6
; Sequence 6, Application US/09803263
; Patent No. 6706476
; GENERAL INFORMATION:
;  APPLICANT: Thirstrup, Kenneth
;  TITLE OF INVENTION: A Process for Amplifying and Labeling Single Stranded cDNA by 5'
;  TITLE OF INVENTION:  Adapter Mediated Amplification
;  FILE REFERENCE: 674513-2003.1
;  CURRENT APPLICATION NUMBER: US/09/803,263
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Poly-a tail
US-09-803-263-6

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 495
US-09-803-263-7/c
; Sequence 7, Application US/09803263
; Patent No. 6706476
; GENERAL INFORMATION:
;  APPLICANT: Thirstrup, Kenneth
;  TITLE OF INVENTION: A Process for Amplifying and Labeling Single Stranded cDNA by 5'
;  TITLE OF INVENTION:  Adapter Mediated Amplification
;  FILE REFERENCE: 674513-2003.1
;  CURRENT APPLICATION NUMBER: US/09/803,263
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Complement of poly-a tail
US-09-803-263-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 496
US-09-994-311-7/c
; Sequence 7, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
              || ||||||| ||||| |
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 497
US-09-142-108C-28/c
; Sequence 28, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/09/142,108C
;  CURRENT FILING DATE:  1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-142-108C-28

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 498
US-09-809-545A-84/c
; Sequence 84, Application US/09809545A
; Patent No. 6800455
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  White, R. Tyler
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.017A
```

```
;  CURRENT APPLICATION NUMBER: US/09/809,545A
;  CURRENT FILING DATE:  2001-03-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-09-809-545A-84

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 499
US-10-352-704-12/c
; Sequence 12, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY: CDS
;             LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-352-704-12

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 500
US-10-352-704-18
; Sequence 18, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-352-704-18

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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```
Qy       3605 AAAAAAACAAAAACAGAA 3622
             ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 501
PCT-US94-05407-4/c
; Sequence 4, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-4

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
             ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 502
US-08-482-918-32/c
; Sequence 32, Application US/08482918
; Patent No. 6207417
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,918
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/33005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-482-918-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
             ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 503
US-09-224-681-32/c
; Sequence 32, Application US/09224681
; Patent No. 6207454
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Method for Enhancing the Efficiency of Gene
;    TITLE OF INVENTION:  Transfer with Stem Cell Factor (SCF) Polypeptide
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/224,681
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/005,893
;      FILING DATE:  12-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/449,653
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/35199
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-224-681-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 504
US-08-336-728A-32/c
; Sequence 32, Application US/08336728A
; Patent No. 6207802
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/336,728A
;      FILING DATE:  09-NOV-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/32956
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-336-728A-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 505
US-09-635-251-32/c
; Sequence 32, Application US/09635251
; Patent No. 6759215
;  GENERAL INFORMATION:
;       APPLICANT: Zsebo, Krisztina M.
;                  Bosselman, Robert A.
;                  Suggs, Sidney V.
;                  Martin, Francis H.
;       TITLE OF INVENTION: Stem Cell Factor
;       NUMBER OF SEQUENCES: 104
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;            STREET: 6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: United States of America
;            ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/635,251
;            FILING DATE: 07-Aug-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/449,182
;            FILING DATE: 24-MAY-1995
;            APPLICATION NUMBER: 08/172,329
;            FILING DATE: 21-DEC-1993
;            APPLICATION NUMBER: 07/982,255
;            FILING DATE: 25-NOV-1992
;            APPLICATION NUMBER: 07/684,535
;            FILING DATE: 04-OCT-1991
;            APPLICATION NUMBER: 07/589,701
;            FILING DATE: 01-OCT-1990
;            APPLICATION NUMBER: 07/573,616
;            FILING DATE: 24-AUG-1990
;            APPLICATION NUMBER: 07/537,198
;            FILING DATE: 11-JUN-1990
;            APPLICATION NUMBER: 07/422,383
;            FILING DATE: 16-OCT-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Clough, David W.
;            REGISTRATION NUMBER: 36,107
```

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;           REFERENCE/DOCKET NUMBER: 01017/32957A
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 312/474-6300
;           TELEFAX: 312/474-0448
;           TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 32:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 20 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-635-251-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 506
PCT-US94-05407-7
; Sequence 7, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 23;
  Best Local Similarity   83.3%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          6 AAAAAAAAAAAAAAAAAA 23


RESULT 507
PCT-US94-05407-8/c
; Sequence 8, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-8

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 23;
  Best Local Similarity   83.3%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 508
US-08-584-040-2554
; Sequence 2554, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
```

```
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2554:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2554

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 3.7e+02;
  Matches    0;  Conservative   13;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              :::::::::::::
Db          1 UUUUUUUUUUUUU 13


RESULT 509
US-09-371-772B-1078
; Sequence 1078, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1078

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 3.7e+02;
  Matches    0;  Conservative   13;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              :::::::::::::
Db          1 UUUUUUUUUUUUU 13


RESULT 510
US-09-685-664B-1078
; Sequence 1078, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1078

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 3.7e+02;
  Matches    0;  Conservative   13;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              :::::::::::::
Db          1 UUUUUUUUUUUUU 13


RESULT 511
US-09-129-603-4/c
; Sequence 4, Application US/09129603A
; Patent No. 6790944
; GENERAL INFORMATION:
;  APPLICANT: Ishiwata, Tetsuyoshi
;  APPLICANT: Sakurada, Mikiko
;  APPLICANT: Nishimura, Ayako
;  APPLICANT: Nakagawa, Satoshi
;  APPLICANT: Kuga, Tetsuro
;  APPLICANT: Nishi, Tatsunari
;  APPLICANT: No. 6790944ura, No. 6790944uo
;  APPLICANT: Sawada, Shigemasa
;  APPLICANT: Nagase, Takahiro
;  APPLICANT: Takei, Masami
;  TITLE OF INVENTION: No. 6790944el Protein
;  FILE REFERENCE: 766.25
;  CURRENT APPLICATION NUMBER: US/09/129,603A
;  CURRENT FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: PCT/JP97/04469
;  EARLIER FILING DATE: 1997-12-05
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: other nucleic acid from homo sapiens, synthesized
;   OTHER INFORMATION: DNA
US-09-129-603-4

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 512
US-09-090-672B-107/c
; Sequence 107, Application US/09090672B
; Patent No. 6828428
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
```

```
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-107

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         17 GAAAAAAAAAAAAAA 2


RESULT 513
US-08-584-040-2549/c
; Sequence 2549, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2549:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2549

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         17 AAAAAAAAAAAAAAAG 2


RESULT 514
US-09-371-772B-1073/c
; Sequence 1073, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1073

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         17 AAAAAAAAAAAAAAAG 2


RESULT 515
US-09-685-664B-1073/c
```

```
; Sequence 1073, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1073

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         17 AAAAAAAAAAAAAAAG 2


RESULT 516
US-08-584-040-2550/c
; Sequence 2550, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2550:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2550

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              ||||||| ||||| ||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 517
US-08-584-040-2551/c
; Sequence 2551, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2551:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
US-08-584-040-2551

  Query Match              0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||||.|||||.|
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 518
US-09-371-772B-1074/c
; Sequence 1074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1074

  Query Match              0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              |||||||.|||||.||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 519
US-09-371-772B-1075/c
; Sequence 1075, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1075

  Query Match              0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||||.|||||.|
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 520
US-09-685-664B-1074/c
; Sequence 1074, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relatec
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1074

  Query Match              0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAG 3620
              |||||||.|||||.||
Db         16 AAAAAAAAAAAAAAAG 1


RESULT 521
US-09-685-664B-1075/c
; Sequence 1075, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
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;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1075

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 522
US-08-373-124A-1060/c
; Sequence 1060, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1060:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-1060

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATA 2408
              ||| |||||| |||||
Db         17 AATGTATATATATATA 2


RESULT 523
US-08-435-628-1060/c
; Sequence 1060, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1060:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-1060

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATA 2408
              ||| |||||| |||||
Db         17 AATGTATATATATATA 2


RESULT 524
```

```
US-09-725-265-16/c
; Sequence 16, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-16

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 4.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 525
US-09-556-127-16/c
; Sequence 16, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-16

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 4.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 526
US-09-725-265-20/c
; Sequence 20, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 4.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTT 2


RESULT 527
US-09-556-127-20/c
; Sequence 20, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
```

```
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-20

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 4.1e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4510
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTT 2


RESULT 528
US-08-332-420-62/c
; Sequence 62, Application US/08332420
; Patent No. 5744300
;  GENERAL INFORMATION:
;    APPLICANT:  Maarten H.K. Linskens, et al.
;    TITLE OF INVENTION:  METHODS AND REAGENTS FOR THE
;    TITLE OF INVENTION:  IDENTIFICATION AND REGULATION
;    TITLE OF INVENTION:  OF SENESCENCE-RELATED GENES
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,420
;      FILING DATE:  October 31, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/235,180
;      FILING DATE:  April 29, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/041
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-332-420-62

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 39;
  Best Local Similarity   70.8%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1804 TGGAATGGAAAAGCAACTTCATTT 1827
              ||||||||   | || | |||| |
Db         24 TGGAATGGGTTAACATCATCATCT 1


RESULT 529
US-08-452-196A-3
; Sequence 3, Application US/08452196A
; Patent No. 5576427
;  GENERAL INFORMATION:
;    APPLICANT:  Cook, Philip D.
;    APPLICANT:  Delecki, Daniel J.
;    APPLICANT:  Guinosso, Charles
;    TITLE OF INVENTION:  ACYCLIC NUCLEOSIDE
;    TITLE OF INVENTION:  ANALOGS AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  SEQUENCES
;    TITLE OF INVENTION:  CONTAINING THEM
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Department
;      STREET:  9 Great Valley Parkway
;      CITY:  Malvern
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19355
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.4 MB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.0B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,196A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/040,326
;      FILING DATE:  30 March 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul E. Dupont
;      REGISTRATION NUMBER:  27,438
;      REFERENCE/DOCKET NUMBER:  2525
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215)889-6338
;      TELEFAX:  (215)889-8800
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Nucleic Acid
;      DESCRIPTION:
;    ANTI-SENSE:  yes
;    ORIGINAL SOURCE:  synthesized
;    FEATURE:
;      LOCATION:  14
;      OTHER INFORMATION:  8-[2,2-bis
;      OTHER INFORMATION:  (methoxymethyl)
;      OTHER INFORMATION:  propoxy]-9-
;      OTHER INFORMATION:  methyladenosine
US-08-452-196A-3

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAANA 15


RESULT 530
US-08-292-620A-363/c
; Sequence 363, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
```

```
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  363:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-363

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 4.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
              ||||||||  |||||
Db         15 GAAAAAAAAAAAAA 2


RESULT 531
US-09-071-845-363/c
; Sequence 363, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  363:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-363

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 4.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
              ||||||||  |||||
Db         15 GAAAAAAAAAAAAA 2


RESULT 532
US-08-893-204C-2/c
; Sequence 2, Application US/08893204C
; Patent No. 6043044
;  GENERAL INFORMATION:
;    APPLICANT:  Hudson, Perry B.
;    APPLICANT:  Hakky, Said I.
;    APPLICANT:  Meyer-Siegler, Katherine
;    APPLICANT:  Hakki, A-Hamid
;    TITLE OF INVENTION:  DIAGNOSTIC AND PROGNOSTIC MARKER
;    TITLE OF INVENTION:  FOR METASTATIC ADEMOCARCINOMA
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rosenberg, Klein & Bilker
;      STREET:  3444 Ellicott Center Drive, Suite 105
;      CITY:  Ellicott City
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  21043
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inches,
;      MEDIUM TYPE:  1.44Mb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows 7.0
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/893,204C
;      FILING DATE:  7/15/97
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rosenberg, Morton
;      REGISTRATION NUMBER:  26,049
;      REFERENCE/DOCKET NUMBER:  MR2493-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (410) 465-6678
;      TELEFAX:  (410) 461-3067
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  yes
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:  synthetic
;    PUBLICATION INFORMATION:
;      AUTHORS:  Katherine Meyer-Siegler
;      AUTHORS:  Perry Hudson
;      TITLE:  Enhanced Expression of Macrophage Migration
;      TITLE:  Inhibitory Factor in Prostatic Adenocarcinoma Metastases
;      JOURNAL:  Urology
;      VOLUME:  48
;      ISSUE:  3
;      PAGES:  448-452
;      DATE:  1996
;      RELEVANT RESIDUES IN SEQ ID NO:  2: FROM 1 TO 15
US-08-893-204C-2

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 4.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
             ||||||||  |||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 533
US-09-788-338-3/c
; Sequence 3, Application US/09788338
; Patent No. 6485916
; GENERAL INFORMATION:
;  APPLICANT: MURAMATSU, TAKAMICHI
;  APPLICANT:  FUJITA, TAKESHI
;  APPLICANT:  KIYAMA, MASAHARU
;  APPLICANT:  IRIE, TAKASHI
;  TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
;  TITLE OF INVENTION:  EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
;  TITLE OF INVENTION:  NUCLEIC ACID SAMPLES THEREBY
;  FILE REFERENCE: NIT-129-02
;  CURRENT APPLICATION NUMBER: US/09/788,338
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: 09/313,637
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: JP 10-153651
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-788-338-3

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 4.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
             |||||||  ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 534
US-09-300-958A-64/c
; Sequence 64, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-64

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 4.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
             |||||||  ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 535
US-09-090-672B-106/c
; Sequence 106, Application US/09090672B
; Patent No. 6828428
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
```

```
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  106:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-106

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 4.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 536
US-09-090-672B-105/c
; Sequence 105, Application US/09090672B
; Patent No. 6828428
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-105

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 4.8e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         14 AAAAAAAAAAAAAC 1


RESULT 537
US-08-937-067-17/c
; Sequence 17, Application US/08937067
; Patent No. 6433155
;  GENERAL INFORMATION:
;    APPLICANT:  Umansky, Samuil
;    APPLICANT:  Melkonyan, Hovsep
;    TITLE OF INVENTION:  A FAMILY OF GENES ENCODING
;    TITLE OF INVENTION:  APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
;    TITLE OF INVENTION:  METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,067
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lehnhardt, Susan K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  23647-20018.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-937-067-17

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 4.8e+02;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              : ||||||| ||||| |
Db         17 SNAAAAAAAAAAAAAAA 1


RESULT 538
US-09-437-076-2/c
; Sequence 2, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
;  APPLICANT: Barber-Guillem, Emilio
;  APPLICANT: Nelson, M. Bud
;  APPLICANT: Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  CURRENT APPLICATION NUMBER: US/09/437,076
;  CURRENT FILING DATE: 1999-11-09
;  EARLIER APPLICATION NUMBER:
```

```
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: Word for Windows
; SEQ ID NO 2
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    NAME/KEY:
;    LOCATION:
;    OTHER INFORMATION: synthesized
US-09-437-076-2

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 4.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         16 AAAAAAAAAAAAAC 3


RESULT 539
US-09-904-744-2/c
; Sequence 2, Application US/09904744
; Patent No. 6828142
; GENERAL INFORMATION:
;  APPLICANT: Barbera-Guillem, Emilio
;  APPLICANT:  Nelson, M. Bud
;  APPLICANT:  Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  TITLE OF INVENTION:  dendrimers in a signal amplification system
;  FILE REFERENCE: B-73
;  CURRENT APPLICATION NUMBER: US/09/904,744
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/437076
;  PRIOR FILING DATE: 1999-11-09
;  PRIOR APPLICATION NUMBER: 60/107828
;  PRIOR FILING DATE: 1998-11-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthesized
US-09-904-744-2

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 4.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| ||||||
Db         16 AAAAAAAAAAAAAC 3


RESULT 540
US-09-130-079-1
; Sequence 1, Application US/09130079
; Patent No. 6270966
;  GENERAL INFORMATION:
;     APPLICANT:  The United States of America, as represented by the
;     APPLICANT:  Secretary, Department of Health and Human Services
;     TITLE OF INVENTION:  RESTRICTION DISPLAY (RD-PCR) OF DIFFERENTIALLY EXPRESS
;     NUMBER OF SEQUENCES:  25
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Knobbe, Martens, Olson & Bear
;       STREET:  620 Newport Center Drive, 16th Floor
;       CITY:  Newport Beach
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92660
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/130,079
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/011/379
;       FILING DATE:  09-FEB-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kirkpatrick, Anita M
;       REGISTRATION NUMBER:  32,617
;       REFERENCE/DOCKET NUMBER:  NIH108.001VPC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-235-8550
;       TELEFAX:  619-235-0176
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  mRNA
US-09-130-079-1

  Query Match             0.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 4.9e+02;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              :||||||| ||||| | |
Db          2 BAAAAAAAAAAAAAAAAA 19


RESULT 541
US-08-851-843A-132/c
; Sequence 132, Application US/08851843A
; Patent No. 6093809
;  GENERAL INFORMATION:
;     APPLICANT:  Cech, Thomas R.
;     APPLICANT:  Lingner, Joachim
;     APPLICANT:  Nakamura, Toru
;     APPLICANT:  Chapman, Karen B.
;     APPLICANT:  Morin, Gregg B.
;     APPLICANT:  Harley, Calvin
;     APPLICANT:  Andrews, William H.
;     TITLE OF INVENTION:  No. 6093809el Telomerase
;     NUMBER OF SEQUENCES:  225
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Center, 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  United States of America
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/851,843A
;       FILING DATE:  06-MAY-1997
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/846,017
;       FILING DATE:  25-APR-1997
;       CLASSIFICATION:
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-851-843A-132

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 542
US-09-250-075-5/c
; Sequence 5, Application US/09250075
; Patent No. 6207819
; GENERAL INFORMATION:
;  APPLICANT:  Manoharan, Muthiah
;  APPLICANT:  Maier, Martin A
;  TITLE OF INVENTION:  Compounds Processes And Intermediates For Synthesis Of
;  TITLE OF INVENTION:  Mixed Backbone Oligomeric Compounds
;  FILE REFERENCE:  ISIS3299
;  CURRENT APPLICATION NUMBER: US/09/250,075
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: 2'-methoxyethoxy (MOE); modified linkage
;   OTHER INFORMATION: Description of Artificial Sequence:  No. 6207819el
;   OTHER INFORMATION: Sequence
US-09-250-075-5

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 543
US-08-854-050-132/c
; Sequence 132, Application US/08854050
; Patent No. 6261836
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6261836el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/854,050
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/851,843
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-854-050-132

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 544
US-09-430-323-132/c
; Sequence 132, Application US/09430323
; Patent No. 6309867
;  GENERAL INFORMATION:
;       APPLICANT: Cech, Thomas R.
;                  Lingner, Joachim
;                  Nakamura, Toru
;                  Chapman, Karen B.
```

```
;                    Morin, Gregg B.
;                    Harley, Calvin
;                    Andrews, William H.
;         TITLE OF INVENTION: No. 6309867el Telomerase
;         NUMBER OF SEQUENCES: 225
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Townsend and Townsend and Crew LLP
;              STREET: Two Embarcadero Center, 8th Floor
;              CITY: San Francisco
;              STATE: California
;              COUNTRY: United States of America
;              ZIP: 94111
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/430,323
;              FILING DATE: 29-Oct-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/854,050
;              FILING DATE: 09-MAY-1997
;              APPLICATION NUMBER: US 08/851,843
;              FILING DATE: 06-MAY-1997
;              APPLICATION NUMBER: US 08/846,017
;              FILING DATE: 25-APR-1997
;              APPLICATION NUMBER: US 08/844,419
;              FILING DATE: 18-APR-1997
;              APPLICATION NUMBER: US 08/724,643
;              FILING DATE: 01-OCT-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Apple,  Randolph T.
;              REGISTRATION NUMBER: 36,429
;              REFERENCE/DOCKET NUMBER: 015389-002930US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 132:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 17 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-430-323-132

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 545
US-09-619-103-23
; Sequence 23, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-23

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 546
US-09-726-096A-5/c
; Sequence 5, Application US/09726096A
; Patent No. 6462184
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT:  Maier, Martin A.
;  TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back
;  TITLE OF INVENTION:  Oligomeric Compounds
;  FILE REFERENCE: ISIS4528
;  CURRENT APPLICATION NUMBER: US/09/726,096A
;  CURRENT FILING DATE:  2000-11-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(19)
;   OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
;   OTHER INFORMATION: internucleoside linkage
US-09-726-096A-5

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 547
US-09-766-253-132/c
; Sequence 132, Application US/09766253
; Patent No. 6808880
;   GENERAL INFORMATION:
;         APPLICANT: Cech, Thomas R.
;                    Lingner, Joachim
;                    Nakamura, Toru
;                    Chapman, Karen B.
;                    Morin, Gregg B.
;                    Harley, Calvin
;                    Andrews, William H.
;         TITLE OF INVENTION: No. 6808880el Telomerase
;         NUMBER OF SEQUENCES: 171
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Townsend and Townsend and Crew LLP
;              STREET: Two Embarcadero Center, 8th Floor
;              CITY: San Francisco
;              STATE: California
;              COUNTRY: United States of America
```

```
;           ZIP: 94111
;         COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/766,253
;           FILING DATE: 19-Jan-2001
;           CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/846,017
;           FILING DATE: 1997-04-25
;           APPLICATION NUMBER: US 08/724,643
;           FILING DATE: 01-OCT-1996
;         ATTORNEY/AGENT INFORMATION:
;           NAME: Apple,  Randolph T.
;           REGISTRATION NUMBER: 36,429
;           REFERENCE/DOCKET NUMBER: 015389-002920US
;         TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (415) 576-0200
;           TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 132:
;         SEQUENCE CHARACTERISTICS:
;           LENGTH: 17 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-766-253-132

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 548
US-08-584-040-2548/c
; Sequence 2548, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2548:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2548

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| || |
Db         17 AAAAAAAAAAAAAAGTA 1


RESULT 549
US-09-371-772B-1072/c
; Sequence 1072, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1072
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1072

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| || |
Db         17 AAAAAAAAAAAAAAGTA 1


RESULT 550
US-09-685-664B-1072/c
; Sequence 1072, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
```

```
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1072
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1072

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| || |
Db         17 AAAAAAAAAAAAAAGTA 1


RESULT 551
US-08-233-130A-10
; Sequence 10, Application US/08233130A
; Patent No. 5587300
;  GENERAL INFORMATION:
;    APPLICANT:  Malter, James S.
;    TITLE OF INVENTION:  Method to Increase Regulatory Molecule
;    TITLE OF INVENTION:  Production
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  203 Textile Buildling, 119 No. 5587300th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,130A
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  119.00010101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1220
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-233-130A-10

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1875 ATGTATGAATGTAAGGA 1891
              ||||||| ||||| | |
Db          1 ATGTATGTATGTATGTA 17


RESULT 552
US-08-233-130A-11/c
; Sequence 11, Application US/08233130A
; Patent No. 5587300
;  GENERAL INFORMATION:
;    APPLICANT:  Malter, James S.
;    TITLE OF INVENTION:  Method to Increase Regulatory Molecule
;    TITLE OF INVENTION:  Production
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch, Gebhardt & Schwappach, P.A.
;      STREET:  203 Textile Buildling, 119 No. 5587300th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,130A
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  119.00010101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1220
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-233-130A-11

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1875 ATGTATGAATGTAAGGA 1891
              ||||||| ||||| | |
Db         17 ATGTATGTATGTATGTA 1


RESULT 553
US-09-637-751A-5/c
; Sequence 5, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
;  APPLICANT:  Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Binary Encoded Sequence Tags
; Patent No. 6383754
;  FILE REFERENCE:  AGL 100
;  CURRENT APPLICATION NUMBER: US/09/637,751A
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
```

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; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-5

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         18 GCAAAAAAAAAAAAAAA 2


RESULT 554
US-09-994-311-5/c
; Sequence 5, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-5

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              | ||||||| ||||| |
Db         18 GCAAAAAAAAAAAAAAA 2


RESULT 555
US-09-142-108C-29/c
; Sequence 29, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/09/142,108C
;  CURRENT FILING DATE:  1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-142-108C-29

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 556
PCT-US91-03680-73/c
; Sequence 73, Application PC/TUS9103680
;  GENERAL INFORMATION:
;    APPLICANT:  Matteucci, Mark D.
;    APPLICANT:  Krawczyk, Steven
;    TITLE OF INVENTION:  SEQUENCE-SPECIFIC NONPHOTOACTIVATED
;    TITLE OF INVENTION:  CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
;    TITLE OF INVENTION:  DUPLEX DNA
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/03680
;      FILING DATE:  19910524
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  4610-0011.40
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  5
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "5-methylcytosine"
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  18
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N4,N4-ethanocytosine"
PCT-US91-03680-73

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| | ||
Db         17 AAAAAAAAAAAAGAAAA 1
```

```
RESULT 557
US-09-142-108C-27/c
; Sequence 27, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/09/142,108C
;  CURRENT FILING DATE:  1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-142-108C-27

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| | |
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 558
PCT-US91-03680-74/c
; Sequence 74, Application PC/TUS9103680
;  GENERAL INFORMATION:
;    APPLICANT:  Matteucci, Mark D.
;    APPLICANT:  Krawczyk, Steven
;    TITLE OF INVENTION:  SEQUENCE-SPECIFIC NONPHOTOACTIVATED
;    TITLE OF INVENTION:  CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
;    TITLE OF INVENTION:  DUPLEX DNA
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/03680
;      FILING DATE:  19910524
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  4610-0011.40
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  5
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  18
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N4,N4-ethanocytosine"
PCT-US91-03680-74

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAA 3622
              |||||| ||||| | ||
Db         17 AAAAAAAAAAAAKAAAA 1


RESULT 559
US-09-725-265-15/c
; Sequence 15, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTGT 1


RESULT 560
US-09-725-265-19/c
; Sequence 19, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
```

```
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-19

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTTCT 1


RESULT 561
US-09-556-127-15/c
; Sequence 15, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-15

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTTGT 1


RESULT 562
US-09-556-127-19/c
; Sequence 19, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/09/556,127
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-19

  Query Match             0.3%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+02;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||| |
Db         17 TATATATTTTTTTTTCT 1


RESULT 563
US-08-832-021-33
; Sequence 33, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
;  APPLICANT: Combates, N.
;  APPLICANT: Pardinas, J.
;  APPLICANT: Parimoo, S.
;  APPLICANT: Prouty, S.
;  APPLICANT: Stenn, K.
;  TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
;  FILE REFERENCE: JBP-382
;  CURRENT APPLICATION NUMBER: US/08/832,021
;  CURRENT FILING DATE: 1997-04-02
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-33

  Query Match             0.3%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTT 4512
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 564
US-09-390-324B-2/c
```

```
; Sequence 2, Application US/09390324B
; Patent No. 6342376
; GENERAL INFORMATION:
;  APPLICANT: Kozian, Detlef
;  APPLICANT:  Reuner, Birgit
;  TITLE OF INVENTION: Two-color differential display as a method for
;  TITLE OF INVENTION:  detecting regulated genes
;  FILE REFERENCE: 2481-1635
;  CURRENT APPLICATION NUMBER: US/09/390,324B
;  CURRENT FILING DATE:  1999-09-07
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-09-390-324B-2

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :||||||| ||||| |
Db         16 BAAAAAAAAAAAAAAA 1


RESULT 565
US-10-015-593-2/c
; Sequence 2, Application US/10015593
; Patent No. 6645741
; GENERAL INFORMATION:
;  APPLICANT: Kozian, Detlef
;  APPLICANT:  Reuner, Birgit
;  TITLE OF INVENTION: Two-color differential display as a method for
;  TITLE OF INVENTION:  detecting regulated genes
;  FILE REFERENCE: 2481-1635
;  CURRENT APPLICATION NUMBER: US/10/015,593
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/390,324
;  PRIOR FILING DATE: 2001-05-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-10-015-593-2

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :||||||| ||||| |
Db         16 BAAAAAAAAAAAAAAA 1


RESULT 566
US-08-584-040-2555
; Sequence 2555, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2555:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-2555

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 5.6e+02;
  Matches    0;  Conservative   12;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTT 4512
              ::::::::::::
Db          1 UUUUUUUUUUUU 12


RESULT 567
US-09-371-772B-1079
; Sequence 1079, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
```

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;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-1079

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 5.6e+02;
  Matches    0;  Conservative   12;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTT 4512
              ::::::::::::
Db          1 UUUUUUUUUUUU 12


RESULT 568
US-09-685-664B-1079
; Sequence 1079, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-1079

  Query Match             0.3%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 5.6e+02;
  Matches    0;  Conservative   12;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTT 4512
              ::::::::::::
Db          1 UUUUUUUUUUUU 12


RESULT 569
US-10-103-614A-4
; Sequence 4, Application US/10103614A
; Patent No. 6716585
; GENERAL INFORMATION:
;  APPLICANT: SALMAN AL-MAHMOOD
;  TITLE OF INVENTION: METHOD FOR IDENTIFYING NOVEL GENES INVOLVED IN THE
;  TITLE OF INVENTION:  REGULATION OF ANGIOGENESIS, STUDY OF SAID GENES AND USE
;  TITLE OF INVENTION:  THEREOF FOR THERAPEUTIC PURPOSES
;  FILE REFERENCE: 1071-02
;  CURRENT APPLICATION NUMBER: US/10/103,614A
;  CURRENT FILING DATE:  2002-08-22
;  PRIOR APPLICATION NUMBER: PCT/FR00/02607
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: FR 99/11790
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   NAME/KEY: modified_base
;   LOCATION: (1)
;   OTHER INFORMATION: a, t, c or g
;   NAME/KEY: modified_base
;   LOCATION: (19)
;   OTHER INFORMATION: a, t, c or g
US-10-103-614A-4

  Query Match             0.3%;  Score 12;  DB 1;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              :|||||| ||||| |
Db          2 VAAAAAAAAAAAAAAA 17


RESULT 570
US-09-120-853-4
; Sequence 4, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
;  APPLICANT: Kamiya, Kinya
;  APPLICANT: Matsuda, Yoko
;  APPLICANT: Uchida, Kiyoshi
;  TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
;  FILE REFERENCE: 07898/030001
;  CURRENT APPLICATION NUMBER: US/09/120,853
;  CURRENT FILING DATE: 1998-07-21
;  EARLIER APPLICATION NUMBER: JP 213838/1997
;  EARLIER FILING DATE: 1997-07-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Artificial
;   OTHER INFORMATION: nucleic acid sequence
US-09-120-853-4

  Query Match             0.3%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+02;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3384 AGAAGTAGGAGGAAACAGTT 3403
              || || | ||||||| || |
Db          1 AGCAGAAAGAGGAAAGAGGT 20


RESULT 571
US-08-452-196A-6
; Sequence 6, Application US/08452196A
; Patent No. 5576427
;  GENERAL INFORMATION:
;    APPLICANT:  Cook, Philip D.
;    APPLICANT:  Delecki, Daniel J.
;    APPLICANT:  Guinosso, Charles
;    TITLE OF INVENTION:  ACYCLIC NUCLEOSIDE
;    TITLE OF INVENTION:  ANALOGS AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  SEQUENCES
;    TITLE OF INVENTION:  CONTAINING THEM
;    NUMBER OF SEQUENCES:  8
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patent Department
;      STREET:  9 Great Valley Parkway
;      CITY:  Malvern
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19355
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.4 MB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.0B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,196A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/040,326
;      FILING DATE:  30 March 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul E. Dupont
;      REGISTRATION NUMBER:  27,438
;      REFERENCE/DOCKET NUMBER:  2525
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215)889-6338
;      TELEFAX:  (215)889-8800
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Nucleic Acid
;      DESCRIPTION:
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:  synthesized
US-08-452-196A-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 572
US-07-971-978-1/c
; Sequence 1, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  6-aza-thymidine substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
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;      LOCATION:  14
;      OTHER INFORMATION:  6-aza-thymidine substitution
US-07-971-978-1

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 573
US-08-756-728A-2
; Sequence 2, Application US/08756728A
; Patent No. 5821354
;  GENERAL INFORMATION:
;    APPLICANT:  Leclerc, Guy
;    APPLICANT:  Martel, Remi
;    TITLE OF INVENTION:  RADIOLABELED DNA OLIGONUCLEOTIDE, METHOD
;    TITLE OF INVENTION:  OF PREPARATION AND THERAPEUTIC USES THEREOF
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,728A
;      FILING DATE:  26-NOV-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1398-1-001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "PRIMER"
;    HYPOTHETICAL:  NO
US-08-756-728A-2

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 574
US-08-663-918-3/c
; Sequence 3, Application US/08663918
; Patent No. 5824793
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeffe
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide N3 {symbol 174 \f "Syt
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/663,918
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-663-918-3

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 575
US-08-663-918-4
; Sequence 4, Application US/08663918
; Patent No. 5824793
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeffe
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide N3 {symbol 174 \f "Syt
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/663,918
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-663-918-4

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 576
US-08-292-620A-361/c
; Sequence 361, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  361:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-361

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 577
US-08-292-620A-362/c
; Sequence 362, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  362:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-362
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```
  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 578
US-08-771-789-3/c
; Sequence 3, Application US/08771789
; Patent No. 5859233
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein
;    APPLICANT:  Karen Fearon
;    APPLICANT:  Sergei Gryaznov
;    APPLICANT:  Sarah McCurdy
;    APPLICANT:  Jeffery Nelson
;    APPLICANT:  Ronald G. Schultz
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide
;    TITLE OF INVENTION:  N3 {symbol 174 \f "Symbol" \s 12|}P5  Phosphoramidates
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,789
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/663,918
;      FILING DATE:  14-JUN-1996
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-771-789-3

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 579
US-08-771-789-4
; Sequence 4, Application US/08771789
; Patent No. 5859233
;  GENERAL INFORMATION:
;    APPLICANT:  Bernard Hirschbein
;    APPLICANT:  Karen Fearon
;    APPLICANT:  Sergei Gryaznov
;    APPLICANT:  Sarah McCurdy
;    APPLICANT:  Jeffery Nelson
;    APPLICANT:  Ronald G. Schultz
;    TITLE OF INVENTION:  Solid Phase Synthesis of Oligonucleotide
;    TITLE OF INVENTION:  N3 {symbol 174 \f "Symbol" \s 12|}P5  Phosphoramidates
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatable
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  Microsoft Word for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,789
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/663,918
;      FILING DATE:  14-JUN-1996
;      APPLICATION NUMBER:  08/603,566
;      FILING DATE:  21-FEB-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  LYNX-035/01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-771-789-4

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 580
US-08-358-556A-10/c
; Sequence 10, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..15
US-08-358-556A-10

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 581
US-08-358-556A-16
; Sequence 16, Application US/08358556A
; Patent No. 5869643
;  GENERAL INFORMATION:
;    APPLICANT:  Chatelain, Francois
;    APPLICANT:  Kumarev, Viktor
;    TITLE OF INVENTION:  Process for Preparing Polynucleotides on
;    TITLE OF INVENTION:  a Solid Support and Apparatus Permitting its
;    TITLE OF INVENTION:  Implementation
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh St. N.W.
;      CITY:  Washington D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,556A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9315164
;      FILING DATE:  16-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10577/P58418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-6666
;      TELEFAX:  (202) 393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..15
US-08-358-556A-16

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 582
US-08-922-170B-5/c
; Sequence 5, Application US/08922170B
; Patent No. 5968822
;  GENERAL INFORMATION:
;    APPLICANT:  Iris Pecker, Israel Vlodavsky and Elena
;    APPLICANT:  Feinstein
;    TITLE OF INVENTION:  POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
;    TITLE OF INVENTION:  HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
;    TITLE OF INVENTION:  SAME IN TRANSDUCED CELLS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark M. Friedman c/o Robert Sheinbein
;      STREET:  2940 Birchtree lane
;      CITY:  Silver Spring
;      STATE:  Maryland
;      COUNTRY:  United States of America
;      ZIP:  20906
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 megabyte, 3.5" microdisk
;      COMPUTER:  Twinhead* Slimnote-890TX
;      OPERATING SYSTEM:  MS DOS version 6.2,
;      OPERATING SYSTEM:  Windows version 3.11
;      SOFTWARE:  Word for Windows version 2.0 converted to
;      SOFTWARE:  an ASCI file
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/922,170B
;      FILING DATE:  2 SEP 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Friedmam, Mark M.
;      REGISTRATION NUMBER:  33,883
;      REFERENCE/DOCKET NUMBER:  910/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  972-3-5625553
;      TELEFAX:  972-3-5625554
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
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```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-922-170B-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 583
US-08-863-639A-5
; Sequence 5, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 584
US-08-863-639A-9/c
; Sequence 9, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-9

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 585
US-08-693-831-1/c
; Sequence 1, Application US/08693831
; Patent No. 6017700
; GENERAL INFORMATION:
;  APPLICANT: Horn, Thomas
;  APPLICANT: Letsinger, Robert L.
;  APPLICANT: Balasubramanian, Tanjore N.
;  TITLE OF INVENTION: CATIONIC OLIGONUCLEOTIDES, AND RELATED METHODS OF
;  TITLE OF INVENTION: SYNTHESIS AND USE
;  FILE REFERENCE: 1117.002
;  CURRENT APPLICATION NUMBER: US/08/693,831
;  CURRENT FILING DATE: 1996-07-31
;  EARLIER APPLICATION NUMBER: US 08/693,831
;  EARLIER FILING DATE: 1996-07-31
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: Description of Artificial Sequence: poly-T
US-08-693-831-1

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 586
US-09-183-619-4/c
; Sequence 4, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
;  APPLICANT: DELLINGER, DOUGLAS J.
;  APPLICANT: DAHM, SUEANN C.
;  APPLICANT: ILSLEY, DIANE D.
;  APPLICANT: ACH, ROBERT A.
;  APPLICANT: TROLL, MARK A.
;  TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
;  FILE REFERENCE: 10981619-1
;  CURRENT APPLICATION NUMBER: US/09/183,619
;  CURRENT FILING DATE: 1998-10-30
;  EARLIER APPLICATION NUMBER: 08/735,381
;  EARLIER FILING DATE: 1996-10-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;    LENGTH: 15
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Reporter probe
US-09-183-619-4

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 587
US-09-071-845-361/c
; Sequence 361, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  361:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-361

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 588
US-09-071-845-362/c
; Sequence 362, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
```

```
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  362:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-362

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 589
US-09-167-375-1
; Sequence 1, Application US/09167375B
; Patent No. 6291438
; GENERAL INFORMATION:
;  APPLICANT: Jui H. Wang
;  TITLE OF INVENTION: Antiviral anticancer poly-substituted phenyl derivatized oligorib
;  TITLE OF INVENTION: methods for their use.
;  FILE REFERENCE: WNGJ 2002 (CIP-1)
;  CURRENT APPLICATION NUMBER: US/09/167,375B
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Retroviral reverse transcriptase inhibitor
US-09-167-375-1

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 590
US-08-150-156A-19/c
; Sequence 19, Application US/08150156A
; Patent No. 6357163
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;    TITLE OF INVENTION:  DIAGNOSTICS AND ANALYTICAL PROCEDURES
;    NUMBER OF SEQUENCES:  40
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/150,156A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0986/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0987/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0510/92
;      FILING DATE:  15-APR-1992
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      DOCUMENT NUMBER:  WO PCT/EP92/01220
;      FILING DATE:  22-MAY-1992
US-08-150-156A-19

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 591
US-08-150-156A-20
; Sequence 20, Application US/08150156A
; Patent No. 6357163
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;    TITLE OF INVENTION:  DIAGNOSTICS AND ANALYTICAL PROCEDURES
;    NUMBER OF SEQUENCES:  40
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/150,156A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0986/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0987/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0510/92
;      FILING DATE:  15-APR-1992
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      DOCUMENT NUMBER:  WO PCT/EP92/01220
;      FILING DATE:  22-MAY-1992
US-08-150-156A-20

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
```

```
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 592
US-08-108-591B-17/c
; Sequence 17, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/08/108,591B
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-17

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 593
US-08-108-591B-18
; Sequence 18, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/08/108,591B
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-18

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 594
US-09-619-103-21
; Sequence 21, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-21

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 595
US-09-300-958A-68/c
; Sequence 68, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-68

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 596
US-08-988-024C-9/c
; Sequence 9, Application US/08988024C
```

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; Patent No. 6635452
; GENERAL INFORMATION:
;  APPLICANT: Monforte, Joseph A.
;  APPLICANT:  Becker, Christopher H.
;  APPLICANT:  Pollart, Daniel J.
;  APPLICANT:  Shaler, Thomas A.
;  TITLE OF INVENTION: Releasable No. 6635452volatile Mass-Label Molecules
;  FILE REFERENCE: 24736-2057
;  CURRENT APPLICATION NUMBER: US/08/988,024C
;  CURRENT FILING DATE:  1997-12-10
;  PRIOR APPLICATION NUMBER: US 60/033,037
;  PRIOR FILING DATE: 1996-12-10
;  PRIOR APPLICATION NUMBER: US 60/046,719
;  PRIOR FILING DATE: 1997-05-16
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-08-988-024C-9

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 597
US-09-435-739-5/c
; Sequence 5, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky, Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 00/20454
;  CURRENT APPLICATION NUMBER: US/09/435,739
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
US-09-435-739-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 598
US-10-091-231-2/c
; Sequence 2, Application US/10091231
; Patent No. 6664388
; GENERAL INFORMATION:
;  APPLICANT: NELSON, Jeffrey S.
;  TITLE OF INVENTION: REAGENTS FOR OLIGONUCLEOTIDE CLEAVAGE AND DEPROTECTION
;  FILE REFERENCE: 4688US
;  CURRENT APPLICATION NUMBER: US/10/091,231
;  CURRENT FILING DATE:  2002-03-04
;  PRIOR APPLICATION NUMBER: US 60/274,309
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-091-231-2

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 599
US-09-930-218-5/c
; Sequence 5, Application US/09930218
; Patent No. 6677137
; GENERAL INFORMATION:
;  APPLICANT: goldshmidt, orit
;  APPLICANT:  pecker, iris
;  APPLICANT:  vlodavsky, israel
;  APPLICANT:  israel, michal
;  TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HA
;  TITLE OF INVENTION:  HEPARANASE ACTIVITY
;  FILE REFERENCE: 01/22335
;  CURRENT APPLICATION NUMBER: US/09/930,218
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/666,390
;  PRIOR FILING DATE: 2000-09-20
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide
US-09-930-218-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 600
US-08-468-719A-17/c
; Sequence 17, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf H.
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
;  FILE REFERENCE: ISPS-1999
;  CURRENT APPLICATION NUMBER: US/08/468,719A
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
```

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;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-17

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 601
US-08-468-719A-18
; Sequence 18, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf H.
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
;  FILE REFERENCE: ISPS-1999
;  CURRENT APPLICATION NUMBER: US/08/468,719A
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-18

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 602
US-08-462-977B-17/c
; Sequence 17, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS-1993
;  CURRENT APPLICATION NUMBER: US/08/462,977B
;  CURRENT FILING DATE:  1995-06-05
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-17

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 603
US-08-462-977B-18
; Sequence 18, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS-1993
;  CURRENT APPLICATION NUMBER: US/08/462,977B
;  CURRENT FILING DATE:  1995-06-05
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-18

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 604
US-09-988-113-5/c
; Sequence 5, Application US/09988113
; Patent No. 6790658
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY A
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 01/22781
;  CURRENT APPLICATION NUMBER: US/09/988,113
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: US 09/776,874
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US09/258,892
;  PRIOR FILING DATE: 1999-03-01
;  PRIOR APPLICATION NUMBER: PCT/US98/17954
;  PRIOR FILING DATE: 1998-08-31
;  PRIOR APPLICATION NUMBER: US 09/109,386
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 08/922,170
;  PRIOR FILING DATE: 1997-09-02
```

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;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 605
US-10-352-704-10/c
; Sequence 10, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..15
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-352-704-10

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 606
US-10-352-704-16
; Sequence 16, Application US/10352704
; Patent No. 6825339
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..15
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-352-704-16

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
```

```
Db          1 AAAAAAAAAAAAAAA 15


RESULT 607
US-09-475-947A-164/c
; Sequence 164, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
;  APPLICANT: Garner, Harold R.
;  APPLICANT:  Wren, Jonathan D.
;  APPLICANT:  Minna, John D.
;  TITLE OF INVENTION: Polymorphic Repeats in Human Genes
;  FILE REFERENCE: UTSD0667
;  CURRENT APPLICATION NUMBER: US/09/475,947A
;  CURRENT FILING DATE:  1999-12-31
;  NUMBER OF SEQ ID NOS: 346
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: human
US-09-475-947A-164

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 5.9e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3968 AAACAATAAAAACAA 3982
              ||| ||||||||  ||
Db         15 AAAAAATAAAAAAAA 1


RESULT 608
US-07-971-978-36/c
; Sequence 36, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
```

```
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  15
;       OTHER INFORMATION:  5-fluoro-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
US-07-971-978-36

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 609
US-07-971-978-42/c
; Sequence 42, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;     APPLICANT:  Cook and Sanghvi
;     TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;     TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;     TITLE OF INVENTION:  Gene Expression
;     NUMBER OF SEQUENCES:  65
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;       ADDRESSEE:  No. 5614617ris
;       STREET:  One Liberty Place - 46th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  U.S.A.
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/971,978
;       FILING DATE:  February 18, 1993
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/558,806
;       FILING DATE:  July 27, 1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Joseph Lucci
;       REGISTRATION NUMBER:  33,307
;       REFERENCE/DOCKET NUMBER:  ISIS-0333
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-568-3100
;       TELEFAX:  215-568-3439
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  1
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  2
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  3
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  5
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  6
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  7
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  8
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  9
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  10
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  11
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  12
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  13
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  14
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  15
;       OTHER INFORMATION:  5-bromo-2'-deoxyuridine
;       OTHER INFORMATION:  substitution
US-07-971-978-42

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2
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RESULT 610
US-07-971-978-60/c
; Sequence 60, Application US/07971978
; Patent No. 5614617
;  GENERAL INFORMATION:
;    APPLICANT:  Cook and Sanghvi
;    TITLE OF INVENTION:  Nuclease Resistant, Pyrimidine
;    TITLE OF INVENTION:  Modified Oligonucleotides that Detect and Modulate
;    TITLE OF INVENTION:  Gene Expression
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5614617ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,978
;      FILING DATE:  February 18, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/558,806
;      FILING DATE:  July 27, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph Lucci
;      REGISTRATION NUMBER:  33,307
;      REFERENCE/DOCKET NUMBER:  ISIS-0333
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  2
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  6
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  7
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  9
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  10
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  12
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  13
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  14
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  15
;      OTHER INFORMATION:  5-iodo-2'-deoxyuridine
;      OTHER INFORMATION:  substitution
US-07-971-978-60

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
                ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 611
US-08-415-370-2/c
; Sequence 2, Application US/08415370
; Patent No. 5801155
;  GENERAL INFORMATION:
;    APPLICANT:  Kutyavin, Igor V.
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Gamper, Howard B.
;    APPLICANT:  Meyer, Jr., Rich B.
;    TITLE OF INVENTION:  COVALENTLY LINKED OLIGONUCLEOTIDE MINOR
;    TITLE OF INVENTION:  GROOVE BINDER CONJUGATES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KLEIN & SZEKERES
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
```

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;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92715
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/415,370
;       FILING DATE:  03-APR-1995
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Szekeres, Gabor L.
;       REGISTRATION NUMBER:  28,675
;       REFERENCE/DOCKET NUMBER:  491-09-PA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  714-854-5502
;       TELEFAX:  714-854-4897
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-415-370-2

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 612
US-08-687-551-15/c
; Sequence 15, Application US/08687551
; Patent No. 5856435
;  GENERAL INFORMATION:
;    APPLICANT:  BAZILE, Didier
;    APPLICANT:  EMILE, Carole
;    APPLICANT:  HELENE, Claude
;    APPLICANT:  SPENLEHAUER, Gilles
;    TITLE OF INVENTION:  NUCLEIC ACID-CONTAINING COMPOSITION, ITS
;    TITLE OF INVENTION:  PREPARATION AND USE
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Rd. 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/687,551
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/01381
;      FILING DATE:  08-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/FR95/00098
;      FILING DATE:  27-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith Ph.D., Julie K.
;      REGISTRATION NUMBER:  38,619
;      REFERENCE/DOCKET NUMBER:  ST94007-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610)454-3839
;      TELEFAX:  (610)454-3808
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
US-08-687-551-15

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 613
US-09-141-764-2/c
; Sequence 2, Application US/09141764
; Patent No. 6084102
;  GENERAL INFORMATION:
;    APPLICANT:  Kutyavin, Igor V.
;    APPLICANT:  Lukhtanov, Eugeny A.
;    APPLICANT:  Gamper, Howard B.
;    APPLICANT:  Meyer, Jr., Rich B.
;    TITLE OF INVENTION:  COVALENTLY LINKED OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  MINOR
;    TITLE OF INVENTION:  GROOVE BINDER CONJUGATES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KLEIN & SZEKERES
;      STREET:  4199 Campus Drive, Suite 700
;      CITY:  Irvine
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92715
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/141,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/415,370
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Szekeres, Gabor L.
;      REGISTRATION NUMBER:  28,675
;      REFERENCE/DOCKET NUMBER:  491-09-PA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-854-5502
;      TELEFAX:  714-854-4897
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-141-764-2

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 614
US-08-851-843A-131
; Sequence 131, Application US/08851843A
; Patent No. 6093809
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6093809el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/851,843A
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-851-843A-131

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 615
US-08-854-050-131
; Sequence 131, Application US/08854050
; Patent No. 6261836
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. 6261836el Telomerase
;    NUMBER OF SEQUENCES:  225
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/854,050
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/851,843
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002930US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-854-050-131

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 616
US-09-430-323-131
; Sequence 131, Application US/09430323
; Patent No. 6309867
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;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. 6309867el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/430,323
;             FILING DATE: 29-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002930US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-430-323-131

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 617
US-09-507-345A-2/c
; Sequence 2, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-507-345A-2

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 618
US-09-507-345A-3/c
; Sequence 3, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by 6-aminohexanoic acid
;             (-NH(CH-2)-6COOH)"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-507-345A-3

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 619
US-09-507-345A-4/c
; Sequence 4, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;       APPLICANT: Kutyavin, Igor V.
;                  Lukhtanov, Eugeny A.
;                  Gamper, Howard B.
;                  Meyer Jr., Rich B.
;       TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                           Groove Binder Conjugates
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = one
;             4-amino-N-methylpyrrol-2-carboxylic acid residue"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-507-345A-4

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 620
US-09-507-345A-5/c
; Sequence 5, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;       APPLICANT: Kutyavin, Igor V.
;                  Lukhtanov, Eugeny A.
;                  Gamper, Howard B.
;                  Meyer Jr., Rich B.
;       TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                           Groove Binder Conjugates
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
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;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = two
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-507-345A-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 621
US-09-507-345A-6/c
; Sequence 6, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = three
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-507-345A-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 622
US-09-507-345A-7/c
; Sequence 7, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = four
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
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;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-507-345A-7

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 623
US-09-507-345A-8/c
; Sequence 8, Application US/09507345A
; Patent No. 6426408
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,345A
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003500US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = five
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-507-345A-8

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 624
US-09-619-103-22
; Sequence 22, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-22

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 625
US-09-739-928-2/c
; Sequence 2, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
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;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 626
US-09-739-928-3/c
; Sequence 3, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by 6-aminohexanoic acid
;             (-NH(CH-2)-6COOH)"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-739-928-3

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 627
US-09-739-928-4/c
; Sequence 4, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
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;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = one
;            4-amino-N-methylpyrrol-2-carboxylic acid residue"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-739-928-4

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 628
US-09-739-928-5/c
; Sequence 5, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;       APPLICANT: Kutyavin, Igor V.
;                  Lukhtanov, Eugeny A.
;                  Gamper, Howard B.
;                  Meyer Jr., Rich B.
;       TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                           Groove Binder Conjugates
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/739,928
;            FILING DATE: 11-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/415,370
;            FILING DATE: 03-APR-1995
;            APPLICATION NUMBER: US 09/141,764
;            FILING DATE: 27-AUG-1998
;            APPLICATION NUMBER: US 09/507,345
;            FILING DATE: 18-FEB-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kezer, William B.
;            REGISTRATION NUMBER: 37,369
;            REFERENCE/DOCKET NUMBER: 17682A-003510US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  16
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = two
;            4-amino-N-methylpyrrol-2-carboxylic acid residues"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-739-928-5

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 629
US-09-739-928-6/c
; Sequence 6, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;       APPLICANT: Kutyavin, Igor V.
;                  Lukhtanov, Eugeny A.
;                  Gamper, Howard B.
;                  Meyer Jr., Rich B.
;       TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                           Groove Binder Conjugates
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/739,928
;            FILING DATE: 11-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/415,370
;            FILING DATE: 03-APR-1995
;            APPLICATION NUMBER: US 09/141,764
;            FILING DATE: 27-AUG-1998
;            APPLICATION NUMBER: US 09/507,345
;            FILING DATE: 18-FEB-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kezer, William B.
;            REGISTRATION NUMBER: 37,369
;            REFERENCE/DOCKET NUMBER: 17682A-003510US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  16
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = thymidine modified by minor groove binder moiety
;            represented by X, where m = three
;            4-amino-N-methylpyrrol-2-carboxylic acid residues"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-739-928-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 630
US-09-739-928-7/c
; Sequence 7, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = four
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-739-928-7

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 631
US-09-739-928-8/c
; Sequence 8, Application US/09739928
; Patent No. 6486308
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = five
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-739-928-8

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         15 AAAAAAAAAAAAAAA 1


RESULT 632
US-09-958-610A-1
; Sequence 1, Application US/09958610A
; Patent No. 6756492
; GENERAL INFORMATION:
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;  APPLICANT: Beier, Markus
;  APPLICANT:  Hoheisel, Jorg
;  TITLE OF INVENTION: Nucleoside Derivatives with Photolabile Protective Groups
;  FILE REFERENCE: 03528.0135.PCUS00
;  CURRENT APPLICATION NUMBER: US/09/958,610A
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: PCT/DE00/011448
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 100 03 631.7
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: DE 199 15. 867.3
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-958-610A-1

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 AAAAAAAAAAAAAAA 15


RESULT 633
US-09-895-585-9/c
; Sequence 9, Application US/09895585
; Patent No. 6759039
; GENERAL INFORMATION:
;  APPLICANT: Tsang, Wen-Ghih
;  APPLICANT:  Zheng, Tianli
;  APPLICANT:  Huang, Chang Jiang
;  APPLICANT:  AmCyte, Inc.
;  TITLE OF INVENTION: Culturing Pancreatic Stem Cells Having a Specified,
;  TITLE OF INVENTION:  Intermediate Stage of Development
;  FILE REFERENCE: 021164-000100US
;  CURRENT APPLICATION NUMBER: US/09/895,585
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/215,634
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/246,306
;  PRIOR FILING DATE: 2000-11-06
;  PRIOR APPLICATION NUMBER: US 60/291,787
;  PRIOR FILING DATE: 2001-05-17
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo-(dT)-16
US-09-895-585-9

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 634
US-09-152-059-70/c
; Sequence 70, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-70

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 635
US-09-766-253-131
; Sequence 131, Application US/09766253
; Patent No. 6808880
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. 6808880el Telomerase
;        NUMBER OF SEQUENCES: 171
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,253
;             FILING DATE: 19-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-766-253-131

Query Match 0.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACA 3619
||||||| ||||| |
Db 1 AAAAAAAAAAAAAAA 15

RESULT 636
US-08-087-387-6/c
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic andtherapeutic applic
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,387
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-087-387-6

Query Match 0.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3606 AAAAAACAAAAACAG 3620
||||||| ||||| ||
Db 16 AAAAAAAAAAAAAAG 2

RESULT 637
US-08-455-627-6/c
; Sequence 6, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-6

Query Match 0.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3606 AAAAAACAAAAACAG 3620
||||||| ||||| ||
Db 16 AAAAAAAAAAAAAAG 2

RESULT 638
US-08-461-271-6/c
; Sequence 6, Application US/08461271
; Patent No. 5741643
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,271
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/087,387
;      FILING DATE:  2-Jul-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
;      TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-461-271-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
              ||||||  |||||  ||
Db         16 AAAAAAAAAAAAAAG 2


RESULT 639
US-08-713-685A-6/c
; Sequence 6, Application US/08713685A
; Patent No. 5817795
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Oligonucleotide clamps having diagnostic
;    TITLE OF INVENTION:  and therapeutic applications
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics
;      STREET:  465 Lincoln Centre Drive
;      CITY:  Foster City
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/713,685A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/461,271
;      FILING DATE:
;      APPLICATION NUMBER:  08/087,387
;      FILING DATE:  2-Jul-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
;      TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-713-685A-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
              ||||||  |||||  ||
Db         16 AAAAAAAAAAAAAAG 2


RESULT 640
US-08-689-856-6/c
; Sequence 6, Application US/08689856
; Patent No. 5830658
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Convergent Synthesis of Branched and Multiply
;    TITLE OF INVENTION:  Connected Macromolecular Structures
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward LLP
;      STREET:  Five Palo Alto Square, 3000 El Camino Real
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/689,856
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,627
;      FILING DATE:  31-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Jackie N.
;      REGISTRATION NUMBER:  35,966
;      REFERENCE/DOCKET NUMBER:  LYNX-003/01 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5000
;      TELEFAX:  415-857-0663
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-689-856-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
              ||||||  |||||  ||
Db         16 AAAAAAAAAAAAAAG 2


RESULT 641
US-09-070-477-6/c
; Sequence 6, Application US/09070477
```

```
; Patent No. 6048974
;  GENERAL INFORMATION:
;    APPLICANT:  Sergei M. Gryaznov
;    TITLE OF INVENTION:  Oligonucleotide clamps having diagnostic
;    TITLE OF INVENTION:  and therapeutic applications
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics
;      STREET:  465 Lincoln Centre Drive
;      CITY:  Foster City
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 3.1/DOS 5.0
;      SOFTWARE:  Microsoft Word for Windows, vers. 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/070,477
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/713,685
;      FILING DATE:
;      APPLICATION NUMBER:  08/461,271
;      FILING DATE:
;      APPLICATION NUMBER:  08/087,387
;      FILING DATE:  2-Jul-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-7855
;      TELEFAX:  (415) 358-7794
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-070-477-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAG 3620
             ||||||  |||||  ||
Db         16 AAAAAAAAAAAAAAG 2


RESULT 642
US-08-821-827C-30/c
; Sequence 30, Application US/08821827C
; Patent No. 6297425
; GENERAL INFORMATION:
;  APPLICANT: Scelonge, Christopher J.
;  APPLICANT:  Bidney, Dennis L.
;  TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
;  TITLE OF INVENTION:  ASPERGILLUS PHOENICES
;  FILE REFERENCE: 0561A
;  CURRENT APPLICATION NUMBER: US/08/821,827C
;  CURRENT FILING DATE:  1997-03-21
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(17)
;   OTHER INFORMATION: n = A,T,C or G
US-08-821-827C-30

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             |||||||  |||||  |
Db         17 AAAAAAAAAAAAAAA 3


RESULT 643
US-09-290-202B-30/c
; Sequence 30, Application US/09290202B
; Patent No. 6303846
; GENERAL INFORMATION:
;  APPLICANT: Scelonge, Christopher J.
;  APPLICANT:  Bidney, Dennis L.
;  TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
;  TITLE OF INVENTION:  ASPERGILLUS PHOENICES
;  FILE REFERENCE: 0561D
;  CURRENT APPLICATION NUMBER: US/09/290,202B
;  CURRENT FILING DATE:  1999-04-12
;  PRIOR APPLICATION NUMBER: 08/821,827
;  PRIOR FILING DATE: 1997-03-21
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(17)
;   OTHER INFORMATION: n = A,T,C or G
US-09-290-202B-30

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             |||||||  |||||  |
Db         17 AAAAAAAAAAAAAAA 3


RESULT 644
US-09-300-958A-63/c
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 17
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 645
US-08-373-124A-2149
; Sequence 2149, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2149:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-2149

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 6e+02;
  Matches    0;  Conservative   13;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::: ::::::: :
Db          1 UUUUUUAUUUUUUAU 15


RESULT 646
US-08-435-628-2149
; Sequence 2149, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2149:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-2149

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 6e+02;
  Matches    0;  Conservative   13;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::: ::::::: :
Db          1 UUUUUUAUUUUUUAU 15
```

```
RESULT 647
US-09-637-751A-6/c
; Sequence 6, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
;  APPLICANT:  Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION:  Binary Encoded Sequence Tags
; Patent No. 6383754
;  FILE REFERENCE:  AGL 100
;  CURRENT APPLICATION NUMBER: US/09/637,751A
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 648
US-09-994-311-6/c
; Sequence 6, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-6

  Query Match             0.3%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| ||||| |
Db         16 AAAAAAAAAAAAAAA 2


RESULT 649
US-09-300-958A-65/c
; Sequence 65, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
;  APPLICANT:  McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION:  Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE:  P-PH 3457
;  CURRENT APPLICATION NUMBER: US/09/300,958A
;  CURRENT FILING DATE:  1999-04-27
;  PRIOR APPLICATION NUMBER:  60/083,331
;  PRIOR FILING DATE:  1998-04-27
;  PRIOR APPLICATION NUMBER:  60/098,070
;  PRIOR FILING DATE:  1998-08-27
;  PRIOR APPLICATION NUMBER:  60/118,624
;  PRIOR FILING DATE:  1999-02-04
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 65
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-65

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 14;
  Best Local Similarity   85.7%;  Pred. No. 6.3e+02;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
             :||||||| |||||
Db         14 BAAAAAAAAAAAAA 1


RESULT 650
US-08-882-649A-7
; Sequence 7, Application US/08882649A
; Patent No. 6344316
;   GENERAL INFORMATION:
;        APPLICANT: Lockhart, David J.
;                   Chee, Mark
;                   Gunderson, Kevin
;                   Chaoqiang, Lai
;                   Wodicka, Lisa
;                   Cronin, Maureen T.
;                   Lee, Danny
;                   Tran, Huu M.
;                   Matsuzaki, Hajime
;                   McGall, Glenn H.
;        TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Joe Liebeschuetz
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/882,649A
;             FILING DATE: 25-Jun-1997
;             CLASSIFICATION: 435-006.000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/010,471
;             FILING DATE: 23-JAN-1996
;             APPLICATION NUMBER: US 60/035,170
;             FILING DATE: 09-JAN-1997
```

```
;             APPLICATION NUMBER: PCT/US97/01603
;             FILING DATE: 22-JAN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-019410US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: YES
;                      (ix)  Features:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-882-649A-7

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+02;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAA 3617
              :||||||| |||||
Db          2 VAAAAAAAAAAAAA 15


RESULT 651
US-08-882-649A-8/c
; Sequence 8, Application US/08882649A
; Patent No. 6344316
;   GENERAL INFORMATION:
;        APPLICANT: Lockhart, David J.
;                   Chee, Mark
;                   Gunderson, Kevin
;                   Chaoqiang, Lai
;                   Wodicka, Lisa
;                   Cronin, Maureen T.
;                   Lee, Danny
;                   Tran, Huu M.
;                   Matsuzaki, Hajime
;                   McGall, Glenn H.
;        TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Joe Liebeschuetz
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/882,649A
;             FILING DATE: 25-Jun-1997
;             CLASSIFICATION: 435-006.000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/010,471
;             FILING DATE: 23-JAN-1996
;             APPLICATION NUMBER: US 60/035,170
;             FILING DATE: 09-JAN-1997
;             APPLICATION NUMBER: PCT/US97/01603
;             FILING DATE: 22-JAN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-019410US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: YES
;                      (ix)  Features:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-882-649A-8

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 16;
  Best Local Similarity   85.7%;  Pred. No. 6.4e+02;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAAC 3618
              ||||||| |||||:
Db         15 AAAAAAAAAAAAAB 2


RESULT 652
US-09-143-212-64
; Sequence 64, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia and Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
;  FILE REFERENCE: RTS-0005
;  CURRENT APPLICATION NUMBER: US/09/143,212B
;  CURRENT FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-64

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 6.4e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3111 TCCCCTGCCACACTGATG 3128
              ||| ||||||  ||| ||
Db          1 TCCTCTGCCAGGCTGGTG 18


RESULT 653
US-08-850-880-10
; Sequence 10, Application US/08850880
; Patent No. 5925545
;  GENERAL INFORMATION:
;    APPLICANT:  Reznikoff, William S
;    APPLICANT:  Gorysin, Igor Y
;    APPLICANT:  Zhou, Hong
;    TITLE OF INVENTION:  System for In Vitro Transposition
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/850,880
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berson, Bennett J
;      REGISTRATION NUMBER:  37094
;      REFERENCE/DOCKET NUMBER:  960296.94142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608/251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Tn5 wild type inside end"
US-08-850-880-10

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 654
US-08-944-916-10
; Sequence 10, Application US/08944916
; Patent No. 5948622
;  GENERAL INFORMATION:
;    APPLICANT:  Reznikoff, William S
;    APPLICANT:  Goryshin, Igor Y
;    APPLICANT:  York, Dona L
;    APPLICANT:  Zhou, Hong
;    TITLE OF INVENTION:  System for In Vitro Transposition
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,916
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/814,877
;      FILING DATE:  09-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/850,880
;      FILING DATE:  02-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berson, Bennett J
;      REGISTRATION NUMBER:  37094
;      REFERENCE/DOCKET NUMBER:  960296.94916
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608/251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Tn5 wild type inside end"
US-08-944-916-10

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 655
US-09-159-363-2
; Sequence 2, Application US/09159363A
; Patent No. 6159736
; GENERAL INFORMATION:
;  APPLICANT: Reznikoff, William S
;  APPLICANT: Goryshin, Igor Y
;  TITLE OF INVENTION: Method for Making Insertional Mutations
;  FILE REFERENCE: 960296.95688
;  CURRENT APPLICATION NUMBER: US/09/159,363A
;  CURRENT FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-09-159-363-2

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 656
US-09-635-969-6
; Sequence 6, Application US/09635969
; Patent No. 6294385
; GENERAL INFORMATION:
;  APPLICANT: Goryshin, Igor Y
;  APPLICANT: Reznikoff, William S
;  TITLE OF INVENTION: METHOD FOR MAKING INSERTIONAL MUTATIONS
;  FILE REFERENCE: 960296.96854
;  CURRENT APPLICATION NUMBER: US/09/635,969
;  CURRENT FILING DATE: 2000-08-10
;  EARLIER APPLICATION NUMBER: 09/159,363
;  EARLIER FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-09-635-969-6

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
```

```
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 657
US-09-632-021-4
; Sequence 4, Application US/09632021
; Patent No. 6406896
; GENERAL INFORMATION:
;  APPLICANT:  Reznikoff, William S
;  APPLICANT:  Naumann, Todd A
;  TITLE OF INVENTION:  Transposase Enzyme and Method for Use
;  FILE REFERENCE:  960296.96471
;  CURRENT APPLICATION NUMBER: US/09/632,021
;  CURRENT FILING DATE:  2000-08-02
;  PRIOR APPLICATION NUMBER:  60/146686
;  PRIOR FILING DATE:  1999-08-02
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-09-632-021-4

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 658
US-09-272-432A-10
; Sequence 10, Application US/09272432A
; Patent No. 6437109
;  GENERAL INFORMATION:
;    APPLICANT:  Reznikoff, William S
;    APPLICANT:  Goryshin, Igor Y
;    APPLICANT:  Zhou, Hong
;    TITLE OF INVENTION:  System for In Vitro Transposition
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/272,432A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berson, Bennett J
;      REGISTRATION NUMBER:  37094
;      REFERENCE/DOCKET NUMBER:  960296.96277
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608/251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Tn5 wild type inside end"
US-09-272-432A-10

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 659
US-09-350-852A-3/c
; Sequence 3, Application US/09350852A
; Patent No. 6596509
; GENERAL INFORMATION:
;  APPLICANT:  Bauer, David W.
;  APPLICANT:  Beer, Steven V.
;  APPLICANT:  Bogdanove, Adam J.
;  APPLICANT:  Collmer, Alan
;  APPLICANT:  Ham, Jong Hyun
;  TITLE OF INVENTION:  RECOMBINANT CONSTRUCTS AND SYSTEMS FOR SECRETION OF
;  TITLE OF INVENTION:  PROTEINS VIA TYPE III SECRETION SYSTEMS
;  FILE REFERENCE:  19603/2061
;  CURRENT APPLICATION NUMBER: US/09/350,852A
;  CURRENT FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  60/092,357
;  PRIOR FILING DATE:  1998-07-10
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  primer
US-09-350-852A-3

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db         19 CTGTCTCTTGATCAGATC 2


RESULT 660
5212080-3
;Patent No. 5212080
;    APPLICANT: NAG, DILIP K.;HUANG, HENRY V.;BERG, DOUGLAS E.
;    TITLE OF INVENTION: METHOD OF DNA SEQUENCOM=NG USING DNA
;TRANSPOSON TN5SEQL
;    NUMBER OF SEQUENCES: 6
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/508,379
;      FILING DATE: 12-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 105,422
;      FILING DATE: 05-OCT-1987
;SEQ ID NO:3:
;      LENGTH: 19
5212080-3

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || ||||| | ||||| |
Db          1 CTGTCTCTTGATCAGATC 18
```

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RESULT 661
5212080-3
;Patent No. 5212080
;    APPLICANT: NAG, DILIP K.;HUANG, HENRY V.;BERG, DOUGLAS E.
;    TITLE OF INVENTION: METHOD OF DNA SEQUENCOM=NG USING DNA
;TRANSPOSON TN5SEQL
;    NUMBER OF SEQUENCES: 6
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/508,379
;      FILING DATE: 12-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 105,422
;      FILING DATE: 05-OCT-1987
;SEQ ID NO:3:
;      LENGTH: 19
5212080-3

  Query Match             0.3%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 6.3e+02;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3281 CTCTCTCTGGGTCAGAAC 3298
              || |||||  | |||||  |
Db          1 CTGTCTCTTGATCAGATC 18


RESULT 662
US-08-173-489C-75
; Sequence 75, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  double stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;      DESCRIPTION:  esterase D gene (Accession # M13450)
;      DESCRIPTION:  nucleotides 962 to 975
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  chromosome 13
;      MAP POSITION:  13q14.1-q14.2
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lee, E Y H P,  Lee, W H.
;      TITLE:  Molecular cloning of the
;      TITLE:  human esterase D gene, a genetic marker of
;      TITLE:  retinoblastoma
;      JOURNAL:  Proceedings of the National Academy of
;      JOURNAL:  Sciences, USA
;      VOLUME:  83
;      PAGES:  6337-6341
;      DATE:  1986
;      RELEVANT RESIDUES IN SEQ ID NO:  75 :FROM 1 TO 14
US-08-173-489C-75

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 663
US-08-173-489C-76/c
; Sequence 76, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 bases
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  third strand derived from esterase D
;      DESCRIPTION:  sequence region in Seq ID No. 586124475
;
```

```
;    HYPOTHETICAL:  Yes
;    ANTI-SENSE:  No
;    PUBLICATION INFORMATION:
;      RELEVANT RESIDUES IN SEQ ID NO:  76 :FROM 1 TO 14
US-08-173-489C-76

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 664
US-09-462-569B-1/c
; Sequence 1, Application US/09462569B
; Patent No. 6392124
; GENERAL INFORMATION:
;  APPLICANT: PONZ ASCASO, Fernando
;  APPLICANT:  TORRES PASCUAL, Vicente
;  APPLICANT:  SANCHEZ SANCHEZ, Florentina
;  APPLICANT:  MARTINEZ HERRERA, David
;  TITLE OF INVENTION: INFECTIOUS VECTORS AND CLONES OF PLANTS DERIVED FROM
;  TITLE OF INVENTION:  THE TURNIP MOSAIC VIRUS (TuMV)
;  FILE REFERENCE: P/613-110
;  CURRENT APPLICATION NUMBER: US/09/462,569B
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER: PCT/ES98/00200
;  PRIOR FILING DATE: 1998-07-09
;  PRIOR APPLICATION NUMBER: ES P 9701522
;  PRIOR FILING DATE: 1997-07-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: synthetic
;    OTHER INFORMATION: construct
US-09-462-569B-1

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 665
US-09-619-103-20
; Sequence 20, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION:  Peptide Acceptor Ligation Methods
;  FILE REFERENCE:  50036/031002
;  CURRENT APPLICATION NUMBER: US/09/619,103
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  60/145,834
;  PRIOR FILING DATE:  1999-07-27
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-20

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 666
US-09-152-059-65/c
; Sequence 65, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: modified_base
;    LOCATION: (7)
;    OTHER INFORMATION: LNA monomer
;    OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-65

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 667
US-09-152-059-66/c
; Sequence 66, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
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;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-66

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 668
US-09-152-059-67/c
; Sequence 67, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-67

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 669
US-09-152-059-68/c
; Sequence 68, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (11)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-68

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 670
US-09-152-059-80/c
; Sequence 80, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
```

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;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-80

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 671
US-09-152-059-81
; Sequence 81, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-81

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13


RESULT 672
US-09-152-059-82
; Sequence 82, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-82

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13


RESULT 673
US-09-152-059-83/c
; Sequence 83, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
```

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;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-83

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 674
US-09-152-059-84
; Sequence 84, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-84

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 675
US-09-152-059-85
; Sequence 85, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-85

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 676
US-09-152-059-86/c
; Sequence 86, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
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;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-86

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 677
US-09-152-059-87
; Sequence 87, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-87

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 678
US-09-152-059-88
; Sequence 88, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-88

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 679
US-09-152-059-89/c
; Sequence 89, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-89

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 680
US-09-152-059-90
; Sequence 90, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-90

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 681
US-09-152-059-91
; Sequence 91, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-91

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 682
US-09-152-059-92/c
; Sequence 92, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
```

```
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (11)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-92

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 683
US-09-152-059-93
; Sequence 93, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-93

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 684
US-09-152-059-94
; Sequence 94, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-94

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 685
US-09-152-059-96
; Sequence 96, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-96

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 686
US-09-152-059-97
; Sequence 97, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-97

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 687
US-09-152-059-98/c
; Sequence 98, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-98

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 688
US-09-152-059-99
; Sequence 99, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-99

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 689
US-09-152-059-100
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; Sequence 100, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-100

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 690
US-09-152-059-101/c
; Sequence 101, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-101

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          14 AAAAAAAAAAAAA 2


RESULT 691
US-09-152-059-102
; Sequence 102, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-102

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 692
US-09-152-059-103
; Sequence 103, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
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;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-103

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 693
US-09-152-059-104/c
; Sequence 104, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-104

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 694
US-09-152-059-105
; Sequence 105, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-105

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 695
US-09-152-059-106
; Sequence 106, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
```

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;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-106

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 696
US-09-152-059-107/c
; Sequence 107, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-107

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 697
US-09-152-059-108
; Sequence 108, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-108

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 698
US-09-152-059-109
; Sequence 109, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
```

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;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-109

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 699
US-09-152-059-110/c
; Sequence 110, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: modified_base
;    LOCATION: (5)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (7)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (9)
;    OTHER INFORMATION: LNA monomer
;    NAME/KEY: modified_base
;    LOCATION: (11)
;    OTHER INFORMATION: LNA monomer
;    OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-110

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 700
US-09-152-059-111
; Sequence 111, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
;    LENGTH: 14
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
US-09-152-059-111

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 701
US-09-152-059-112
; Sequence 112, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
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;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-112

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 702
US-09-152-059-113/c
; Sequence 113, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(13)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-113

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 703
US-09-152-059-114
; Sequence 114, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-114

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 704
US-09-152-059-115
; Sequence 115, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;   LENGTH: 14
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-115

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 705
US-09-152-059-117/c
; Sequence 117, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-117

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 706
US-09-152-059-118
; Sequence 118, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-118

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 707
US-09-152-059-119
; Sequence 119, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-119

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
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  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 708
US-09-152-059-120/c
; Sequence 120, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-120

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 709
US-09-152-059-121
; Sequence 121, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-121

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 710
US-09-152-059-122
; Sequence 122, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-122

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 711
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US-09-152-059-123/c
; Sequence 123, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-123

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 712
US-09-152-059-124
; Sequence 124, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-124

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 713
US-09-152-059-125
; Sequence 125, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-125

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 714
US-09-152-059-126/c
; Sequence 126, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
```

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;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-126

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 715
US-09-152-059-127
; Sequence 127, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-127

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 716
US-09-152-059-128
; Sequence 128, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-128

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 717
US-09-152-059-129/c
; Sequence 129, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
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;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-129

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 718
US-09-152-059-130
; Sequence 130, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-130

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13


RESULT 719
US-09-152-059-131
; Sequence 131, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-131

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         1 AAAAAAAAAAAAA 13


RESULT 720
US-09-152-059-132/c
; Sequence 132, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
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;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-132

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 721
US-09-152-059-133
; Sequence 133, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-133

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 722
US-09-152-059-134
; Sequence 134, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-134

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 723
US-09-152-059-135/c
; Sequence 135, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
;   LENGTH: 14
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-135

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 724
US-09-152-059-136
; Sequence 136, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-136

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 725
US-09-152-059-137
; Sequence 137, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-137

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 726
US-09-152-059-138/c
; Sequence 138, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6)..(9)
;   OTHER INFORMATION: LNA monomer
```

```
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-138

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 727
US-09-152-059-139
; Sequence 139, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-139

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 728
US-09-152-059-140
; Sequence 140, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-140

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 729
US-09-152-059-141/c
; Sequence 141, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: LNA monomer
;   NAME/KEY: modified_base
;   LOCATION: (11)
```

```
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-141

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 730
US-09-152-059-142
; Sequence 142, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-142

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 731
US-09-152-059-143
; Sequence 143, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-143

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 732
US-09-152-059-144/c
; Sequence 144, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(13)
;   OTHER INFORMATION: LNA monomer
;   OTHER INFORMATION: Description of Artificial Sequence: LNA modified
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-144

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db         14 AAAAAAAAAAAAA 2


RESULT 733
US-09-152-059-145
; Sequence 145, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-145

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 734
US-09-152-059-146
; Sequence 146, Application US/09152059
; Patent No. 6794499
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-146

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAA 3617
              ||||||| |||||
Db          1 AAAAAAAAAAAAA 13


RESULT 735
US-09-859-736-7/c
; Sequence 7, Application US/09859736
; Patent No. 6838244
; GENERAL INFORMATION:
;  APPLICANT: LI, WAN-LIANG ROBERT
;  APPLICANT:  ZHOU, JIAN S.
;  TITLE OF INVENTION: FLUORESCENT OLIGONUCLEOTIDES AND USES THEREOF
;  FILE REFERENCE: 16517.248
;  CURRENT APPLICATION NUMBER: US/09/859,736
;  CURRENT FILING DATE:  2001-05-18
;  PRIOR APPLICATION NUMBER: 60/205,452
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: dT oligonucleotide
US-09-859-736-7

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  Best Local Similarity   92.3%;  Pred. No. 6.8e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         14 AAAAAAAAAAAAA 2


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;Patent No. 5453496
;    APPLICANT: CARUTHERS, MARVIN H.;MARSHALL, WILLIAM S.;BRILL,
;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
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;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
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5453496-4

  Query Match             0.3%;  Score 11.4;  DB 1;  Length 14;
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Db         14 AAAAAAAAAAAAA 2


RESULT 737
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;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
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;      FILING DATE: 31-MAR-1989
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RESULT 738
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;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
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;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
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RESULT 739
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;    APPLICANT: CARUTHERS, MARVIN H.;MARSHALL, WILLIAM S.;BRILL,
;WOLFGANG;NIELSEN, JOHN
;    TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
;    NUMBER OF SEQUENCES: 7
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/138,140
;      FILING DATE: 15-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 793,171
;      FILING DATE: 18-NOV-1991
;      APPLICATION NUMBER: 545,238
;      FILING DATE: 27-JUN-1990
;      APPLICATION NUMBER: 332,247
;      FILING DATE: 31-MAR-1989
;      APPLICATION NUMBER: 198,886
;      FILING DATE: 26-MAY-1988
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5453496-5

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Qy       3605 AAAAAAACAAAAA 3617
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Search completed: October 24, 2005, 15:42:56
Job time : 21 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 15:53:33 ; Search time 62 Seconds
(without alignments)
3.675 Million cell updates/sec

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Perfect score: 4324
Sequence: 1 gtactacaaacctggcttgc.....aataaaagtgaagtgaatct 4324

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1406 seqs, 26347 residues

Total number of hits satisfying chosen parameters: 2812

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1607 summaries

Database : rng.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	30	0.7	30	1	ACC62353	Human NOV3 probe S
	3	25	0.6	25	1	ABZ84148	Toxicologically re
c	4	25	0.6	25	1	ABZ84357	Toxicologically re
c	5	25	0.6	25	1	ABZ84141	Toxicologically re
c	6	24.4	0.6	27	1	ADR47292	Stearoyl-CoA desat
c	7	24.4	0.6	27	1	ADR47296	Stearoyl-CoA desat
	8	24	0.6	24	1	ABZ84363	Toxicologically re
	9	24	0.6	24	1	ADQ90669	Mouse Real Time PC
	10	23.8	0.6	27	1	ABQ82441	Human NOV10 probe
	11	23.8	0.6	27	1	ABQ82444	Human NOV10 probe
	12	23	0.5	23	1	ADC72189	Human stearyl coen
	13	23	0.5	23	1	ADC72188	Human stearyl coen
	14	23	0.5	23	1	ADE27638	Stearoyl-CoA desat
	15	23	0.5	23	1	ADE27640	Stearoyl-CoA desat
	16	23	0.5	23	1	ADE27637	Stearoyl-CoA desat
	17	23	0.5	23	1	ADE27639	Stearoyl-CoA desat
	18	23	0.5	23	1	ADG29600	SCD siNA-target RN
	19	23	0.5	23	1	ADG29602	SCD siNA-target RN
	20	23	0.5	23	1	ADG29599	SCD siNA-target RN
	21	23	0.5	23	1	ADG29601	SCD siNA-target RN
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	24	21.4	0.5	23	1	ADE27652	Stearoyl-CoA desat
	25	21	0.5	21	1	ACA90035	Cardiovascular dis
c	26	21	0.5	21	1	ACC62354	Human NOV3 reverse
	27	21	0.5	21	1	ADE27671	Stearoyl-CoA desat
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	30	21	0.5	21	1	ADE27644	Stearoyl-CoA desat
	31	21	0.5	21	1	ADG30282	SCD-targeted siNA
	32	21	0.5	23	1	ADG30274	SCD-targeted siNA
c	33	20.8	0.5	26	1	AAV54646	Mortierella sp. de
c	34	20.6	0.5	22	1	ADE27653	Stearoyl-CoA desat
c	35	20.6	0.5	22	1	ADE27661	Stearoyl-CoA desat
	36	20.2	0.5	21	1	ADC72195	Human stearyl coen
c	37	20.2	0.5	21	1	ADC72198	Human stearyl coen
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c	121	19.4	0.4	21	1	AAZ77065	Human biallelic ma
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c	221	19	0.4	19	1	ADE27539	Stearoyl-CoA desat
c	222	19	0.4	19	1	ADE27540	Stearoyl-CoA desat
c	223	19	0.4	19	1	ADE27562	Stearoyl-CoA desat
c	224	19	0.4	19	1	ADE27581	Stearoyl-CoA desat
c	225	19	0.4	19	1	ADE27596	Stearoyl-CoA desat
c	226	19	0.4	19	1	ADE27603	Stearoyl-CoA desat
c	227	19	0.4	19	1	ADE27609	Stearoyl-CoA desat
c	228	19	0.4	19	1	ADE27616	Stearoyl-CoA desat
	229	19	0.4	19	1	ADE27112	Stearoyl-CoA desat
	230	19	0.4	19	1	ADE27135	Stearoyl-CoA desat
	231	19	0.4	19	1	ADE27151	Stearoyl-CoA desat
	232	19	0.4	19	1	ADE27170	Stearoyl-CoA desat
	233	19	0.4	19	1	ADE27181	Stearoyl-CoA desat
	234	19	0.4	19	1	ADE27201	Stearoyl-CoA desat
	235	19	0.4	19	1	ADE27212	Stearoyl-CoA desat
	236	19	0.4	19	1	ADE27256	Stearoyl-CoA desat
	237	19	0.4	19	1	ADE27279	Stearoyl-CoA desat
	238	19	0.4	19	1	ADE27327	Stearoyl-CoA desat
	239	19	0.4	19	1	ADE27329	Stearoyl-CoA desat
c	240	19	0.4	19	1	ADE27400	Stearoyl-CoA desat
c	241	19	0.4	19	1	ADE27411	Stearoyl-CoA desat
c	242	19	0.4	19	1	ADE27428	Stearoyl-CoA desat
c	243	19	0.4	19	1	ADE27433	Stearoyl-CoA desat
c	244	19	0.4	19	1	ADE27443	Stearoyl-CoA desat
c	245	19	0.4	19	1	ADE27464	Stearoyl-CoA desat
c	246	19	0.4	19	1	ADE27470	Stearoyl-CoA desat
c	247	19	0.4	19	1	ADE27472	Stearoyl-CoA desat
c	248	19	0.4	19	1	ADE27490	Stearoyl-CoA desat
c	249	19	0.4	19	1	ADE27501	Stearoyl-CoA desat
c	250	19	0.4	19	1	ADE27523	Stearoyl-CoA desat
c	251	19	0.4	19	1	ADE27575	Stearoyl-CoA desat
c	252	19	0.4	19	1	ADE27601	Stearoyl-CoA desat

c 253	19	0.4	19	1	ADE27620	Stearoyl-CoA desat
254	19	0.4	19	1	ADE27172	Stearoyl-CoA desat
255	19	0.4	19	1	ADE27175	Stearoyl-CoA desat
256	19	0.4	19	1	ADE27263	Stearoyl-CoA desat
257	19	0.4	19	1	ADE27271	Stearoyl-CoA desat
258	19	0.4	19	1	ADE27286	Stearoyl-CoA desat
259	19	0.4	19	1	ADE27289	Stearoyl-CoA desat
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261	19	0.4	19	1	ADE27315	Stearoyl-CoA desat
262	19	0.4	19	1	ADE27334	Stearoyl-CoA desat
263	19	0.4	19	1	ADE27335	Stearoyl-CoA desat
264	19	0.4	19	1	ADE27345	Stearoyl-CoA desat
c 265	19	0.4	19	1	ADE27491	Stearoyl-CoA desat
c 266	19	0.4	19	1	ADE27493	Stearoyl-CoA desat
c 267	19	0.4	19	1	ADE27516	Stearoyl-CoA desat
c 268	19	0.4	19	1	ADE27527	Stearoyl-CoA desat
c 269	19	0.4	19	1	ADE27534	Stearoyl-CoA desat
c 270	19	0.4	19	1	ADE27536	Stearoyl-CoA desat
c 271	19	0.4	19	1	ADE27541	Stearoyl-CoA desat
c 272	19	0.4	19	1	ADE27577	Stearoyl-CoA desat
c 273	19	0.4	19	1	ADE27588	Stearoyl-CoA desat
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c 275	19	0.4	19	1	ADE27602	Stearoyl-CoA desat
c 276	19	0.4	19	1	ADE27611	Stearoyl-CoA desat
c 277	19	0.4	19	1	ADE27628	Stearoyl-CoA desat
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279	19	0.4	19	1	ADE27134	Stearoyl-CoA desat
280	19	0.4	19	1	ADE27140	Stearoyl-CoA desat
281	19	0.4	19	1	ADE27145	Stearoyl-CoA desat
282	19	0.4	19	1	ADE27147	Stearoyl-CoA desat
283	19	0.4	19	1	ADE27159	Stearoyl-CoA desat
284	19	0.4	19	1	ADE27167	Stearoyl-CoA desat
285	19	0.4	19	1	ADE27176	Stearoyl-CoA desat
286	19	0.4	19	1	ADE27215	Stearoyl-CoA desat
287	19	0.4	19	1	ADE27276	Stearoyl-CoA desat
288	19	0.4	19	1	ADE27282	Stearoyl-CoA desat
289	19	0.4	19	1	ADE27296	Stearoyl-CoA desat
290	19	0.4	19	1	ADE27308	Stearoyl-CoA desat
291	19	0.4	19	1	ADE27314	Stearoyl-CoA desat
292	19	0.4	19	1	ADE27322	Stearoyl-CoA desat
293	19	0.4	19	1	ADE27343	Stearoyl-CoA desat
c 294	19	0.4	19	1	ADE27412	Stearoyl-CoA desat
c 295	19	0.4	19	1	ADE27413	Stearoyl-CoA desat
c 296	19	0.4	19	1	ADE27453	Stearoyl-CoA desat
c 297	19	0.4	19	1	ADE27505	Stearoyl-CoA desat
c 298	19	0.4	19	1	ADE27507	Stearoyl-CoA desat
c 299	19	0.4	19	1	ADE27529	Stearoyl-CoA desat
c 300	19	0.4	19	1	ADE27550	Stearoyl-CoA desat
c 301	19	0.4	19	1	ADE27563	Stearoyl-CoA desat
c 302	19	0.4	19	1	ADE27622	Stearoyl-CoA desat
c 303	19	0.4	19	1	ADE27625	Stearoyl-CoA desat
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305	19	0.4	19	1	ADE27121	Stearoyl-CoA desat
306	19	0.4	19	1	ADE27125	Stearoyl-CoA desat
307	19	0.4	19	1	ADE27133	Stearoyl-CoA desat
308	19	0.4	19	1	ADE27142	Stearoyl-CoA desat
309	19	0.4	19	1	ADE27205	Stearoyl-CoA desat
310	19	0.4	19	1	ADE27225	Stearoyl-CoA desat
311	19	0.4	19	1	ADE27235	Stearoyl-CoA desat
312	19	0.4	19	1	ADE27236	Stearoyl-CoA desat
313	19	0.4	19	1	ADE27251	Stearoyl-CoA desat
314	19	0.4	19	1	ADE27261	Stearoyl-CoA desat
315	19	0.4	19	1	ADE27280	Stearoyl-CoA desat
316	19	0.4	19	1	ADE27300	Stearoyl-CoA desat
317	19	0.4	19	1	ADE27328	Stearoyl-CoA desat
c 318	19	0.4	19	1	ADE27401	Stearoyl-CoA desat
c 319	19	0.4	19	1	ADE27421	Stearoyl-CoA desat
c 320	19	0.4	19	1	ADE27423	Stearoyl-CoA desat
c 321	19	0.4	19	1	ADE27439	Stearoyl-CoA desat
c 322	19	0.4	19	1	ADE27442	Stearoyl-CoA desat
c 323	19	0.4	19	1	ADE27444	Stearoyl-CoA desat
c 324	19	0.4	19	1	ADE27465	Stearoyl-CoA desat
c 325	19	0.4	19	1	ADE27474	Stearoyl-CoA desat
c 326	19	0.4	19	1	ADE27478	Stearoyl-CoA desat
c 327	19	0.4	19	1	ADE27498	Stearoyl-CoA desat
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c 333	19	0.4	19	1	ADE27579	Stearoyl-CoA desat
c 334	19	0.4	19	1	ADE27582	Stearoyl-CoA desat
c 335	19	0.4	19	1	ADE27630	Stearoyl-CoA desat
c 336	19	0.4	19	1	ADE27633	Stearoyl-CoA desat
337	19	0.4	19	1	ADE27113	Stearoyl-CoA desat
338	19	0.4	19	1	ADE27123	Stearoyl-CoA desat
339	19	0.4	19	1	ADE27203	Stearoyl-CoA desat
340	19	0.4	19	1	ADE27211	Stearoyl-CoA desat
341	19	0.4	19	1	ADE27213	Stearoyl-CoA desat
342	19	0.4	19	1	ADE27227	Stearoyl-CoA desat
343	19	0.4	19	1	ADE27246	Stearoyl-CoA desat
344	19	0.4	19	1	ADE27259	Stearoyl-CoA desat
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347	19	0.4	19	1	ADE27283	Stearoyl-CoA desat
348	19	0.4	19	1	ADE27301	Stearoyl-CoA desat
349	19	0.4	19	1	ADE27316	Stearoyl-CoA desat
350	19	0.4	19	1	ADE27324	Stearoyl-CoA desat
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c 352	19	0.4	19	1	ADE27396	Stearoyl-CoA desat
c 353	19	0.4	19	1	ADE27397	Stearoyl-CoA desat
c 354	19	0.4	19	1	ADE27426	Stearoyl-CoA desat
c 355	19	0.4	19	1	ADE27427	Stearoyl-CoA desat
c 356	19	0.4	19	1	ADE27430	Stearoyl-CoA desat
c 357	19	0.4	19	1	ADE27437	Stearoyl-CoA desat
c 358	19	0.4	19	1	ADE27440	Stearoyl-CoA desat
c 359	19	0.4	19	1	ADE27445	Stearoyl-CoA desat
c 360	19	0.4	19	1	ADE27457	Stearoyl-CoA desat
c 361	19	0.4	19	1	ADE27568	Stearoyl-CoA desat
c 362	19	0.4	19	1	ADE27585	Stearoyl-CoA desat
c 363	19	0.4	19	1	ADE27586	Stearoyl-CoA desat
364	19	0.4	19	1	ADE27120	Stearoyl-CoA desat
365	19	0.4	19	1	ADE27137	Stearoyl-CoA desat
366	19	0.4	19	1	ADE27141	Stearoyl-CoA desat
367	19	0.4	19	1	ADE27146	Stearoyl-CoA desat
368	19	0.4	19	1	ADE27174	Stearoyl-CoA desat
369	19	0.4	19	1	ADE27179	Stearoyl-CoA desat
370	19	0.4	19	1	ADE27194	Stearoyl-CoA desat
371	19	0.4	19	1	ADE27214	Stearoyl-CoA desat
372	19	0.4	19	1	ADE27220	Stearoyl-CoA desat
373	19	0.4	19	1	ADE27230	Stearoyl-CoA desat
374	19	0.4	19	1	ADE27239	Stearoyl-CoA desat
375	19	0.4	19	1	ADE27242	Stearoyl-CoA desat
376	19	0.4	19	1	ADE27258	Stearoyl-CoA desat
377	19	0.4	19	1	ADE27292	Stearoyl-CoA desat
378	19	0.4	19	1	ADE27326	Stearoyl-CoA desat
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380	19	0.4	19	1	ADE27338	Stearoyl-CoA desat
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382	19	0.4	19	1	ADE27341	Stearoyl-CoA desat
c 383	19	0.4	19	1	ADE27434	Stearoyl-CoA desat
c 384	19	0.4	19	1	ADE27447	Stearoyl-CoA desat
c 385	19	0.4	19	1	ADE27448	Stearoyl-CoA desat
c 386	19	0.4	19	1	ADE27454	Stearoyl-CoA desat
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394	19	0.4	19	1	ADE27153	Stearoyl-CoA desat
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398	19	0.4	19	1	ADE27217	Stearoyl-CoA desat

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	424	19	0.4	19	1	ADE27169
	425	19	0.4	19	1	ADE27197
	426	19	0.4	19	1	ADE27198
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	428	19	0.4	19	1	ADE27218
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	430	19	0.4	19	1	ADE27238
	431	19	0.4	19	1	ADE27247
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	433	19	0.4	19	1	ADE27306
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c	437	19	0.4	19	1	ADE27419
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c	439	19	0.4	19	1	ADE27460
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c	445	19	0.4	19	1	ADE27513
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	456	19	0.4	19	1	ADE27111
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	467	19	0.4	19	1	ADE27253
	468	19	0.4	19	1	ADE27270
	469	19	0.4	19	1	ADE27272
	470	19	0.4	19	1	ADE27295
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Stearoyl-CoA desat
Stearoyl-CoA desat
Stearoyl-CoA desat

c 545	19	0.4	19	1	ADE27510	Stearoyl-CoA desat
c 546	19	0.4	19	1	ADE27518	Stearoyl-CoA desat
c 547	19	0.4	19	1	ADE27528	Stearoyl-CoA desat
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c 550	19	0.4	19	1	ADE27626	Stearoyl-CoA desat
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552	19	0.4	19	1	ADE27117	Stearoyl-CoA desat
553	19	0.4	19	1	ADE27128	Stearoyl-CoA desat
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c 562	19	0.4	19	1	ADE27402	Stearoyl-CoA desat
c 563	19	0.4	19	1	ADE27406	Stearoyl-CoA desat
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c 565	19	0.4	19	1	ADE27455	Stearoyl-CoA desat
c 566	19	0.4	19	1	ADE27484	Stearoyl-CoA desat
c 567	19	0.4	19	1	ADE27489	Stearoyl-CoA desat
c 568	19	0.4	19	1	ADE27496	Stearoyl-CoA desat
c 569	19	0.4	19	1	ADE27511	Stearoyl-CoA desat
c 570	19	0.4	19	1	ADE27515	Stearoyl-CoA desat
c 571	19	0.4	19	1	ADE27525	Stearoyl-CoA desat
c 572	19	0.4	19	1	ADE27553	Stearoyl-CoA desat
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c 578	19	0.4	19	1	ADE27634	Stearoyl-CoA desat
579	19	0.4	19	1	ADE27115	Stearoyl-CoA desat
580	19	0.4	19	1	ADE27126	Stearoyl-CoA desat
581	19	0.4	19	1	ADE27130	Stearoyl-CoA desat
582	19	0.4	19	1	ADE27138	Stearoyl-CoA desat
583	19	0.4	19	1	ADE27144	Stearoyl-CoA desat
584	19	0.4	19	1	ADE27182	Stearoyl-CoA desat
585	19	0.4	19	1	ADE27183	Stearoyl-CoA desat
586	19	0.4	19	1	ADE27184	Stearoyl-CoA desat
587	19	0.4	19	1	ADE27189	Stearoyl-CoA desat
588	19	0.4	19	1	ADE27193	Stearoyl-CoA desat
589	19	0.4	19	1	ADE27240	Stearoyl-CoA desat
590	19	0.4	19	1	ADE27243	Stearoyl-CoA desat
591	19	0.4	19	1	ADE27257	Stearoyl-CoA desat
592	19	0.4	19	1	ADE27265	Stearoyl-CoA desat
593	19	0.4	19	1	ADE27281	Stearoyl-CoA desat
594	19	0.4	19	1	ADE27288	Stearoyl-CoA desat
595	19	0.4	19	1	ADE27299	Stearoyl-CoA desat
596	19	0.4	19	1	ADE27305	Stearoyl-CoA desat
c 597	19	0.4	19	1	ADE27431	Stearoyl-CoA desat
c 598	19	0.4	19	1	ADE27459	Stearoyl-CoA desat
c 599	19	0.4	19	1	ADE27486	Stearoyl-CoA desat
c 600	19	0.4	19	1	ADE27492	Stearoyl-CoA desat
c 601	19	0.4	19	1	ADE27494	Stearoyl-CoA desat
c 602	19	0.4	19	1	ADE27495	Stearoyl-CoA desat
c 603	19	0.4	19	1	ADE27524	Stearoyl-CoA desat
c 604	19	0.4	19	1	ADE27543	Stearoyl-CoA desat
c 605	19	0.4	19	1	ADE27554	Stearoyl-CoA desat
c 606	19	0.4	19	1	ADE27635	Stearoyl-CoA desat
607	19	0.4	21	1	AAQ75609	Reverse transcript
c 608	19	0.4	21	1	ADE27648	Stearoyl-CoA desat
609	19	0.4	21	1	ADE27641	Stearoyl-CoA desat
610	19	0.4	21	1	ADE27642	Stearoyl-CoA desat
c 611	19	0.4	21	1	ADG30278	SCD-targeted siNA
c 612	19	0.4	21	1	ADG30286	SCD-targeted siNA
613	19	0.4	21	1	ADG30280	SCD-targeted siNA
614	19	0.4	21	1	ADG30279	SCD-targeted siNA
c 615	19	0.4	22	1	ADE27662	Stearoyl-CoA desat
c 616	19	0.4	22	1	ADE27654	Stearoyl-CoA desat
617	19	0.4	23	1	ADE27657	Stearoyl-CoA desat
618	19	0.4	23	1	ADE27649	Stearoyl-CoA desat
619	19	0.4	23	1	ADG30272	SCD-targeted siNA
620	19	0.4	23	1	ADG30271	SCD-targeted siNA
c 621	18.4	0.4	20	1	ABZ89487	Human oligonucleot
c 622	18.4	0.4	20	1	ABD25717	AI034360-derived o
c 623	18.4	0.4	20	1	ADL59750	Human ESM-1 antise
624	18.4	0.4	21	1	AAQ75617	Reverse transcript
c 625	18.4	0.4	21	1	ADF83488	Human MC1R gene-sp
c 626	18.4	0.4	23	1	AAQ75028	LCR oligo 2. Synt
627	18.4	0.4	23	1	AAQ75029	LCR oligo 3. Synt
628	18	0.4	18	1	AAV54171	Nucleotide sequenc
629	18	0.4	18	1	AAZ90641	Human adipose tiss
630	18	0.4	20	1	AAQ75559	Reverse transcript
631	18	0.4	21	1	AAQ75607	Reverse transcript
632	18	0.4	21	1	AAQ75608	Reverse transcript
633	18	0.4	21	1	AAQ75610	Reverse transcript
634	18	0.4	21	1	ADK01302	Rat DNA microarray
c 635	18	0.4	22	1	ACA89735	Herbicide resistan
636	17.8	0.4	21	1	AAQ75648	Reverse transcript
637	17.8	0.4	21	1	AAQ75777	Reverse transcript
638	17.8	0.4	22	1	AAF99703	Immunostimulatory
639	17.8	0.4	22	1	ABS78424	Angiogenesis inhib
640	17.8	0.4	22	1	ACH03242	Immunostimulatory
641	17.8	0.4	22	1	ADB37205	Immunostimulatory
642	17.8	0.4	22	1	ADK61705	Base containing SS
c 643	17.8	0.4	22	1	ADK61713	Base containing SS
c 644	17.8	0.4	22	1	ADR23192	Human D16S475.R11
c 645	17.4	0.4	19	1	ADN34219	Upper strand of cy
646	17.4	0.4	19	1	ADN34458	Lower strand of cy
c 647	17.4	0.4	19	1	ADK70862	5' mRNA DNA prepar
648	17.4	0.4	20	1	AAQ75561	Reverse transcript
649	17.4	0.4	20	1	AAQ97426	Phage lambda (1841
c 650	17.4	0.4	20	1	ABL57547	Synthetic deoxyrib
651	17.4	0.4	20	1	AAI70284	Phage lambda genom
652	17.4	0.4	20	1	ABL45057	Human chromosome 1
c 653	17.4	0.4	20	1	ABA97632	Poly n nucleotide
654	17.4	0.4	20	1	ADB25743	Mouse connective t
655	17.4	0.4	20	1	ABZ85669	Human oligonucleot
c 656	17.4	0.4	20	1	ABZ85532	Human oligonucleot
c 657	17.4	0.4	20	1	ABZ89014	Human oligonucleot
c 658	17.4	0.4	20	1	ABD21762	Human stanniocalci
c 659	17.4	0.4	20	1	ABD25244	AI051839-derived o
660	17.4	0.4	20	1	ABD21899	Human stanniocalci
c 661	17.4	0.4	20	1	ADG86989	Human PPAR antisen
662	17.4	0.4	20	1	ADG86844	Human PPAR antisen
c 663	17.4	0.4	20	1	ADH70655	Human Vbeta gene r
664	17.4	0.4	20	1	ADJ25433	Human endothelial
665	17.4	0.4	20	1	ADJ25040	Human endothelial
c 666	17.4	0.4	20	1	ADL59745	Human ESM-1 antise
c 667	17.4	0.4	20	1	ADL59751	Human ESM-1 antise
c 668	17.4	0.4	20	1	ADL34927	Human PPAR-delta t
669	17.4	0.4	20	1	ADL34782	Antisense oligonuc
670	17.4	0.4	21	1	AAQ61989	HIV replication in
671	17.4	0.4	21	1	AAQ75657	Reverse transcript
672	17.4	0.4	21	1	AAQ75618	Reverse transcript
673	17.4	0.4	21	1	AAQ75625	Reverse transcript
674	17.4	0.4	21	1	AAQ75641	Reverse transcript
675	17.4	0.4	21	1	AAQ75615	Reverse transcript
676	17.4	0.4	21	1	AAQ75705	Reverse transcript
677	17.4	0.4	21	1	AAQ75737	Reverse transcript
678	17.4	0.4	21	1	AAQ75621	Reverse transcript
679	17.4	0.4	21	1	AAQ75613	Reverse transcript
680	17.4	0.4	21	1	AAQ75616	Reverse transcript
681	17.4	0.4	21	1	AAT35001	HIV inhibitor #4.
682	17.4	0.4	21	1	AAT76098	Human histidine de
683	17.4	0.4	21	1	AAX53903	Histidine decarbox
684	17.4	0.4	21	1	AAA33346	Low adenosine anti
685	17.4	0.4	21	1	AAF19468	Human histidine de
c 686	17.4	0.4	21	1	ABS98544	Human acetyl choli
687	17.4	0.4	21	1	ABZ95162	Human histidine de
688	17.4	0.4	21	1	ADK01304	Rat DNA microarray
689	17.4	0.4	21	1	ABD19062	Human histidine de
690	17	0.4	17	1	AAA30181	PCR primer GT15G u

	691	17	0.4	17	1	AAZ35714	Murine gene anchor
	692	17	0.4	17	1	AAX82721	Human IgA nephropa
	693	17	0.4	17	1	AAZ36740	Anchored oligo(dT)
	694	17	0.4	17	1	AAA25448	Oestrogen receptor
	695	17	0.4	17	1	AAC64204	PCR anchor primer,
	696	17	0.4	17	1	AAC64183	PCR anchor primer,
	697	17	0.4	17	1	AAC64173	PCR anchor primer,
	698	17	0.4	17	1	AAC64163	PCR anchor primer,
	699	17	0.4	17	1	AAC64215	PCR anchor primer,
	700	17	0.4	17	1	AAC64232	PCR anchor primer,
	701	17	0.4	17	1	AAC92294	Human pollinosis-a
	702	17	0.4	17	1	AAC91721	PCR anchor primer,
	703	17	0.4	17	1	AAC82876	Human pollinosis-a
	704	17	0.4	17	1	AAH47128	Nucleotide sequenc
	705	17	0.4	17	1	ABK49636	Human Acetyltransf
	706	17	0.4	17	1	ABL59040	Nucleotide sequenc
	707	17	0.4	17	1	ABN99831	Human allergic dis
	708	17	0.4	17	1	AAL49950	Human B1153 expres
	709	17	0.4	17	1	AAL47236	Allergic disease e
	710	17	0.4	17	1	ABK49758	Human atopic derma
c	711	17	0.4	17	1	ADB42614	Tumour suppression
	712	17	0.4	17	1	ADB44070	Tumour suppression
	713	17	0.4	17	1	ADC84470	PCR primer for amp
	714	17	0.4	17	1	ADE30798	Cholesterol homeos
	715	17	0.4	17	1	ADI50896	Human tumour suppr
	716	17	0.4	17	1	ACC53202	Human tumour suppr
	717	17	0.4	17	1	ACC51607	Human tumour suppr
	718	17	0.4	17	1	ADI13011	PCR primer GT15G u
	719	17	0.4	18	1	AAV54168	Nucleotide sequenc
	720	17	0.4	18	1	AAV54174	Nucleotide sequenc
	721	17	0.4	18	1	AAV54165	Nucleotide sequenc
	722	17	0.4	18	1	AAZ90644	Human adipose tiss
	723	17	0.4	18	1	AAZ90650	Human adipose tiss
	724	17	0.4	18	1	AAZ90647	Human adipose tiss
	725	17	0.4	19	1	AAQ75547	Reverse transcript
	726	17	0.4	20	1	AAQ75560	Reverse transcript
	727	17	0.4	20	1	AAQ75562	Reverse transcript
	728	17	0.4	20	1	AAT04917	Mammalian stem cel
	729	17	0.4	20	1	AAV15104	Human VEGF antisen
c	730	17	0.4	20	1	AAZ09195	Oligonucleotide 7
c	731	17	0.4	20	1	AAX15599	Fragment of upstre
	732	17	0.4	20	1	AAX15764	Antisense oligonuc
	733	17	0.4	20	1	AAA13752	Stem cell factor u
	734	17	0.4	20	1	AAH41331	Universal stem cel
	735	17	0.4	20	1	AAS04111	Human SCF (stem ce
	736	17	0.4	20	1	AAF89091	Mammalian stem cel
	737	17	0.4	20	1	AAH23889	Human SCF (stem ce
	738	17	0.4	20	1	AAS04212	Human SCF (stem ce
	739	17	0.4	20	1	AAS10447	Human stem cell fa
c	740	17	0.4	20	1	ABL57070	Molecular beacon t
	741	17	0.4	20	1	AAD35464	Rat SCF 5' cDNA am
	742	17	0.4	20	1	ABS73848	SCF universal olig
c	743	17	0.4	20	1	AAD57844	Target oligonucleo
	744	17	0.4	20	1	ADE52460	Stem cell factor (
c	745	17	0.4	20	1	ADF23330	Binding partner sc
c	746	17	0.4	20	1	ABZ85535	Human oligonucleot
c	747	17	0.4	20	1	ABD21765	Human stanniocalci
c	748	17	0.4	20	1	ADL59746	Human ESM-1 antise
c	749	17	0.4	20	1	ADL59742	Human ESM-1 antise
	750	17	0.4	20	1	ADM14803	Human mPGES-1 chim
	751	17	0.4	20	1	ADM14429	Human mPGES-1 chim
	752	17	0.4	20	1	ADM14371	Human mPGES-1 chim
	753	17	0.4	20	1	ADM14467	Human mPGES-1 chim
	754	17	0.4	20	1	ADP99302	Stem cell factor,
	755	17	0.4	21	1	AAQ75611	Reverse transcript
	756	17	0.4	21	1	AAQ75622	Reverse transcript
	757	17	0.4	21	1	AAQ75620	Reverse transcript
	758	17	0.4	21	1	AAQ75614	Reverse transcript
	759	17	0.4	21	1	AAQ75612	Reverse transcript
	760	17	0.4	21	1	AAQ75619	Reverse transcript
c	761	17	0.4	21	1	AAV35395	HIV-1 gag protein
c	762	17	0.4	21	1	ABL57071	Molecular beacon t
c	763	17	0.4	21	1	ABS97681	Histamine N-methyl
c	764	17	0.4	21	1	ABS97669	Histamine N-methyl
	765	17	0.4	21	1	ADK01334	Rat DNA microarray
	766	17	0.4	21	1	ADK01303	Rat DNA microarray
	767	17	0.4	21	1	ADK01301	Rat DNA microarray
	768	16.8	0.4	20	1	AAQ75569	Reverse transcript
	769	16.8	0.4	20	1	AAQ75601	Reverse transcript
	770	16.8	0.4	20	1	AAV40326	Maize oligonucleot
	771	16.8	0.4	20	1	AAA66772	Dog genomic marker
	772	16.8	0.4	20	1	ABL57565	Nucleic acid probe
c	773	16.8	0.4	20	1	ABL95912	Probe poly u for a
c	774	16.8	0.4	20	1	ACC44056	Oligo ISIS 124647
	775	16.8	0.4	20	1	ABZ59435	Human src-c chimer
	776	16.8	0.4	20	1	ABZ89549	Human oligonucleot
c	777	16.8	0.4	20	1	ABZ88498	Human oligonucleot
c	778	16.8	0.4	20	1	ABD24728	AI038433-derived o
	779	16.8	0.4	20	1	ABD25779	AI085559-derived o
	780	16.8	0.4	20	1	ADH67295	Human glucocortico
	781	16.8	0.4	20	1	ADH66257	Human glucocortico
	782	16.8	0.4	20	1	ADH67152	Human glucocortico
	783	16.8	0.4	20	1	ADJ61323	Oligonucleotide as
	784	16.8	0.4	20	1	ADJ61324	Oligonucleotide as
	785	16.8	0.4	20	1	ADJ61325	Oligonucleotide as
	786	16.8	0.4	20	1	ADK61702	Base containing SS
	787	16.8	0.4	20	1	ADJ25304	Human endothelial
c	788	16.8	0.4	20	1	ADL58138	Human ESM-1 antise
	789	16.8	0.4	20	1	ADM14520	Human mPGES-1 chim
	790	16.8	0.4	20	1	ADO46716	Human oligonucleot
	791	16.8	0.4	20	1	ADO46715	Human oligonucleot
	792	16.8	0.4	20	1	ADO46713	Human oligonucleot
	793	16.8	0.4	20	1	ADO46714	Human oligonucleot
	794	16.8	0.4	20	1	ADP69247	Human mitoNEET-spe
	795	16.8	0.4	20	1	ADP69305	Human mitoNEET-spe
	796	16.8	0.4	20	1	ADP69379	Human mitoNEET-spe
	797	16.8	0.4	20	1	ADP69193	Human mitoNEET-spe
	798	16.8	0.4	21	1	AAQ75633	Reverse transcript
	799	16.8	0.4	21	1	AAQ75778	Reverse transcript
	800	16.8	0.4	21	1	AAQ75650	Reverse transcript
	801	16.8	0.4	21	1	AAQ75665	Reverse transcript
	802	16.8	0.4	21	1	AAQ75713	Reverse transcript
	803	16.8	0.4	21	1	AAQ75728	Reverse transcript
	804	16.8	0.4	21	1	AAQ75649	Reverse transcript
	805	16.8	0.4	21	1	AAQ75775	Reverse transcript
	806	16.8	0.4	21	1	AAQ75776	Reverse transcript
	807	16.8	0.4	21	1	AAQ75745	Reverse transcript
	808	16.8	0.4	21	1	AAQ75647	Reverse transcript
	809	16.8	0.4	21	1	AAT86582	Phosphorothioate o
	810	16.8	0.4	21	1	AAT86583	Phosphorothioate o
	811	16.8	0.4	21	1	AAV40583	Human TSC gene exo
c	812	16.8	0.4	21	1	ABS98543	Human acetyl choli
c	813	16.8	0.4	21	1	ACA89736	Herbicide resistan
	814	16.8	0.4	21	1	ADK01328	Rat DNA microarray
	815	16.8	0.4	21	1	ADK01312	Rat DNA microarray
c	816	16.8	0.4	21	1	ADH28008	Human chromosome 1
c	817	16.8	0.4	21	1	ADH70964	Human Vbeta PCR pr
	818	16.8	0.4	21	1	ADH70613	Human Vbeta gene r
	819	16.4	0.4	18	1	AAQ20108	Cross-linking olig
	820	16.4	0.4	18	1	AAQ30447	Oligomer TNFR942 f
	821	16.4	0.4	18	1	AAV54170	Nucleotide sequenc
	822	16.4	0.4	18	1	AAV54172	Nucleotide sequenc
	823	16.4	0.4	18	1	AAZ90642	Human adipose tiss
	824	16.4	0.4	18	1	AAZ90640	Human adipose tiss
	825	16.4	0.4	18	1	ABL56900	Nucleic acid probe
c	826	16.4	0.4	18	1	ABX79779	EST polymorphic DN
c	827	16.4	0.4	18	1	ADL95317	Anti-proliferative
	828	16.4	0.4	19	1	AAA83338	cdk8 ribozyme bind
	829	16.4	0.4	19	1	AAH58500	Cell-cycle depende
c	830	16.4	0.4	19	1	ADO14573	Human PDGFr-target
	831	16.4	0.4	19	1	ADO14884	Human PDGFr-target
	832	16.4	0.4	20	1	AAQ75591	Reverse transcript
	833	16.4	0.4	20	1	AAQ75563	Reverse transcript
	834	16.4	0.4	20	1	AAQ75575	Reverse transcript
	835	16.4	0.4	20	1	AAQ75567	Reverse transcript
	836	16.4	0.4	20	1	AAQ75571	Reverse transcript

c 837	16.4	0.4	20	1	ABL57552	Synthetic deoxyrib
c 838	16.4	0.4	20	1	ABL57553	Synthetic deoxyrib
c 839	16.4	0.4	20	1	ABL57554	Synthetic deoxyrib
c 840	16.4	0.4	20	1	ABL57548	Synthetic deoxyrib
841	16.4	0.4	20	1	ABQ79871	Nucleotide sequenc
c 842	16.4	0.4	20	1	ABA97633	Poly o nucleotide
c 843	16.4	0.4	20	1	ABA97638	Poly t nucleotide
c 844	16.4	0.4	20	1	ABA97639	Poly u nucleotide
c 845	16.4	0.4	20	1	ABA97637	Poly s nucleotide
846	16.4	0.4	20	1	AAD35095	HT15-C downstream
c 847	16.4	0.4	20	1	ABI96151	Capture oligonucle
c 848	16.4	0.4	20	1	AAL61371	Human FXR antisens
c 849	16.4	0.4	20	1	ABZ89872	Human oligonucleot
c 850	16.4	0.4	20	1	ABZ89301	Human oligonucleot
851	16.4	0.4	20	1	ABZ89719	Human oligonucleot
c 852	16.4	0.4	20	1	ABD26102	AA463249-derived o
853	16.4	0.4	20	1	ABD25949	AA906703-derived o
c 854	16.4	0.4	20	1	ABD25531	AI125651-derived o
855	16.4	0.4	20	1	ADJ25197	Human endothelial
c 856	16.4	0.4	20	1	ADL59739	Human ESM-1 antise
c 857	16.4	0.4	20	1	ADO52643	Farnesoid X recept
c 858	16.4	0.4	20	1	ADO52650	Farnesoid X recept
c 859	16.4	0.4	20	1	ADO52628	Farnesoid X recept
860	16.2	0.4	19	1	ADM11779	Environmental poll
c 861	16	0.4	16	1	ADH70350	Human Vbeta gene r
862	16	0.4	17	1	AAV37934	Primer of the spec
863	16	0.4	17	1	AAV49503	Human eosinophil c
864	16	0.4	17	1	AAA30179	PCR primer GT15A u
865	16	0.4	17	1	AAA30180	PCR primer GT15C u
866	16	0.4	17	1	AAX82722	Human IgA nephropa
867	16	0.4	17	1	AAX82720	Human IgA nephropa
868	16	0.4	17	1	AAA25449	Oestrogen receptor
869	16	0.4	17	1	AAA25451	Oestrogen receptor
870	16	0.4	17	1	AAA25452	Oestrogen receptor
871	16	0.4	17	1	AAA25447	Oestrogen receptor
872	16	0.4	17	1	AAC64202	PCR anchor primer,
873	16	0.4	17	1	AAC64203	PCR anchor primer,
874	16	0.4	17	1	AAC64181	PCR anchor primer,
875	16	0.4	17	1	AAC64182	PCR anchor primer,
876	16	0.4	17	1	AAC64171	PCR anchor primer,
877	16	0.4	17	1	AAC64172	PCR anchor primer,
878	16	0.4	17	1	AAC64161	PCR anchor primer,
879	16	0.4	17	1	AAC64162	PCR anchor primer,
880	16	0.4	17	1	AAC64213	PCR anchor primer,
881	16	0.4	17	1	AAC64214	PCR anchor primer,
882	16	0.4	17	1	AAC64231	PCR anchor primer,
883	16	0.4	17	1	AAC64230	PCR anchor primer,
884	16	0.4	17	1	AAC92292	Human pollinosis-a
885	16	0.4	17	1	AAC92293	Human pollinosis-a
886	16	0.4	17	1	AAC91720	PCR anchor primer,
887	16	0.4	17	1	AAC91719	PCR anchor primer,
888	16	0.4	17	1	AAC82875	Human pollinosis-a
889	16	0.4	17	1	AAC82874	Human pollinosis-a
890	16	0.4	17	1	AAH47127	Nucleotide sequenc
891	16	0.4	17	1	AAH47126	Nucleotide sequenc
892	16	0.4	17	1	ABK49634	Human Acetyltransf
893	16	0.4	17	1	ABK49635	Human Acetyltransf
894	16	0.4	17	1	ABL59038	Nucleotide sequenc
895	16	0.4	17	1	ABL59039	Nucleotide sequenc
896	16	0.4	17	1	ABN99829	Human allergic dis
897	16	0.4	17	1	ABN99830	Human allergic dis
898	16	0.4	17	1	AAL49948	Human B1153 expres
899	16	0.4	17	1	AAL49949	Human B1153 expres
900	16	0.4	17	1	AAL47234	Allergic disease e
901	16	0.4	17	1	AAL47235	Allergic disease e
902	16	0.4	17	1	ABK49757	Human atopic derma
903	16	0.4	17	1	ABK49756	Human atopic derma
904	16	0.4	17	1	ADB04273	Human MDZ7 scannin
905	16	0.4	17	1	ADB04272	Human MDZ7 scannin
906	16	0.4	17	1	ADB41269	Tumour suppression
907	16	0.4	17	1	ADB45964	Tumour suppression
908	16	0.4	17	1	ADC84469	PCR primer for amp
909	16	0.4	17	1	ADC84468	PCR primer for amp
910	16	0.4	17	1	ADE77745	DNA oligo (SeqID 5
911	16	0.4	17	1	ADF47483	Gene prediction ta
912	16	0.4	17	1	ADI48898	Human tumour suppr
913	16	0.4	17	1	ACC53203	Human tumour suppr
914	16	0.4	17	1	ADI13009	PCR primer GT15A u
915	16	0.4	17	1	ADI13010	PCR primer GT15C u
916	16	0.4	17	1	ADP86141	CpG immunostimulat
917	16	0.4	17	1	ADR05333	Silkworm juvenile
c 918	16	0.4	18	1	AAN30173	L1 region of the b
919	16	0.4	18	1	AAT94669	Anchored poly(T) o
920	16	0.4	18	1	AAV54175	Nucleotide sequenc
921	16	0.4	18	1	AAV54173	Nucleotide sequenc
922	16	0.4	18	1	AAV54164	Nucleotide sequenc
923	16	0.4	18	1	AAV54166	Nucleotide sequenc
924	16	0.4	18	1	AAV54169	Nucleotide sequenc
925	16	0.4	18	1	AAV54167	Nucleotide sequenc
926	16	0.4	18	1	AAZ90649	Human adipose tiss
927	16	0.4	18	1	AAZ90648	Human adipose tiss
928	16	0.4	18	1	AAZ90646	Human adipose tiss
929	16	0.4	18	1	AAZ90645	Human adipose tiss
930	16	0.4	18	1	AAZ90643	Human adipose tiss
931	16	0.4	18	1	AAZ90651	Human adipose tiss
932	16	0.4	18	1	AAA58386	Polynucleotide # 2
933	16	0.4	18	1	AAF75596	Binary encoded seq
934	16	0.4	18	1	AAF75597	Binary encoded seq
935	16	0.4	18	1	AAD16463	K. singaporensis i
936	16	0.4	19	1	AAQ75549	Reverse transcript
937	16	0.4	19	1	AAQ75548	Reverse transcript
938	16	0.4	19	1	AAQ75550	Reverse transcript
c 939	16	0.4	19	1	ACA98771	Human CYP2C8 SNP d
940	16	0.4	19	1	ACA98774	Human CYP2C8 SNP d
c 941	16	0.4	19	1	ADE29541	Mitogen activated
942	16	0.4	19	1	ADE29704	Mitogen activated
943	16	0.4	19	1	ADR81681	Hepatitis C virus
944	16	0.4	20	1	AAQ75566	Reverse transcript
945	16	0.4	20	1	AAQ75574	Reverse transcript
946	16	0.4	20	1	AAQ75568	Reverse transcript
947	16	0.4	20	1	AAQ75570	Reverse transcript
948	16	0.4	20	1	AAQ75572	Reverse transcript
949	16	0.4	20	1	AAQ75564	Reverse transcript
950	16	0.4	20	1	AAQ75565	Reverse transcript
951	16	0.4	20	1	AAQ75573	Reverse transcript
c 952	16	0.4	20	1	AAX38448	E. coli SecA antis
953	16	0.4	20	1	AAF83959	BAP28 gene fragmen
954	16	0.4	20	1	AAD12369	Human caspase 8 mR
955	16	0.4	20	1	ABA05915	Hepatitis B virus
956	16	0.4	20	1	ABA05916	Hepatitis B virus
c 957	16	0.4	20	1	AAD55499	Human FGFR-3 antis
958	16	0.4	20	1	ADD24998	Human caspase-8 an
c 959	16	0.4	20	1	ABZ89676	Human oligonucleot
c 960	16	0.4	20	1	ABZ88938	Human oligonucleot
c 961	16	0.4	20	1	ABZ88618	Human oligonucleot
c 962	16	0.4	20	1	ABD24848	AI092623-derived o
c 963	16	0.4	20	1	ABD25168	AI041482-derived o
964	16	0.4	20	1	ADH67348	Human glucocortico
965	16	0.4	20	1	ADH66659	Human glucocortico
966	16	0.4	20	1	ADH66380	Human glucocortico
967	16	0.4	20	1	ADH66379	Human glucocortico
968	16	0.4	20	1	ADH67400	Human glucocortico
969	16	0.4	20	1	ADK94634	Primer of the inve
970	16	0.4	20	1	ADK74647	Chimeric phosphoro
971	16	0.4	20	1	ADK73558	Chimeric phosphoro
972	16	0.4	20	1	ADK73725	Chimeric phosphoro
973	16	0.4	20	1	ADK74442	Chimeric phosphoro
974	16	0.4	20	1	ADK74413	Chimeric phosphoro
975	16	0.4	20	1	ADK19329	Immunostimulatory
976	16	0.4	20	1	ADK19330	Immunostimulatory
c 977	16	0.4	20	1	ADL59743	Human ESM-1 antise
978	16	0.4	20	1	ADM14246	Human mPGES-1 chim
979	16	0.4	20	1	ADM14751	Human mPGES-1 chim
c 980	15.8	0.4	19	1	ADE27324	Stearoyl-CoA desat
981	15.8	0.4	19	1	ADE27614	Stearoyl-CoA desat
982	15.8	0.4	19	1	AAQ75557	Reverse transcript

c 983	15.8	0.4	19	1	AAV28402	Wild type transpos
c 984	15.8	0.4	19	1	AAZ06438	Wildtype Inside En
c 985	15.8	0.4	19	1	AAA11741	Transposon Tn5 ins
986	15.8	0.4	19	1	AAA86321	PCBA HH ribozyme b
c 987	15.8	0.4	19	1	AAD21281	Inside end (IE) te
c 988	15.8	0.4	19	1	AAC85194	Tn5 transposase in
c 989	15.8	0.4	19	1	AAC91689	Transposon Tn5 IS5
990	15.8	0.4	19	1	AAH61483	PCNA HH ribozyme b
c 991	15.8	0.4	19	1	ACA90054	Cardiovascular dis
c 992	15.8	0.4	19	1	ABZ22886	Oligonucleotide kh
c 993	15.8	0.4	19	1	AAD58808	Tn5 transposon ele
994	15.8	0.4	19	1	ADF36101	Human VEGFR1 short
c 995	15.8	0.4	19	1	ADF36528	Human VEGFR1 short
c 996	15.8	0.4	19	1	ADH16535	Human BACE transcr
997	15.8	0.4	19	1	ADH16860	Human BACE siNA lo
998	15.8	0.4	19	1	ADH70642	Human Vbeta gene r
c 999	15.8	0.4	19	1	ADH70567	Human Vbeta gene r
1000	15.8	0.4	19	1	ADH70449	Human Vbeta gene r
1001	15.8	0.4	19	1	ADM97645	Human MIA-2 coding
c1002	15.8	0.4	19	1	ADQ16517	Transposon Tn5 inn
1003	15.6	0.4	17	1	AAV19118	Anchored oligo(T)
1004	15.6	0.4	18	1	ABK98126	Triple helix formi
1005	15.6	0.4	19	1	ACA98775	Human CYP2C8 SNP d
c1006	15.6	0.4	19	1	ACA98772	Human CYP2C8 SNP d
1007	15.4	0.4	17	1	AAT12451	Antiviral phosphor
1008	15.4	0.4	17	1	AAX69799	Human flt1 VEGF re
1009	15.4	0.4	17	1	AAA25446	Oestrogen receptor
c1010	15.4	0.4	17	1	ABT35107	Tumour suppression
1011	15.4	0.4	17	1	ADB04274	Human MDZ7 scannin
1012	15.4	0.4	17	1	ABZ61148	Human K-Ras DNAzym
c1013	15.4	0.4	17	1	ACC52668	Human tumour suppr
1014	15.4	0.4	17	1	ADP86140	CpG immunostimulat
1015	15.4	0.4	17	1	ADP86143	CpG immunostimulat
1016	15.4	0.4	18	1	AAQ30446	Oligomer TNFR941 f
c1017	15.4	0.4	18	1	AAQ25501	Purine rich HUMNFR
1018	15.4	0.4	18	1	AAV35391	HIV-1 gag protein
c1019	15.4	0.4	18	1	AAV07750	Phosphorothioate o
1020	15.4	0.4	18	1	AAV21967	Nuclease resistant
c1021	15.4	0.4	18	1	AAV21967	Nuclease resistant
1022	15.4	0.4	18	1	AAX19941	Primer SEQ ID NO:1
c1023	15.4	0.4	18	1	AAX19941	Primer SEQ ID NO:1
1024	15.4	0.4	18	1	AAX87332	Reverse transcript
c1025	15.4	0.4	18	1	AAX89278	PDE8A specific pri
c1026	15.4	0.4	18	1	AAA72005	Human PDE8A specif
1027	15.4	0.4	18	1	ABL57540	Nucleic acid probe
1028	15.4	0.4	18	1	ABL57543	Nucleic acid probe
1029	15.4	0.4	18	1	AAC87202	Escherichia coli f
1030	15.4	0.4	18	1	ABK13935	5'-PCR primer used
1031	15.4	0.4	18	1	ABL38718	Immunostimulatory
c1032	15.4	0.4	18	1	ABL38718	Immunostimulatory
c1033	15.4	0.4	18	1	ABL31389	Human HLA genotypi
1034	15.4	0.4	18	1	ACF36339	Nucleotide sequenc
1035	15.4	0.4	18	1	ACF36364	Nucleotide sequenc
1036	15.4	0.4	18	1	ADC64943	Camellia sinensis
1037	15.4	0.4	18	1	ADC64942	Camellia sinensis
1038	15.4	0.4	18	1	ADC64941	Camellia sinensis
1039	15.4	0.4	18	1	AAD63454	Tea non-dormant (N
1040	15.4	0.4	18	1	AAD63452	Tea non-dormant (N
1041	15.4	0.4	18	1	AAD63453	Tea non-dormant (N
c1042	15.4	0.4	18	1	ADM06395	Human PCR primer S
1043	15.4	0.4	18	1	ADM16963	T11A PCR primer, t
1044	15.4	0.4	18	1	ADM16964	T11C PCR primer, t
1045	15.4	0.4	18	1	ADM16965	T11G PCR primer, t
1046	15.4	0.4	18	1	ADM91739	Primer #3 of the i
1047	15.4	0.4	18	1	ADM91741	Primer #5 of the i
1048	15.4	0.4	18	1	ADM91740	Primer #4 of the i
c1049	15.4	0.4	18	1	ADH43299	Human PDE8A specif
c1050	15.4	0.4	18	1	ADK69848	Human cyclic PDE8A
1051	15.4	0.4	19	1	AAQ75551	Reverse transcript
1052	15.4	0.4	19	1	AAQ75555	Reverse transcript
c1053	15.4	0.4	19	1	AAX32228	Probe specific for
1054	15.4	0.4	19	1	AAA83339	cdk8 ribozyme bind
1055	15.4	0.4	19	1	AAA82668	cdk2 ribozyme bind
1056	15.4	0.4	19	1	AAA82667	cdk2 ribozyme bind
c1057	15.4	0.4	19	1	AAH42195	PCR primer for cDN
1058	15.4	0.4	19	1	AAH57829	Cell-cycle depende
1059	15.4	0.4	19	1	AAH57830	Cell-cycle depende
1060	15.4	0.4	19	1	AAH58501	Cell-cycle depende
1061	15.4	0.4	19	1	ABK90423	Human UGT1a1 promo
c1062	15.4	0.4	19	1	ABK90423	Human UGT1a1 promo
1063	15.4	0.4	19	1	AAL50681	Human uridine diph
c1064	15.4	0.4	19	1	AAL50681	Human uridine diph
c1065	15.4	0.4	19	1	ABL51521	Tailing reaction r
c1066	15.4	0.4	19	1	ADA45468	Human BAP1 DNA pro
1067	15.4	0.4	19	1	ADF36974	Human VEGFR2 short
c1068	15.4	0.4	19	1	ADF36650	Human VEGFR2 short
1069	15.4	0.4	19	1	ADR81918	Hepatitis C virus
1070	15.2	0.4	16	1	AAD44149	Oligo-dT PCR prime
1071	15.2	0.4	17	1	AAX18388	RT-PCR primer of t
1072	15.2	0.4	17	1	AAS14174	Modified Poly-T Pr
1073	15.2	0.4	17	1	AAD44151	Oligo-AT PCR prime
1074	15.2	0.4	18	1	AAX18389	RT-PCR primer of t
1075	15.2	0.4	18	1	ADP04929	PCR primer 1 used
c1076	15.2	0.4	19	1	AAT94431	Template mRNA poly
1077	15.2	0.4	19	1	AAX18390	RT-PCR primer of t
1078	15.2	0.4	19	1	AAZ99489	Primer HOOK for cD
1079	15.2	0.4	19	1	AAD15201	3' sequencing prim
1080	15.2	0.4	19	1	AAH21968	Mouse total gene e
1081	15.2	0.4	19	1	AAS06525	Mouse microglia an
1082	15.2	0.4	19	1	ABK71509	CNS related 3' seq
1083	15.2	0.4	19	1	ABQ73231	Rabbit atheroscler
1084	15.2	0.4	19	1	AAD34663	PCR primer #4 used
1085	15.2	0.4	19	1	AAD40279	HOOK PCR primer us
1086	15.2	0.4	19	1	ABZ68389	Reverse transcript
1087	15.2	0.4	19	1	ACC79402	M13 sequencing pri
1088	15.2	0.4	19	1	AAD49149	3' sequencing prim
1089	15.2	0.4	19	1	AAD50267	3' sequencing prim
1090	15.2	0.4	19	1	ADC21495	Human PRDI-BF1 RT-
c1091	15.2	0.4	19	1	ADF74670	DNA oligo (30) use
1092	15.2	0.4	19	1	ADL24850	Intestinal epithel
1093	15.2	0.4	19	1	ADM16445	RNA intron poly-py
1094	15.2	0.4	20	1	ABL57554	Synthetic deoxyrib
c1095	15.2	0.4	20	1	ABQ79871	Nucleotide sequenc
1096	15.2	0.4	20	1	ABA97633	Poly o nucleotide
1097	15.2	0.4	20	1	ABA97639	Poly u nucleotide
1098	15.2	0.4	21	1	ABS98544	Human acetyl choli
c1099	15	0.3	15	1	AAQ79185	Nuclease resistant
c1100	15	0.3	15	1	AAQ79184	Nuclease resistant
1101	15	0.3	15	1	AAT52136	Human ICAM hammerh
1102	15	0.3	15	1	AAT52138	Human ICAM hammerh
c1103	15	0.3	15	1	AAX65144	Mouse B7-1 hammerh
c1104	15	0.3	15	1	AAV01604	Oligonucleotide co
1105	15	0.3	15	1	AAV01603	Oligonucleotide co
1106	15	0.3	15	1	AAV07431	Synthetic peptide-
1107	15	0.3	15	1	AAT86675	Oligonucleotide li
1108	15	0.3	15	1	AAT86605	Oligonucleotide se
1109	15	0.3	15	1	AAX00787	N3-P5 phosphoramid
c1110	15	0.3	15	1	AAX00788	N3-P5 phosphoramid
1111	15	0.3	15	1	AAX18364	RT-PCR primer of t
1112	15	0.3	15	1	AAZ61854	HCV 3' non core re
1113	15	0.3	15	1	AAZ64910	Substrate for HH r
1114	15	0.3	15	1	AAA46502	PCR primer used to
1115	15	0.3	15	1	AAA75048	Primer used to rev
1116	15	0.3	15	1	AAA07792	Nucleic acid seque
1117	15	0.3	15	1	AAA07794	Nucleic acid seque
1118	15	0.3	15	1	AAA07828	Nucleic acid seque
1119	15	0.3	15	1	AAA07790	Nucleic acid seque
1120	15	0.3	15	1	AAA07789	Nucleic acid seque
1121	15	0.3	15	1	AAA07795	Nucleic acid seque
1122	15	0.3	15	1	AAA07797	Nucleic acid seque
1123	15	0.3	15	1	AAA07799	Nucleic acid seque
1124	15	0.3	15	1	AAA07802	Nucleic acid seque
1125	15	0.3	15	1	AAA07825	Nucleic acid seque
1126	15	0.3	15	1	AAA07831	Nucleic acid seque
1127	15	0.3	15	1	AAA07803	Nucleic acid seque
1128	15	0.3	15	1	AAA07834	Nucleic acid seque

1129	15	0.3	15	1	AAA07796	Nucleic acid seque
1130	15	0.3	15	1	AAA07800	Nucleic acid seque
1131	15	0.3	15	1	AAA07793	Nucleic acid seque
1132	15	0.3	15	1	AAA07798	Nucleic acid seque
1133	15	0.3	15	1	AAA07788	Nucleic acid seque
1134	15	0.3	15	1	AAA07791	Nucleic acid seque
1135	15	0.3	15	1	AAA07801	Nucleic acid seque
1136	15	0.3	15	1	AAA62350	Oligonucleotide #2
1137	15	0.3	15	1	AAA62347	Oligonucleotide #3
1138	15	0.3	15	1	AAA62348	Oligonucleotide #4
1139	15	0.3	15	1	AAH20308	Oligo dT15 EDTA la
1140	15	0.3	15	1	AAF30882	Oligonucleotide po
1141	15	0.3	15	1	AAH20511	Oligonucleotide b)
1142	15	0.3	15	1	AAF49041	IGF-I oligonucleot
1143	15	0.3	15	1	AAH49243	PNA-forming oligon
1144	15	0.3	15	1	ABL40743	Chicken heparanase
1145	15	0.3	15	1	ABA97403	Nucleotide sequenc
c1146	15	0.3	15	1	AAL49453	Mutation detection
c1147	15	0.3	15	1	AAL49455	Mutation detection
1148	15	0.3	15	1	AAD29506	Primer used for th
c1149	15	0.3	15	1	AAD22531	Retroviral reverse
c1150	15	0.3	15	1	ABQ82140	Acceptor vector pH
1151	15	0.3	15	1	ABX00240	Hepatitis C virus
1152	15	0.3	15	1	ABX03406	Hepatitis C virus
1153	15	0.3	15	1	ABL57064	Hydrazide precurso
1154	15	0.3	15	1	ABL57054	Hydrazide phosphor
1155	15	0.3	15	1	ABL57063	Hydrazide precurso
1156	15	0.3	15	1	ABL57066	Amino-C6-modified
1157	15	0.3	15	1	ABL57059	Hydrazide precurso
1158	15	0.3	15	1	ABL57061	Hydrazide precurso
1159	15	0.3	15	1	ABL57056	Hydrazide phosphor
1160	15	0.3	15	1	ABL57060	Hydrazide precurso
1161	15	0.3	15	1	ABK98141	Triple helix formi
1162	15	0.3	15	1	ABK98184	Triple helix formi
c1163	15	0.3	15	1	ABV74142	5' End of cDNA lib
1164	15	0.3	15	1	ABV74141	Oligonucleotide us
1165	15	0.3	15	1	ABV75865	Oligonucleotide T1
c1166	15	0.3	15	1	ADA14836	Hairpin target seq
1167	15	0.3	15	1	ADB68520	Single-base mismat
1168	15	0.3	15	1	ADC18592	Annealing control
1169	15	0.3	15	1	ADF44290	HPV labelling 3'-e
1170	15	0.3	15	1	AAD63523	Chicken heparanase
1171	15	0.3	15	1	ADF91234	cDNA synthesis ass
1172	15	0.3	15	1	ADG88842	Human hpa cDNA amp
1173	15	0.3	15	1	ABZ37501	Oligonucleotide SE
1174	15	0.3	15	1	ADG28662	Annealing control
c1175	15	0.3	15	1	ADH70349	Human Vbeta gene r
c1176	15	0.3	15	1	ADH70351	Human Vbeta gene r
c1177	15	0.3	15	1	ADH50577	Bacterial DNA prim
1178	15	0.3	15	1	ADI34486	Nucleotide sequenc
1179	15	0.3	15	1	ADL16374	Human heparanase c
1180	15	0.3	15	1	ADM48711	Human hp3 DNA ampl
1181	15	0.3	15	1	ADL33722	LNA oligomer #1.
1182	15	0.3	15	1	ADO81112	Sheep prion protei
1183	15	0.3	15	1	ADO81158	Prion protein poly
1184	15	0.3	15	1	ADO81108	Sheep prion protei
1185	15	0.3	15	1	ADO78367	RNA oligonucleotid
1186	15	0.3	15	1	ADO78368	RNA oligonucleotid
1187	15	0.3	15	1	ADQ81798	Oligonucleotide sy
1188	15	0.3	16	1	AAX18365	RT-PCR primer of t
1189	15	0.3	16	1	AAX18366	RT-PCR primer of t
1190	15	0.3	16	1	AAX18367	RT-PCR primer of t
c1191	15	0.3	16	1	AAX07568	Homo sapiens fetal
c1192	15	0.3	16	1	AAC66068	DNA chip primer #4
1193	15	0.3	16	1	ABA04585	Oligonucleotide #5
1194	15	0.3	16	1	AAF30895	Oligonucleotide-mi
1195	15	0.3	16	1	AAF30880	Oligonucleotide po
1196	15	0.3	16	1	AAH42481	Oligonucleotide us
c1197	15	0.3	16	1	ABL57075	Molecular beacon t
1198	15	0.3	16	1	ABA97402	Nucleotide sequenc
1199	15	0.3	16	1	ABK87931	Anchored oligo-dT
1200	15	0.3	16	1	AAD56451	2'F-ANA antisense
1201	15	0.3	16	1	AAL54078	Oligo-homodeoxyrib
c1202	15	0.3	16	1	AAD57845	Target oligonucleo
1203	15	0.3	16	1	ADB68508	PNA-HypNA hybridis
1204	15	0.3	16	1	ADB68519	DNA hybridisation
c1205	15	0.3	16	1	ADF23331	Binding partner sc
1206	15	0.3	16	1	ADI34487	Nucleotide sequenc
1207	15	0.3	17	1	AAX69800	Human flt1 VEGF re
1208	15	0.3	17	1	AAX69801	Human flt1 VEGF re
c1209	15	0.3	17	1	AAX72892	Mouse flk-1 VEGF r
1210	15	0.3	17	1	AAX69802	Human flt1 VEGF re
1211	15	0.3	17	1	AAX18371	RT-PCR primer of t
1212	15	0.3	17	1	AAX18370	RT-PCR primer of t
1213	15	0.3	17	1	AAZ89372	RNA detecting prim
1214	15	0.3	17	1	AAZ36739	Anchored oligo(dT)
1215	15	0.3	17	1	AAA25450	Oestrogen receptor
1216	15	0.3	17	1	AAA25453	Oestrogen receptor
1217	15	0.3	17	1	AAA98232	Human retrovirus H
1218	15	0.3	17	1	AAA50197	2'-Methoxyethoxy-m
1219	15	0.3	17	1	ABK13941	5'-PCR primer used
c1220	15	0.3	17	1	ABK19050	Human ERG DNAzyme
1221	15	0.3	17	1	ABK98192	Triple helix formi
1222	15	0.3	17	1	ABX79793	EST polymorphic DN
1223	15	0.3	17	1	ADB04271	Human MDZ7 scannin
1224	15	0.3	17	1	ADB04270	Human MDZ7 scannin
1225	15	0.3	17	1	ABZ70578	Primer. Synthetic
1226	15	0.3	17	1	AAD56441	Antisense oligo #2
1227	15	0.3	17	1	AAD56448	2'F-ANA antisense
1228	15	0.3	17	1	AAD56449	2'F-ANA antisense
1229	15	0.3	17	1	AAD56447	2'F-ANA antisense
1230	15	0.3	17	1	AAD56450	2'F-ANA antisense
1231	15	0.3	17	1	ADB98902	LRP5 mutagenic PCR
1232	15	0.3	17	1	ACF36345	Nucleotide sequenc
1233	15	0.3	17	1	ACF36370	Nucleotide sequenc
1234	15	0.3	17	1	ADI34488	Nucleotide sequenc
c1235	15	0.3	17	1	ADO04016	Annealing primer u
c1236	15	0.3	17	1	ADP71261	Oligo #13 for gase
1237	15	0.3	17	1	ADP71260	Oligo #12 for gase
1238	15	0.3	17	1	ADP86177	CpG immunostimulat
1239	15	0.3	17	1	ADP86146	CpG immunostimulat
1240	15	0.3	17	1	ADP86154	CpG immunostimulat
1241	15	0.3	17	1	ADP86178	CpG immunostimulat
1242	15	0.3	17	1	ADP86185	CpG immunostimulat
1243	15	0.3	17	1	ADP86145	CpG immunostimulat
1244	15	0.3	17	1	ADP86137	CpG immunostimulat
1245	15	0.3	17	1	ADP86183	CpG immunostimulat
1246	15	0.3	17	1	ADP86144	CpG immunostimulat
1247	15	0.3	17	1	ADP86131	CpG immunostimulat
1248	15	0.3	17	1	ADP86184	CpG immunostimulat
c1249	15	0.3	18	1	AAQ34110	Sequence of a micr
1250	15	0.3	18	1	AAQ75025	PCR primer. Synth
1251	15	0.3	18	1	AAT94667	Anchored poly(T) o
1252	15	0.3	18	1	AAT94668	Anchored poly(T) o
c1253	15	0.3	18	1	AAV37712	Human protein AQ2_
1254	15	0.3	18	1	AAV21970	Nuclease resistant
1255	15	0.3	18	1	AAX19943	Primer SEQ ID NO:3
c1256	15	0.3	18	1	AAX19942	Primer SEQ ID NO:2
1257	15	0.3	18	1	AAX18373	RT-PCR primer of t
1258	15	0.3	18	1	AAX18372	RT-PCR primer of t
c1259	15	0.3	18	1	AAA40563	Human adult ovary
c1260	15	0.3	18	1	AAA58385	Polynucleotide # 1
c1261	15	0.3	18	1	AAZ87161	Oligoarabinonucleo
1262	15	0.3	18	1	AAZ87162	Oligoarabinonucleo
1263	15	0.3	18	1	AAZ87166	Deoxyarabinonucleo
c1264	15	0.3	18	1	AAZ87167	Deoxyarabinonucleo
1265	15	0.3	18	1	AAD03565	Oligonucleotide #6
c1266	15	0.3	18	1	AAD17014	Oligonucleotide A1
1267	15	0.3	18	1	AAF75598	Binary encoded seq
c1268	15	0.3	18	1	AAD20091	mRNA fragment used
1269	15	0.3	18	1	AAF99708	Immunostimulatory
1270	15	0.3	18	1	AAF99734	Immunostimulatory
1271	15	0.3	18	1	AAF82472	Phagemid vector pC
1272	15	0.3	18	1	ABK51158	Human cytomegalovi
1273	15	0.3	18	1	AAS94743	Rat secreted facto
1274	15	0.3	18	1	ABS78455	Angiogenesis inhib

1275	15	0.3	18	1	ABS78429	Angiogenesis inhib
1276	15	0.3	18	1	ABL39401	Immunostimulatory
1277	15	0.3	18	1	AAD41497	Oligonucleotide us
1278	15	0.3	18	1	ABS53437	Poly d(T) primer.
1279	15	0.3	18	1	ABA93239	Adaptor oligonucle
1280	15	0.3	18	1	AAD52799	Primer used to pre
c1281	15	0.3	18	1	AAD56466	Target RNA #1 used
1282	15	0.3	18	1	AAD56440	Antisense oligo #1
1283	15	0.3	18	1	AAD56446	2'F-ANA antisense
1284	15	0.3	18	1	ACH03247	Immunostimulatory
1285	15	0.3	18	1	AAD57871	Antisense oligo #1
1286	15	0.3	18	1	AAD57878	Antisense DNA-RNA
1287	15	0.3	18	1	AAD57879	Antisense DNA-RNA
1288	15	0.3	18	1	AAD57877	Antisense DNA-RNA
c1289	15	0.3	18	1	AAD57890	Target RNA #1 used
1290	15	0.3	18	1	ADB37210	Immunostimulatory
1291	15	0.3	18	1	ADB37236	Immunostimulatory
c1292	15	0.3	18	1	ADE77617	Human probe NEG fo
1293	15	0.3	18	1	ADI34489	Nucleotide sequenc
c1294	15	0.3	18	1	ADH78590	Test element oligo
1295	15	0.3	18	1	ADL95318	Anti-proliferative
c1296	15	0.3	18	1	ADO28710	Single stranded cD
1297	15	0.3	18	1	ADO28711	Single stranded cD
1298	15	0.3	18	1	ADO26684	Synthetic leader s
c1299	15	0.3	18	1	ADO26682	Synthetic leader s
1300	15	0.3	18	1	ADP86130	CpG immunostimulat
1301	15	0.3	18	1	ADR32355	Rat KDR cytosolic
1302	15	0.3	18	1	ADR57967	Nucleotide #4 for
1303	15	0.3	19	1	ADE27471	Stearoyl-CoA desat
c1304	15	0.3	19	1	ADE27181	Stearoyl-CoA desat
1305	15	0.3	19	1	ADE27470	Stearoyl-CoA desat
c1306	15	0.3	19	1	ADE27180	Stearoyl-CoA desat
1307	14.8	0.3	18	1	AAQ20109	Cross-linking olig
1308	14.8	0.3	18	1	AAQ30448	Oligomer TNFR943 f
1309	14.8	0.3	18	1	AAX15198	Triple helix formi
1310	14.8	0.3	18	1	AAV21969	Nuclease resistant
1311	14.8	0.3	18	1	AAX91065	CAT gene target RN
1312	14.8	0.3	18	1	AAH63154	Shrimp white spot
1313	14.8	0.3	18	1	AAD14847	Human PS-133 EST-s
c1314	14.8	0.3	18	1	AAI64450	SSR motif #10. Un
1315	14.8	0.3	18	1	ABT21493	Multiplex group PC
1316	14.8	0.3	18	1	ABZ10686	Haematopoietic cel
1317	14.8	0.3	18	1	ABZ11102	Haematopoietic cel
1318	14.8	0.3	18	1	ABZ10510	Haematopoietic cel
1319	14.8	0.3	18	1	ADB54892	Hybridisation olig
1320	14.8	0.3	18	1	ADC70239	Primer oligo used
1321	14.8	0.3	18	1	ADC70018	Primer oligo used
1322	14.8	0.3	18	1	ADE84378	Human lymphoid cel
1323	14.8	0.3	18	1	ADE84488	Human lymphoid cel
c1324	14.8	0.3	18	1	ADF92108	Human cytokeratin
c1325	14.8	0.3	18	1	ADH70321	Human Vbeta gene r
c1326	14.8	0.3	18	1	ADH70679	Human Vbeta gene r
c1327	14.8	0.3	18	1	ADQ15984	Human HES-6 transc
1328	14.8	0.3	18	1	ADS90292	Oligonucleotide of
c1329	14.8	0.3	18	1	ADS90530	Oligonucleotide of
c1330	14.8	0.3	20	1	ADB25743	Mouse connective t
1331	14.8	0.3	20	1	AAD55499	Human FGFR-3 antis
c1332	14.8	0.3	24	1	ADG75988	Immunostimulatory
1333	14.6	0.3	15	1	AAS99971	Human NPR1 gene al
c1334	14.6	0.3	15	1	ABK32799	Human APPBP1 gene,
c1335	14.4	0.3	16	1	AAQ83416	c-fos antisense ol
1336	14.4	0.3	16	1	AAX18360	RT-PCR primer of t
1337	14.4	0.3	16	1	AAX18368	RT-PCR primer of t
1338	14.4	0.3	16	1	AAX82792	Chicken cytochrome
c1339	14.4	0.3	16	1	AAX82793	Chicken cytochrome
1340	14.4	0.3	16	1	ABL57076	Molecular beacon t
1341	14.4	0.3	16	1	ABK90419	Human UGT1a1 promo
c1342	14.4	0.3	16	1	ABK90419	Human UGT1a1 promo
1343	14.4	0.3	16	1	AAL50677	Human uridine diph
c1344	14.4	0.3	16	1	AAL50677	Human uridine diph
c1345	14.4	0.3	16	1	ABL45022	Human chromosome 1
1346	14.4	0.3	16	1	AAD44147	Oligo-dT PCR prime
1347	14.4	0.3	16	1	AAD57846	Target oligonucleo
1348	14.4	0.3	16	1	ADF23332	Binding partner sc
1349	14.4	0.3	16	1	ADI20623	Putative eRNA sequ
1350	14.4	0.3	16	1	ADH70346	Human Vbeta gene r
c1351	14.4	0.3	16	1	ADH70346	Human Vbeta gene r
1352	14.4	0.3	16	1	ADH70379	Human Vbeta gene r
1353	14.4	0.3	16	1	ADH70276	Human Vbeta gene r
1354	14.4	0.3	16	1	ADH70347	Human Vbeta gene r
1355	14.4	0.3	16	1	ADR33544	Human nicking agen
c1356	14.4	0.3	16	1	ADR33311	Human nicking agen
1357	14.4	0.3	16	1	ADS15827	Control probe targ
1358	14.4	0.3	17	1	AAT81559	Human c-myb hammer
1359	14.4	0.3	17	1	AAX69798	Human flt1 VEGF re
c1360	14.4	0.3	17	1	AAX69804	Human flt1 VEGF re
c1361	14.4	0.3	17	1	AAX69803	Human flt1 VEGF re
c1362	14.4	0.3	17	1	AAX73165	Mouse flk-1 VEGF r
1363	14.4	0.3	17	1	AAA19027	Human TIE-2 substr
1364	14.4	0.3	17	1	AAA22602	Integrin subunit b
1365	14.4	0.3	17	1	AAA22593	Integrin subunit b
1366	14.4	0.3	17	1	AAA19024	Human TIE-2 substr
1367	14.4	0.3	17	1	AAA22603	Integrin subunit b
1368	14.4	0.3	17	1	AAA22594	Integrin subunit b
1369	14.4	0.3	17	1	AAA19026	Human TIE-2 substr
1370	14.4	0.3	17	1	AAA19025	Human TIE-2 substr
1371	14.4	0.3	17	1	AAZ21177	Mouse inhibitor fo
1372	14.4	0.3	17	1	AAA25445	Oestrogen receptor
c1373	14.4	0.3	17	1	ABK02864	Human CD20 Hammerh
1374	14.4	0.3	17	1	ABK90422	Human UGT1a1 promo
c1375	14.4	0.3	17	1	ABK90422	Human UGT1a1 promo
1376	14.4	0.3	17	1	AAL50679	Human uridine diph
c1377	14.4	0.3	17	1	AAL50679	Human uridine diph
1378	14.4	0.3	17	1	ABK49298	Norwalk-like virus
1379	14.4	0.3	17	1	ABK19272	Human ERG Amberzym
1380	14.4	0.3	17	1	ABS75218	Human PAPP-Ea asso
1381	14.4	0.3	17	1	ABS75219	Human PAPP-Ea asso
c1382	14.4	0.3	17	1	ABK55689	Human CLCA1 gene e
1383	14.4	0.3	17	1	ADB04275	Human MDZ7 scannin
c1384	14.4	0.3	17	1	ACD65318	HCV minus strand D
c1385	14.4	0.3	17	1	ACC66072	Murine oligonucleo
c1386	14.4	0.3	17	1	ACC65071	Murine oligonucleo
1387	14.4	0.3	17	1	ABZ23260	PCR primer used to
c1388	14.4	0.3	17	1	ACC53486	Human tumour suppr
c1389	14.4	0.3	17	1	ADH70415	Human Vbeta gene r
c1390	14.4	0.3	17	1	ADI87036	HCV DNAzyme substr
c1391	14.4	0.3	17	1	ADP86138	CpG immunostimulat
1392	14.4	0.3	17	1	ADP86139	CpG immunostimulat
1393	14.4	0.3	18	1	ABX79779	EST polymorphic DN
1394	14.4	0.3	18	1	AAQ38707	First chimeric pri
c1395	14.4	0.3	18	1	AAX70270	Human flt1 VEGF re
1396	14.4	0.3	18	1	AAT96107	First chimeric pri
c1397	14.4	0.3	18	1	AAT49044	Rapamycin-dependen
1398	14.4	0.3	18	1	AAA06980	Human Smad5 phosph
1399	14.4	0.3	18	1	AAZ69782	Human biallelic ma
1400	14.4	0.3	18	1	AAZ88678	Chimeric primer #1
c1401	14.4	0.3	18	1	AAZ93494	TRADD antisense ol
1402	14.4	0.3	18	1	AAC70742	Single nucleotide
1403	14.4	0.3	18	1	AAC70757	Single nucleotide
1404	14.4	0.3	18	1	AAC70760	Single nucleotide
1405	14.4	0.3	18	1	AAC70748	Single nucleotide
1406	14.4	0.3	18	1	AAC70745	Single nucleotide
1407	14.4	0.3	18	1	AAC70730	Single nucleotide
1408	14.4	0.3	18	1	AAC70733	Single nucleotide
1409	14.4	0.3	18	1	AAC70754	Single nucleotide
1410	14.4	0.3	18	1	ABL57542	Nucleic acid probe
1411	14.4	0.3	18	1	ABL56899	Nucleic acid probe
c1412	14.4	0.3	18	1	AAD24812	B. thuringiensis c
1413	14.4	0.3	18	1	AAD24813	B. thuringiensis c
1414	14.4	0.3	18	1	ABA99596	Canine epididymis-
c1415	14.4	0.3	18	1	ABT43442	Neuroblastoma-rela
c1416	14.4	0.3	18	1	ABT43153	Neuroblastoma-rela
c1417	14.4	0.3	18	1	ABT32308	Neuroblastoma-rela
c1418	14.4	0.3	18	1	ADE13403	HLA class I allele
c1419	14.4	0.3	18	1	ADE43545	Human IDE sequenci
c1420	14.4	0.3	18	1	ADG76788	Human olfactory re

c1421	14.4	0.3	18	1	ADH70777	Human Vbeta gene r
c1422	14.4	0.3	18	1	ADH54023	Human neurodegener
c1423	14.4	0.3	18	1	ADL09253	HLA locus-specific
1424	14.4	0.3	18	1	ADO56496	Human cyclin-depen
1425	14.2	0.3	15	1	AAA47676	Oligo d(T) primer
c1426	14.2	0.3	15	1	AAD44150	Oligo-AT PCR prime
1427	14.2	0.3	16	1	AAX18387	RT-PCR primer of t
1428	14.2	0.3	16	1	AAF82119	Human TSA7005 gene
1429	14.2	0.3	16	1	AAH27758	Primer used in hum
1430	14.2	0.3	16	1	AAD44145	Oligo-dT PCR prime
1431	14.2	0.3	16	1	AAD44143	Oligo-dT PCR prime
c1432	14.2	0.3	19	1	ADH70642	Human Vbeta gene r
1433	14.2	0.3	19	1	ABL51521	Tailing reaction r
c1434	14.2	0.3	20	1	ABZ85669	Human oligonucleot
c1435	14.2	0.3	20	1	ABD21899	Human stanniocalci
c1436	14.2	0.3	20	1	ABL57565	Nucleic acid probe
1437	14.2	0.3	20	1	ABL95912	Probe poly u for a
1438	14.2	0.3	20	1	ABL57553	Synthetic deoxyrib
1439	14.2	0.3	20	1	ABL57548	Synthetic deoxyrib
1440	14.2	0.3	20	1	ABA97638	Poly t nucleotide
c1441	14.2	0.3	20	1	ABZ89719	Human oligonucleot
c1442	14.2	0.3	20	1	ABD25949	AA906703-derived o
c1443	14.2	0.3	21	1	ADK01328	Rat DNA microarray
1444	14	0.3	17	1	AAX69803	Human flt1 VEGF re
c1445	13.8	0.3	17	1	AAX69802	Human flt1 VEGF re
c1446	13.8	0.3	17	1	ABX79793	EST polymorphic DN
c1447	13.8	0.3	17	1	ADB04270	Human MDZ7 scannin
c1448	13.8	0.3	17	1	ADP71260	Oligo #12 for gase
c1449	13.8	0.3	17	1	ADP86184	CpG immunostimulat
c1450	13.8	0.3	18	1	AAV54175	Nucleotide sequenc
c1451	13.8	0.3	18	1	AAZ90651	Human adipose tiss
c1452	13.8	0.3	18	1	ABL57540	Nucleic acid probe
1453	13.8	0.3	18	1	AAA58385	Polynucleotide # 1
1454	13.8	0.3	18	1	ADH70777	Human Vbeta gene r
1455	13.8	0.3	20	1	ABZ77072	Human stearoyl-CoA
c1456	13.8	0.3	20	1	AAD35095	HT15-C downstream
1457	13.6	0.3	20	1	ABT07496	Rat protein phosph
1458	13.6	0.3	20	1	AAZ09195	Oligonucleotide 7
1459	13.6	0.3	20	1	ABZ89872	Human oligonucleot
1460	13.6	0.3	20	1	ABD26102	AA463249-derived o
c1461	13.6	0.3	20	1	AAQ75574	Reverse transcript
c1462	13.6	0.3	20	1	AAQ75572	Reverse transcript
c1463	13.6	0.3	20	1	AAF83959	BAP28 gene fragmen
c1464	13.6	0.3	20	1	ADK73725	Chimeric phosphoro
c1465	13.6	0.3	20	1	ADM14751	Human mPGES-1 chim
1466	13.6	0.3	21	1	ABS98543	Human acetyl choli
c1467	13.4	0.3	16	1	ABL57076	Molecular beacon t
c1468	13.4	0.3	16	1	AAD57846	Target oligonucleo
c1469	13.4	0.3	16	1	ADF23332	Binding partner sc
c1470	13.4	0.3	16	1	ADS15827	Control probe targ
c1471	13.4	0.3	17	1	ADP86146	CpG immunostimulat
c1472	13.4	0.3	17	1	ADP86185	CpG immunostimulat
c1473	13.4	0.3	18	1	AAQ38707	First chimeric pri
c1474	13.4	0.3	18	1	AAT96107	First chimeric pri
c1475	13.4	0.3	18	1	AAZ88678	Chimeric primer #1
c1476	13.4	0.3	19	1	AAZ99489	Primer HOOK for cD
c1477	13.4	0.3	19	1	AAD15201	3' sequencing prim
c1478	13.4	0.3	19	1	AAH21968	Mouse total gene e
c1479	13.4	0.3	19	1	AAS06525	Mouse microglia an
c1480	13.4	0.3	19	1	ABK71509	CNS related 3' seq
c1481	13.4	0.3	19	1	ABQ73231	Rabbit atheroscler
c1482	13.4	0.3	19	1	AAD34663	PCR primer #4 used
c1483	13.4	0.3	19	1	AAD40279	HOOK PCR primer us
c1484	13.4	0.3	19	1	ABZ68389	Reverse transcript
c1485	13.4	0.3	19	1	ACC79402	M13 sequencing pri
c1486	13.4	0.3	19	1	AAD49149	3' sequencing prim
c1487	13.4	0.3	19	1	AAD50267	3' sequencing prim
c1488	13.4	0.3	19	1	ADC21495	Human PRDI-BF1 RT-
1489	13.4	0.3	19	1	ADF74670	DNA oligo (30) use
c1490	13.4	0.3	19	1	ADL24850	Intestinal epithel
c1491	13.4	0.3	19	1	ADM16445	RNA intron poly-py
c1492	13.2	0.3	18	1	AAV54170	Nucleotide sequenc
c1493	13.2	0.3	18	1	AAZ90640	Human adipose tiss
1494	13.2	0.3	18	1	ADL95317	Anti-proliferative
c1495	13.2	0.3	18	1	AAV54167	Nucleotide sequenc
c1496	13.2	0.3	18	1	AAZ90643	Human adipose tiss
1497	13.2	0.3	18	1	AAV07750	Phosphorothioate o
1498	13.2	0.3	18	1	AAQ34110	Sequence of a micr
c1499	13.2	0.3	18	1	AAQ75025	PCR primer. Synth
c1500	13.2	0.3	18	1	AAT94668	Anchored poly(T) o
1501	13.2	0.3	18	1	AAV37712	Human protein AQ2_
c1502	13.2	0.3	18	1	AAV21970	Nuclease resistant
c1503	13.2	0.3	18	1	AAX19943	Primer SEQ ID NO:3
1504	13.2	0.3	18	1	AAX19942	Primer SEQ ID NO:2
1505	13.2	0.3	18	1	AAA40563	Human adult ovary
1506	13.2	0.3	18	1	AAZ87161	Oligoarabinonucleo
c1507	13.2	0.3	18	1	AAZ87162	Oligoarabinonucleo
c1508	13.2	0.3	18	1	AAZ87166	Deoxyarabinonucleo
1509	13.2	0.3	18	1	AAZ87167	Deoxyarabinonucleo
c1510	13.2	0.3	18	1	AAD03565	Oligonucleotide #6
1511	13.2	0.3	18	1	AAD17014	Oligonucleotide A1
c1512	13.2	0.3	18	1	AAF75598	Binary encoded seq
c1513	13.2	0.3	18	1	AAF99708	Immunostimulatory
c1514	13.2	0.3	18	1	AAF99734	Immunostimulatory
c1515	13.2	0.3	18	1	AAF82472	Phagemid vector pC
c1516	13.2	0.3	18	1	AAS94743	Rat secreted facto
c1517	13.2	0.3	18	1	ABS78455	Angiogenesis inhib
c1518	13.2	0.3	18	1	ABS78429	Angiogenesis inhib
c1519	13.2	0.3	18	1	ABL39401	Immunostimulatory
c1520	13.2	0.3	18	1	AAD41497	Oligonucleotide us
c1521	13.2	0.3	18	1	ABS53437	Poly d(T) primer.
c1522	13.2	0.3	18	1	ABA93239	Adaptor oligonucle
1523	13.2	0.3	18	1	AAD56466	Target RNA #1 used
c1524	13.2	0.3	18	1	AAD56440	Antisense oligo #1
c1525	13.2	0.3	18	1	AAD56446	2'F-ANA antisense
c1526	13.2	0.3	18	1	ACH03247	Immunostimulatory
c1527	13.2	0.3	18	1	AAD57871	Antisense oligo #1
c1528	13.2	0.3	18	1	AAD57878	Antisense DNA-RNA
c1529	13.2	0.3	18	1	AAD57879	Antisense DNA-RNA
c1530	13.2	0.3	18	1	AAD57877	Antisense DNA-RNA
1531	13.2	0.3	18	1	AAD57890	Target RNA #1 used
c1532	13.2	0.3	18	1	ADB37210	Immunostimulatory
c1533	13.2	0.3	18	1	ADB37236	Immunostimulatory
1534	13.2	0.3	18	1	ADE77617	Human probe NEG fo
c1535	13.2	0.3	18	1	ADI34489	Nucleotide sequenc
1536	13.2	0.3	18	1	ADH78590	Test element oligo
1537	13.2	0.3	18	1	ADO28710	Single stranded cD
c1538	13.2	0.3	18	1	ADO28711	Single stranded cD
c1539	13.2	0.3	18	1	ADO26684	Synthetic leader s
1540	13.2	0.3	18	1	ADO26682	Synthetic leader s
c1541	13.2	0.3	18	1	ADP86130	CpG immunostimulat
c1542	13.2	0.3	18	1	ADR32355	Rat KDR cytosolic
c1543	13.2	0.3	18	1	ADR57967	Nucleotide #4 for
c1544	13.2	0.3	19	1	ADE27190	Stearoyl-CoA desat
1545	13.2	0.3	19	1	ADE27480	Stearoyl-CoA desat
1546	13.2	0.3	19	1	ACA98771	Human CYP2C8 SNP d
c1547	13.2	0.3	19	1	ACA98774	Human CYP2C8 SNP d
c1548	13.2	0.3	19	1	AAQ75557	Reverse transcript
c1549	13.2	0.3	19	1	AAQ75555	Reverse transcript
1550	13.2	0.3	20	1	ABL57547	Synthetic deoxyrib
1551	13.2	0.3	20	1	ABA97632	Poly n nucleotide
1552	13.2	0.3	20	1	ADH70655	Human Vbeta gene r
c1553	13.2	0.3	20	1	AAT04917	Mammalian stem cel
c1554	13.2	0.3	20	1	AAA13752	Stem cell factor u
c1555	13.2	0.3	20	1	AAH41331	Universal stem cel
c1556	13.2	0.3	20	1	AAS04111	Human SCF (stem ce
c1557	13.2	0.3	20	1	AAF89091	Mammalian stem cel
c1558	13.2	0.3	20	1	AAH23889	Human SCF (stem ce
c1559	13.2	0.3	20	1	AAS04212	Human SCF (stem ce
c1560	13.2	0.3	20	1	AAS10447	Human stem cell fa
c1561	13.2	0.3	20	1	AAD35464	Rat SCF 5' cDNA am
c1562	13.2	0.3	20	1	ABS73848	SCF universal olig
c1563	13.2	0.3	20	1	ADE52460	Stem cell factor (
1564	13.2	0.3	20	1	ADL59742	Human ESM-1 antise
c1565	13.2	0.3	20	1	ADM14467	Human mPGES-1 chim
c1566	13.2	0.3	20	1	ADP99302	Stem cell factor,

c1567	13.2	0.3	20	1	AAQ75601	Reverse transcript
c1568	13.2	0.3	20	1	ADP69379	Human mitoNEET-spe
c1569	13.2	0.3	20	1	AAQ75591	Reverse transcript
1570	13.2	0.3	20	1	ABL57552	Synthetic deoxyrib
1571	13.2	0.3	20	1	ABA97637	Poly s nucleotide
1572	13.2	0.3	20	1	ABZ88618	Human oligonucleot
1573	13.2	0.3	20	1	ABD24848	AI092623-derived o
c1574	13.2	0.3	20	1	ADH67348	Human glucocortico
c1575	13.2	0.3	20	1	ADH67400	Human glucocortico
c1576	13.2	0.3	20	1	ADK74647	Chimeric phosphoro
c1577	13.2	0.3	20	1	ADK73558	Chimeric phosphoro
c1578	13.2	0.3	20	1	ADK74442	Chimeric phosphoro
1579	13.2	0.3	20	1	ADL59743	Human ESM-1 antise
c1580	13.2	0.3	20	1	ADM14246	Human mPGES-1 chim
c1581	13.2	0.3	21	1	ADK01302	Rat DNA microarray
c1582	13.2	0.3	21	1	AAQ75777	Reverse transcript
c1583	13.2	0.3	21	1	AAQ75737	Reverse transcript
c1584	13.2	0.3	21	1	ADK01304	Rat DNA microarray
1585	13.2	0.3	21	1	AAV35395	HIV-1 gag protein
c1586	13.2	0.3	21	1	ADK01334	Rat DNA microarray
c1587	13.2	0.3	21	1	ADK01303	Rat DNA microarray
c1588	13.2	0.3	21	1	ADK01301	Rat DNA microarray
c1589	13.2	0.3	21	1	AAQ75778	Reverse transcript
c1590	13.2	0.3	21	1	AAQ75775	Reverse transcript
c1591	13.2	0.3	21	1	AAQ75776	Reverse transcript
c1592	13.2	0.3	21	1	AAQ75745	Reverse transcript
c1593	13.2	0.3	21	1	ADK01312	Rat DNA microarray
1594	13.2	0.3	23	1	AAQ75028	LCR oligo 2. Synt
c1595	13.2	0.3	23	1	AAQ75029	LCR oligo 3. Synt
c1596	13	0.3	17	1	AAD44151	Oligo-AT PCR prime
1597	13	0.3	17	1	AAX69804	Human flt1 VEGF re
1598	13	0.3	19	1	ADE27483	Stearoyl-CoA desat
c1599	13	0.3	19	1	ADE27193	Stearoyl-CoA desat
c1600	13	0.3	21	1	AAQ75611	Reverse transcript
c1601	13	0.3	21	1	AAQ75620	Reverse transcript
c1602	13	0.3	21	1	AAQ75614	Reverse transcript
1603	12.8	0.3	16	1	ADH70350	Human Vbeta gene r
1604	12.8	0.3	16	1	ABL57075	Molecular beacon t
1605	12.8	0.3	16	1	AAD57845	Target oligonucleo
1606	12.8	0.3	16	1	ADF23331	Binding partner sc
c1607	12.8	0.3	16	1	ADH70347	Human Vbeta gene r

ALIGNMENTS

RESULT 1
AAT28105
ID AAT28105 standard; DNA; 39 BP.
XX
AC AAT28105;
XX
DT 31-DEC-1996 (first entry)
XX
DE Probe 10F1 isolated from fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 8; Page 38; 135pp; English.
XX
CC AAT28076-T28113, and AAT28131-T28173 represent novel senescent-related
CC gene sequences isolated from fibroblasts using the method of the
CC invention. In the method of the invention, mRNA is isolated from a
CC senescent cell, and a young quiescent cell, and the mRNAs are amplified
CC (using primers such as those shown in AAT28044-T28075) in separate
CC reaction mixtures. The amplified sequences are then separated by size or
CC charge, and the products are analysed to identify a gene from young
CC quiescent cells and dividing cells, that is present at a different level
CC from senescent cells. To enhance the method even more, it can be
CC performed in conjuncture with an enhanced differential display (EDD)
CC method (an mRNA preparation method) on the fibroblasts. The method can be
CC used for the rapid and efficient identification and isolation of
CC senescence-related genes and gene products, and to detect and distinguish
CC between senescent and non-senescent cells. It can also be used to destroy
CC cells expressing senescence specific (or related) gene products, and to
CC screen for compounds capable of altering gene expression in senescent
CC cells. The method can also be used to ameliorate problems associated with
CC the accumulation of senescent cells such as age-related lipofuscin
CC accumulation in the retina, and in the treatment of AIDS. Also, the
CC method can be used to distinguish young cells from senescent cells in
CC donor tissue, which is useful in removing senescent melanocytes
CC overexpressing melanin which cause hypopigmentation, or liver spots
XX
SQ Sequence 39 BP; 11 A; 7 C; 6 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 39; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1412 AGATGATGATGTTAACCCATTCCAGTACAGTATTCTTTT 1450
              |||||||||||||||||||||||||||||||||||||||
Db          1 AGATGATGATGTTAACCCATTCCAGTACAGTATTCTTTT 39
```

RESULT 2
ACC62353
ID ACC62353 standard; DNA; 30 BP.
XX
AC ACC62353;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human NOV3 probe SEQ ID NO:228.
XX
KW Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X; probe; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO2003023001-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028538.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318184P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 14-DEC-2001; 2001US-0341144P.
PR 26-FEB-2002; 2002US-0359599P.
PR 05-MAR-2002; 2002US-0361663P.
PR 03-MAY-2002; 2002US-0377908P.
PR 17-MAY-2002; 2002US-0381483P.
PR 29-MAY-2002; 2002US-0383863P.
PR 02-JUL-2002; 2002US-0393332P.
PR 17-JUL-2002; 2002US-0396412P.
PR 13-AUG-2002; 2002US-0403517P.
PR 06-SEP-2002; 2002US-00236417.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
PI Malyankar UM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M;
PI Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
PI Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong M;
XX
DR WPI; 2003-313241/30.
XX
PT Novel human proteins and nucleic acid encoding the proteins, useful for
PT diagnosis, treatment and prevention of disorders involving the human
PT protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS Example C; Page 289; 460pp; English.
XX
CC The present invention describes isolated human NOVX proteins, where X is
CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
CC antiparkinsonian and antilipaemic activities, and can be used in gene
CC therapy. NOVX proteins are useful for treating or preventing a pathology
CC associated with a NOVX protein in humans and for treating a syndrome
CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human trypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
SQ Sequence 30 BP; 12 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.7%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4136 TCAAGATTCTAAAGCTCAATTCAAGTGACA 4165
||||||||||||||||||||||||||||||
Db 1 TCAAGATTCTAAAGCTCAATTCAAGTGACA 30

RESULT 3
ABZ84148
ID ABZ84148 standard; DNA; 25 BP.
XX
AC ABZ84148;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant human PCR primer #1307.
XX
KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003016500-A2.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US026514.
XX
PR 16-AUG-2001; 2001US-0313080P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
PI Alen P;
XX
DR WPI; 2003-268322/26.
XX
PT Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
XX
PS Claim 1; Page 333; 455pp; English.
XX
CC The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in ABZ82842
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC ; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent or isolating cells from a human subject who
CC was exposed to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for
CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX

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SQ   Sequence 25 BP; 4 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4906 CCGTGTGTCCCAGATGCTGTCATTA 4930
             |||||||||||||||||||||||||
Db          1 CCGTGTGTCCCAGATGCTGTCATTA 25


RESULT 4
ABZ84357/c
ID   ABZ84357 standard; DNA; 25 BP.
XX
AC   ABZ84357;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant human PCR primer #1516.
XX
KW   Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 343; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 25 BP; 11 A; 9 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5046 GCCTTTTCTGTGATTGGGTGGGATT 5070
             |||||||||||||||||||||||||
Db         25 GCCTTTTCTGTGATTGGGTGGGATT 1


RESULT 5
ABZ84141/c
ID   ABZ84141 standard; DNA; 25 BP.
XX
AC   ABZ84141;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant human PCR primer #1300.
XX
KW   Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 333; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 25 BP; 11 A; 9 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 26;
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  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5046 GCCTTTTCTGTGATTGGGTGGGATT 5070
              |||||||||||||||||||||||||
Db         25 GCCTTTTCTGTGATTGGGTGGGATT 1


RESULT 6
ADR47292/c
ID   ADR47292 standard; DNA; 27 BP.
XX
AC   ADR47292;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase (SCD) related PCR primer H.
XX
KW   degree; unsaturated fatty acid; beef; body fat; milk fat;
KW   stearoyl-CoA desaturase; SCD; single nucleotide polymorphism; SNP;
KW   diary product; taste; texture; meat; Japanese black cattle; butter;
KW   breeding; hybrid; primer; ss.
XX
OS   Unidentified.
XX
PN   WO2004074515-A1.
XX
PD   02-SEP-2004.
XX
PF   17-FEB-2004; 2004WO-JP001756.
XX
PR   20-FEB-2003; 2003JP-00042076.
XX
PA   (NEWI-) NEW IND RES ORG.
XX
PI   Tsuji S,  Mannen H,  Taniguchi M;
XX
DR   WPI; 2004-652969/63.
XX
PT   Determining degree of unsaturated fatty acid in beef body fat or milk
PT   fat, useful for determining whether Bos taurus is capable of providing
PT   diary products having good taste and texture, based on stearoyl-CoA
PT   desaturase (SCD) genotype.
XX
PS   Disclosure; SEQ ID NO 10; 39pp; Japanese.
XX
CC   The invention relates to a novel method for determining the degree of an
CC   unsaturated fatty acid in beef body fat or milk fat, based on the
CC   stearoyl-CoA desaturase (SCD) genotype. The method involves detecting
CC   single nucleotide polymorphisms (SNPs) of the SCD gene, provided in the
CC   specification, which relate to the degree of unsaturation in beef body
CC   fat. The determination involves amplifying a template gene region
CC   prepared from genomic DNA or cDNA obtained from Bos taurus; digesting the
CC   obtained amplified fragment using a restriction enzyme; and determining
CC   the genotype of SCD based on the presence or absence of the digestion.
CC   The method is useful for determining whether a B. taurus is capable of
CC   providing diary products having good taste and texture, which involves
CC   determining the capability based on the results of the method. The method
CC   is useful for determining the quality of meat or milk obtained from B.
CC   taurus, e.g. Japanese black cattle. The method is useful in fields such
CC   as dairy industries for obtaining quality butter and other dairy products
CC   having e.g. good taste, texture. The method is useful for identifying a
CC   B. taurus capable of producing milk having high content of unsaturated
CC   fatty acids (with low melting point) or capable of providing meat with
CC   good taste and texture. The identified B. taurus can be employed in
CC   breeding programmes for obtaining hybrid varieties. This polynucleotide
CC   sequence represents a primer used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 5 A; 7 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 24.4;  DB 1;  Length 27;
  Best Local Similarity   96.2%;  Pred. No. 36;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1235 TATGACCGGAAGAAAGTCTCCAAGGC 1260
              |||||||||||||||| ||||||||
Db         27 TATGACCGGAAGAAAGTATCCAAGGC 2


RESULT 7
ADR47296/c
ID   ADR47296 standard; DNA; 27 BP.
XX
AC   ADR47296;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase (SCD) related PCR primer L.
XX
KW   degree; unsaturated fatty acid; beef; body fat; milk fat;
KW   stearoyl-CoA desaturase; SCD; single nucleotide polymorphism; SNP;
KW   diary product; taste; texture; meat; Japanese black cattle; butter;
KW   breeding; hybrid; primer; ss.
XX
OS   Unidentified.
XX
PN   WO2004074515-A1.
XX
PD   02-SEP-2004.
XX
PF   17-FEB-2004; 2004WO-JP001756.
XX
PR   20-FEB-2003; 2003JP-00042076.
XX
PA   (NEWI-) NEW IND RES ORG.
XX
PI   Tsuji S,  Mannen H,  Taniguchi M;
XX
DR   WPI; 2004-652969/63.
XX
PT   Determining degree of unsaturated fatty acid in beef body fat or milk
PT   fat, useful for determining whether Bos taurus is capable of providing
PT   diary products having good taste and texture, based on stearoyl-CoA
PT   desaturase (SCD) genotype.
XX
PS   Disclosure; SEQ ID NO 14; 39pp; Japanese.
XX
CC   The invention relates to a novel method for determining the degree of an
CC   unsaturated fatty acid in beef body fat or milk fat, based on the
CC   stearoyl-CoA desaturase (SCD) genotype. The method involves detecting
CC   single nucleotide polymorphisms (SNPs) of the SCD gene, provided in the
CC   specification, which relate to the degree of unsaturation in beef body
CC   fat. The determination involves amplifying a template gene region
CC   prepared from genomic DNA or cDNA obtained from Bos taurus; digesting the
CC   obtained amplified fragment using a restriction enzyme; and determining
CC   the genotype of SCD based on the presence or absence of the digestion.
CC   The method is useful for determining whether a B. taurus is capable of
CC   providing diary products having good taste and texture, which involves
CC   determining the capability based on the results of the method. The method
CC   is useful for determining the quality of meat or milk obtained from B.
CC   taurus, e.g. Japanese black cattle. The method is useful in fields such
CC   as dairy industries for obtaining quality butter and other dairy products
CC   having e.g. good taste, texture. The method is useful for identifying a
CC   B. taurus capable of producing milk having high content of unsaturated
CC   fatty acids (with low melting point) or capable of providing meat with
CC   good taste and texture. The identified B. taurus can be employed in
CC   breeding programmes for obtaining hybrid varieties. This polynucleotide
CC   sequence represents a primer used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 5 A; 7 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 24.4;  DB 1;  Length 27;
  Best Local Similarity   96.2%;  Pred. No. 36;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       1235 TATGACCGGAAGAAAGTCTCCAAGGC 1260
              ||||||||||||||||| ||||||||
Db         27 TATGACCGGAAGAAAGTATCCAAGGC 2


RESULT 8
ABZ84363
ID   ABZ84363 standard; DNA; 24 BP.
XX
AC   ABZ84363;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant human PCR primer #1522.
XX
KW   Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 343; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 24 BP; 3 A; 8 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4687 CCACTGACTTGCTGTGTGACCCTG 4710
              ||||||||||||||||||||||||
Db          1 CCACTGACTTGCTGTGTGACCCTG 24


RESULT 9
ADQ90669
ID   ADQ90669 standard; DNA; 24 BP.
XX
AC   ADQ90669;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Mouse Real Time PCR primer #3.
XX
KW   Mouse; Real Time PCR; PCR; primer; ss; liver steatosis;
KW   ciliary neurotrophic factor receptor; CNTF; Axokine; liver function;
KW   ALT/AST ratio; stearoyl-CoA desaturase-1; SCD-1; insulin; complex lipid;
KW   alcohol consumption; obesity; hepatotoxin exposure; hepatotropic.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2004142868-A1.
XX
PD   22-JUL-2004.
XX
PF   16-JAN-2004; 2004US-00758783.
XX
PR   21-JAN-2003; 2003US-0441464P.
XX
PA   (SLEE/) SLEEMAN M W.
XX
PI   Sleeman MW;
XX
DR   WPI; 2004-579966/56.
XX
PT   Treating, inhibiting or ameliorating liver steatosis in a subject
PT   comprises administering to the subject an agent capable of activating a
PT   ciliary neurotrophic factor receptor.
XX
PS   Example 1; SEQ ID NO 3; 9pp; English.
XX
CC   The invention relates to a method of treating or improving liver
CC   steatosis in a subject comprising administering to the subject an agent
CC   capable of activating a ciliary neurotrophic factor (CNTF) receptor. The
CC   agent is CNTF or a modified CNTF. The modified CNTF is Axokine. The
CC   treatment results in improved liver function as determined by ALT/AST
CC   ratio, reduced stearoyl-CoA desaturase-1 (SCD-1) gene expression or
CC   activity, enhanced biochemical responsiveness of the liver to insulin
CC   and/or reduced synthesis of complex lipids. The liver steatosis results
CC   from alcohol consumption, obesity and/or exposure to a hepatotoxin. The
CC   method is useful for treating, inhibiting and/or ameliorating liver
CC   steatosis in a subject. This sequence represents a Real Time PCR primer
CC   used in the method of the invention.
XX
SQ   Sequence 24 BP; 3 A; 8 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        903 TGCTGATGTGCTTCATCCTGCCCA 926
              ||||||||||||||||||||||||
Db          1 TGCTGATGTGCTTCATCCTGCCCA 24


RESULT 10
ABQ82441
ID   ABQ82441 standard; DNA; 27 BP.
XX
AC   ABQ82441;
XX
DT   17-DEC-2002  (first entry)
XX
```

DE Human NOV10 probe SEQ ID NO:327.
XX
KW Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
KW cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide;
KW antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;
KW antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy;
KW cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
KW stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
KW Pick's disease; vesicular transport disease; cystic fibrosis; goitre;
KW diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine;
KW ulcerative colitis; gastric disorder; duodenal disorder; infection;
KW autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
KW rheumatoid arthritis; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200262999-A2.
XX
PD 15-AUG-2002.
XX
PF 31-DEC-2001; 2001WO-US049976.
XX
PR 29-DEC-2000; 2000US-0258928P.
PR 02-JAN-2001; 2001US-0259415P.
PR 04-JAN-2001; 2001US-0259785P.
PR 20-FEB-2001; 2001US-0269814P.
PR 09-MAR-2001; 2001US-0279863P.
PR 29-MAR-2001; 2001US-0279832P.
PR 29-MAR-2001; 2001US-0279833P.
PR 13-APR-2001; 2001US-0283889P.
PR 18-APR-2001; 2001US-0284447P.
PR 25-APR-2001; 2001US-0286683P.
PR 29-MAY-2001; 2001US-0294080P.
PR 16-AUG-2001; 2001US-0312915P.
PR 17-AUG-2001; 2001US-0313325P.
PR 17-SEP-2001; 2001US-0322699P.
PR 26-NOV-2001; 2001US-0333350P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
PI Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
PI Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
PI Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
PI Gunther E, Smithson G, Millet I, Macdougall JR;
XX
DR WPI; 2002-732706/79.
XX
PT New NOVX polypeptides and polynucleotides useful for treating NOVX-
PT associated disorders, such as cancers, neurological disorders, disorders
PT of vesicular transport, gastrointestinal disorders, and autoimmune
PT diseases.
XX
PS Example 2; Page 404; 444pp; English.
XX
CC The present invention describes novel human proteins designated NOVX,
CC where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective,
CC cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular,
CC antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide,
CC immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,
CC protozoacide and antihelminthic activities, and can be used in gene
CC therapy. The NOVX proteins, nucleotides or antibodies can be used in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from NOVX-associated disorder, such as cancers
CC (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle,
CC ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke,
CC ischaemic cerebrovascular disease, Alzheimer's disease or Pick's
CC disease), disorders of vesicular transport (e.g. cystic fibrosis,
CC diabetes mellitus, Grave's disease, or goitre), gastrointestinal
CC disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
CC autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
CC anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic
CC and protozoal infections. The NOVX proteins can be used as immunogens to
CC produce antibodies and as vaccines. The NOVX nucleotide sequences may be
CC used in chromosome mapping, identifying individuals from minute
CC biological samples (tissue typing), and in forensic identification of a
CC biological sample. The present sequence represents a probe for a human
CC NOVX protein, which is used in an example from the present invention
XX
SQ Sequence 27 BP; 3 A; 9 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 23.8; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1143 CCTTTCCCTATGACTACTCTGCCAGTG 1169
||||||||| |||||||||||| ||||
Db 1 CCTTTCCCTTTGACTACTCTGCGAGTG 27

RESULT 11
ABQ82444
ID ABQ82444 standard; DNA; 27 BP.
XX
AC ABQ82444;
XX
DT 17-DEC-2002 (first entry)
XX
DE Human NOV10 probe SEQ ID NO:330.
XX
KW Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
KW cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide;
KW antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;
KW antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy;
KW cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
KW stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
KW Pick's disease; vesicular transport disease; cystic fibrosis; goitre;
KW diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine;
KW ulcerative colitis; gastric disorder; duodenal disorder; infection;
KW autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
KW rheumatoid arthritis; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200262999-A2.
XX
PD 15-AUG-2002.
XX
PF 31-DEC-2001; 2001WO-US049976.
XX
PR 29-DEC-2000; 2000US-0258928P.
PR 02-JAN-2001; 2001US-0259415P.
PR 04-JAN-2001; 2001US-0259785P.
PR 20-FEB-2001; 2001US-0269814P.
PR 09-MAR-2001; 2001US-0279863P.
PR 29-MAR-2001; 2001US-0279832P.
PR 29-MAR-2001; 2001US-0279833P.
PR 13-APR-2001; 2001US-0283889P.
PR 18-APR-2001; 2001US-0284447P.
PR 25-APR-2001; 2001US-0286683P.
PR 29-MAY-2001; 2001US-0294080P.
PR 16-AUG-2001; 2001US-0312915P.
PR 17-AUG-2001; 2001US-0313325P.
PR 17-SEP-2001; 2001US-0322699P.
PR 26-NOV-2001; 2001US-0333350P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
PI Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
PI Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
PI Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
PI Gunther E, Smithson G, Millet I, Macdougall JR;
XX
DR WPI; 2002-732706/79.
XX

```
PT   New NOVX polypeptides and polynucleotides useful for treating NOVX-
PT   associated disorders, such as cancers, neurological disorders, disorders
PT   of vesicular transport, gastrointestinal disorders, and autoimmune
PT   diseases.
XX
PS   Example 2; Page 404; 444pp; English.
XX
CC   The present invention describes novel human proteins designated NOVX,
CC   where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective,
CC   cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular,
CC   antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide,
CC   immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,
CC   protozoacide and antihelminthic activities, and can be used in gene
CC   therapy. The NOVX proteins, nucleotides or antibodies can be used in the
CC   manufacture of a medicament for treating a syndrome associated with a
CC   human disease selected from NOVX-associated disorder, such as cancers
CC   (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle,
CC   ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke,
CC   ischaemic cerebrovascular disease, Alzheimer's disease or Pick's
CC   disease), disorders of vesicular transport (e.g. cystic fibrosis,
CC   diabetes mellitus, Grave's disease, or goitre), gastrointestinal
CC   disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
CC   autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
CC   anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic
CC   and protozoal infections. The NOVX proteins can be used as immunogens to
CC   produce antibodies and as vaccines. The NOVX nucleotide sequences may be
CC   used in chromosome mapping, identifying individuals from minute
CC   biological samples (tissue typing), and in forensic identification of a
CC   biological sample. The present sequence represents a probe for a human
CC   NOVX protein, which is used in an example from the present invention
XX
SQ   Sequence 27 BP; 3 A; 9 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 23.8;  DB 1;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 46;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1143 CCTTTCCCTATGACTACTCTGCCAGTG 1169
              ||||||||| |||||||||||| ||||
Db          1 CCTTTCCCTTTGACTACTCTGCGAGTG 27


RESULT 12
ADC72189
ID   ADC72189 standard; DNA; 23 BP.
XX
AC   ADC72189;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human stearyl coenzyme A desaturase siRNA target sequence SCD3.
XX
KW   p53 pathway modulating agent; stearyl coenzyme A desaturase; SCD;
KW   p53 gene; cancer; signal integrator; DNA damage; hypoxia;
KW   nucleotide deprivation; oncogene activation; cytostatic; gene therapy;
KW   defective p53 function; angiogenic; apoptotic;
KW   cell proliferative disorder; human; small interfering RNA; siRNA; ds;
KW   SCD3.
XX
OS   Homo sapiens.
XX
PN   WO2003074662-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006087.
XX
PR   01-MAR-2002; 2002US-0361196P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Belvin M,  Francis-Lang H,  Friedman L,  Plowman GD,  Heuer TS;
XX
DR   WPI; 2003-748276/70.
XX
PT   Identifying a candidate p53 pathway-modulating agent as therapeutic
PT   targets for disorders related to defective p53 function e.g. cancer by
PT   contacting an assay system having SCD polypeptide or nucleic acid, with a
PT   test agent.
XX
PS   Example 6; SEQ ID NO 15; 44pp; English.
XX
CC   This invention relates to a novel method of identifying candidate p53
CC   pathway modulating agent which comprises contacting an assay system
CC   comprising stearyl coenzyme A desaturase (SCD) polypeptide or nucleic
CC   acid, or their functionally active fragment or derivative, with a test
CC   agent under conditions where, but for the presence of the test agent, the
CC   system provides a reference activity. The p53 gene is mutated in over 50
CC   different types of human cancers and is believed to be the most commonly
CC   mutated gene in human cancer. The human p53 protein normally functions as
CC   a central integrator of signals including DNA damage, hypoxia, nucleotide
CC   deprivation and oncogene activation. Modulators of p53 may have
CC   cytostatic activity or be useful in gene therapy. The methods of the
CC   invention are useful for identifying modulators of the p53 pathway as
CC   therapeutic targets for disorders associated with defective p53 function,
CC   such as angiogenic, apoptotic or cell proliferative disorders, for
CC   example cancer. The modulators are useful as research reagents,
CC   diagnostics and therapeutics. The present sequence (SCD3) is that of a
CC   region of a human Stearoyl-CoA desaturase sequence (see ADC72205) which
CC   was selected for small interfering RNA (siRNA) generation in the
CC   exemplification of the invention.
XX
SQ   Sequence 23 BP; 6 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1247 AAAGTCTCCAAGGCCGCCATCTT 1269
              |||||||||||||||||||||||
Db          1 AAAGTCTCCAAGGCCGCCATCTT 23


RESULT 13
ADC72188
ID   ADC72188 standard; DNA; 23 BP.
XX
AC   ADC72188;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human stearyl coenzyme A desaturase siRNA target sequence SCD2.
XX
KW   p53 pathway modulating agent; stearyl coenzyme A desaturase; SCD;
KW   p53 gene; cancer; signal integrator; DNA damage; hypoxia;
KW   nucleotide deprivation; oncogene activation; cytostatic; gene therapy;
KW   defective p53 function; angiogenic; apoptotic;
KW   cell proliferative disorder; human; small interfering RNA; siRNA; ds;
KW   SCD2.
XX
OS   Homo sapiens.
XX
PN   WO2003074662-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006087.
XX
PR   01-MAR-2002; 2002US-0361196P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Belvin M,  Francis-Lang H,  Friedman L,  Plowman GD,  Heuer TS;
XX
DR   WPI; 2003-748276/70.
XX
```

```
PT   Identifying a candidate p53 pathway-modulating agent as therapeutic
PT   targets for disorders related to defective p53 function e.g. cancer by
PT   contacting an assay system having SCD polypeptide or nucleic acid, with a
PT   test agent.
XX
PS   Example 6; SEQ ID NO 14; 44pp; English.
XX
CC   This invention relates to a novel method of identifying candidate p53
CC   pathway modulating agent which comprises contacting an assay system
CC   comprising stearyl coenzyme A desaturase (SCD) polypeptide or nucleic
CC   acid, or their functionally active fragment or derivative, with a test
CC   agent under conditions where, but for the presence of the test agent, the
CC   system provides a reference activity. The p53 gene is mutated in over 50
CC   different types of human cancers and is believed to be the most commonly
CC   mutated gene in human cancer. The human p53 protein normally functions as
CC   a central integrator of signals including DNA damage, hypoxia, nucleotide
CC   deprivation and oncogene activation. Modulators of p53 may have
CC   cytostatic activity or be useful in gene therapy. The methods of the
CC   invention are useful for identifying modulators of the p53 pathway as
CC   therapeutic targets for disorders associated with defective p53 function,
CC   such as angiogenic, apoptotic or cell proliferative disorders, for
CC   example cancer. The modulators are useful as research reagents,
CC   diagnostics and therapeutics. The present sequence (SCD2) is that of a
CC   region of a human Stearoyl-CoA desaturase sequence (see ADC72205) which
CC   was selected for small interfering RNA (siRNA) generation in the
CC   exemplification of the invention.
XX
SQ   Sequence 23 BP; 5 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        964 AAACAGTGTGTTCGTTGCCACTT 986
              |||||||||||||||||||||||
Db          1 AAACAGTGTGTTCGTTGCCACTT 23


RESULT 14
ADE27638
ID   ADE27638 standard; RNA; 23 BP.
XX
AC   ADE27638;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:582.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 582; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 7 A; 3 C; 9 G; 0 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 52;
  Matches   19;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2518 ACTGCTGGACATGAGATGGAGAG 2540
              ||:||:|||||:||||:||||||
Db          1 ACUGCUGGACAUGAGAUGGAGAG 23


RESULT 15
ADE27640
ID   ADE27640 standard; RNA; 23 BP.
XX
AC   ADE27640;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:584.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

```
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 584; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 6 A; 7 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 52;
  Matches   18;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4772 CTGACCTACCTCAAAGGGCAGTT 4794
              |:||||:|||:||||||||||::
Db          1 CUGACCUACCUCAAAGGGCAGUU 23


RESULT 16
ADE27637
ID   ADE27637 standard; RNA; 23 BP.
XX
AC   ADE27637;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:581.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 581; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 4 A; 4 C; 7 G; 0 T; 8 U; 0 Other;

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   65.2%;  Pred. No. 52;
  Matches   15;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        993 GATATGCTGTGGTGCTTAATGCC 1015
              ||:|:||:|:||:||::||:|||
Db          1 GAUAUGCUGUGGUGCUUAAUGCC 23


RESULT 17
ADE27639
ID   ADE27639 standard; RNA; 23 BP.
XX
AC   ADE27639;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:583.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
```

XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 583; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 23 BP; 5 A; 4 C; 9 G; 0 T; 5 U; 0 Other;

Query Match 0.5%; Score 23; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 52;
Matches 18; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3783 TAGAGGCTACAGGGGTTAGCCTG 3805
              :||||||:|||||||::||||:|
Db          1 UAGAGGCUACAGGGGUUAGCCUG 23
```

RESULT 18
ADG29600
ID ADG29600 standard; RNA; 23 BP.
XX
AC ADG29600;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD siNA-target RNA - SEQ ID 166.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; target; ss; SCD.
XX
OS Unidentified.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX

PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 166; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA
CC target DNA of the invention.
XX
SQ Sequence 23 BP; 7 A; 3 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 0.5%; Score 23; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2518 ACTGCTGGACATGAGATGGAGAG 2540
              ||:||:|||||:||||:||||||
Db          1 ACUGCUGGACAUGAGAUGGAGAG 23
```

RESULT 19
ADG29602
ID ADG29602 standard; RNA; 23 BP.
XX
AC ADG29602;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD siNA-target RNA - SEQ ID 168.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; target; ss; SCD.
XX
OS Unidentified.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX

PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 168; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA
CC target DNA of the invention.
XX
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.5%; Score 23; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 52;
Matches 18; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 4772 CTGACCTACCTCAAAGGGCAGTT 4794
|:||||:|||:||||||||||::
Db 1 CUGACCUACCUCAAAGGGCAGUU 23

RESULT 20
ADG29599
ID ADG29599 standard; RNA; 23 BP.
XX
AC ADG29599;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD siNA-target RNA - SEQ ID 165.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; target; ss; SCD.
XX
OS Unidentified.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX

PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 165; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA
CC target DNA of the invention.
XX
SQ Sequence 23 BP; 4 A; 4 C; 7 G; 0 T; 8 U; 0 Other;

Query Match 0.5%; Score 23; DB 1; Length 23;
Best Local Similarity 65.2%; Pred. No. 52;
Matches 15; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 993 GATATGCTGTGGTGCTTAATGCC 1015
||:|:||:|:||:||::||:|||
Db 1 GAUAUGCUGUGGUGCUUAAUGCC 23

RESULT 21
ADG29601
ID ADG29601 standard; RNA; 23 BP.
XX
AC ADG29601;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD siNA-target RNA - SEQ ID 167.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; target; ss; SCD.
XX
OS Unidentified.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX

```
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 167; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA
CC   target DNA of the invention.
XX
SQ   Sequence 23 BP; 5 A; 4 C; 9 G; 0 T; 5 U; 0 Other;

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 52;
  Matches   18;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3783 TAGAGGCTACAGGGGTTAGCCTG 3805
              :||||||:|||||||::||||:|
Db          1 UAGAGGCUACAGGGGUUAGCCUG 23


RESULT 22
ACC62352
ID   ACC62352 standard; DNA; 22 BP.
XX
AC   ACC62352;
XX
DT   23-JUN-2003  (first entry)
XX
DE   Human NOV3 forward PCR primer SEQ ID NO:227.
XX
KW   Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW   anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW   haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW   neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW   gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW   congenital heart defect; aortic stenosis; valve disease; transplantation;
KW   tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW   prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW   fertility; haemophilia; hypercoagulation; graft versus host disease;
KW   idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW   Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW   cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia;
KW   metabolic syndrome X; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003023001-A2.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028538.
XX
PR   07-SEP-2001; 2001US-0318120P.
PR   07-SEP-2001; 2001US-0318184P.
PR   10-SEP-2001; 2001US-0318430P.
PR   17-SEP-2001; 2001US-0322636P.
PR   17-SEP-2001; 2001US-0322781P.
PR   17-SEP-2001; 2001US-0322816P.
PR   17-SEP-2001; 2001US-0322817P.
PR   19-SEP-2001; 2001US-0323519P.
PR   20-SEP-2001; 2001US-0323631P.
PR   20-SEP-2001; 2001US-0323636P.
PR   25-SEP-2001; 2001US-0324969P.
PR   25-SEP-2001; 2001US-0325091P.
PR   26-SEP-2001; 2001US-0324990P.
PR   14-DEC-2001; 2001US-0341144P.
PR   26-FEB-2002; 2002US-0359599P.
PR   05-MAR-2002; 2002US-0361663P.
PR   03-MAY-2002; 2002US-0377908P.
PR   17-MAY-2002; 2002US-0381483P.
PR   29-MAY-2002; 2002US-0383863P.
PR   02-JUL-2002; 2002US-0393332P.
PR   17-JUL-2002; 2002US-0396412P.
PR   13-AUG-2002; 2002US-0403517P.
PR   06-SEP-2002; 2002US-00236417.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Agee ML,  Alsobrook JP,  Anderson DW,  Berghs C,  Boldog FL;
PI   Burgess CE,  Casman SJ,  Catterton E,  Chant JS,  Chaudhuri A;
PI   Crabtree J,  Dipippo VA,  Edinger SR,  Eisen AJ,  Ellerman K;
PI   Gangolli EA,  Gerlach VL,  Giot L,  Gorman L,  Guo X,  Gusev VY,  Ji W;
PI   Kekuda R,  Khramtsov NV,  Leach MD,  Lepley DM,  Li L,  Liu X;
PI   Malyankar UM,  Miller CE,  Ooi CE,  Ort T,  Padigaru M,  Patturajan M;
PI   Pena CEA,  Rieger DK,  Rothenberg ME,  Shenoy SG,  Shimkets RA;
PI   Spaderna SK,  Spytek KA,  Taupier RJ,  Twomlow N,  Vernet CAM,  Voss EZ;
PI   Zerhusen BD,  Zhong M;
XX
DR   WPI; 2003-313241/30.
XX
PT   Novel human proteins and nucleic acid encoding the proteins, useful for
PT   diagnosis, treatment and prevention of disorders involving the human
PT   protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS   Example C; Page 289; 460pp; English.
XX
CC   The present invention describes isolated human NOVX proteins, where X is
CC   1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC   ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC   hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC   antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC   antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
CC   antiparkinsonian and antilipaemic activities, and can be used in gene
CC   therapy. NOVX proteins are useful for treating or preventing a pathology
CC   associated with a NOVX protein in humans and for treating a syndrome
CC   associated with the human disease. NOVX nucleic acids, proteins and
CC   antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC   atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC   valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC   congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC   disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC   hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC   disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC   infectious disease, anorexia, cancer-associated cachexia, cancer,
CC   Alzheimer's disease, Parkinson's disease, immune disorders,
CC   haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC   ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC   sequences, which are used in examples from the present invention.
CC   ABR54277 represents a human trypsinogen protein given in comparison with
CC   the human NOV35b protein in the exemplification of the present invention
XX
SQ   Sequence 22 BP; 7 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4112 TCTGCTGAGTAAGGAACACGAT 4133
              ||||||||||||||||||||||
Db          1 TCTGCTGAGTAAGGAACACGAT 22
```

```
RESULT 23
ADE27660
ID   ADE27660 standard; RNA; 23 BP.
XX
AC   ADE27660;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:604.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 604; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 6 A; 6 C; 5 G; 2 T; 2 U; 2 Other;

  Query Match             0.5%;  Score 21.4;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 1e+02;
  Matches   19;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4773 TGACCTACCTCAAAGGGCAGTTT 4795
              :||||:|||:|||||||||||||:
Db          1 BGACCUACCUCAAAGGGCAGTTB 23
```

```
RESULT 24
ADE27652
ID   ADE27652 standard; RNA; 23 BP.
XX
AC   ADE27652;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:596.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 596; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 6 A; 6 C; 5 G; 2 T; 2 U; 2 Other;

  Query Match             0.5%;  Score 21.4;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 1e+02;
  Matches   19;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4773 TGACCTACCTCAAAGGGCAGTTT 4795
              :||||:|||:|||||||||||||:
Db          1 BGACCUACCUCAAAGGGCAGTTB 23
```

RESULT 25
ACA90035
ID ACA90035 standard; DNA; 21 BP.
XX
AC ACA90035;
XX
DT 10-JUL-2003 (first entry)
XX
DE Cardiovascular disease differential gene expression related primer #82.
XX
KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
KW myocardial infarction; cardiant; antiarteriosclerotic; antianginal;
KW gene therapy; differential gene expression; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003031650-A2.
XX
PD 17-APR-2003.
XX
PF 02-OCT-2002; 2002WO-EP011034.
XX
PR 08-OCT-2001; 2001GB-00024145.
XX
PA (FARB) BAYER AG.
XX
PI Munnes M, Gehrmann M, Wick M, Schmitz G;
XX
DR WPI; 2003-403108/38.
XX
PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
PT of a polynucleotide in a biological sample comprises detecting a
PT hybridization complex.
XX
PS Example 3; Page 105; 454pp; English.
XX
CC The invention describes a method of predicting, diagnosing or prognosing
CC a cardiovascular disease by detection of a polynucleotide in a biological
CC sample comprises hybridising at least one of the polynucleotide to a
CC nucleic acid material of a biological sample, thus forming a
CC hybridisation complex, and detecting the hybridisation complex. The
CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
CC are useful for preparing compositions for preventing, predicting or
CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
CC This sequence represents a primer used to identify genes differentially
CC regulated in individuals with cardiovascular disease
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1262 GCCATCTTGGCCAGGATTAAA 1282
              |||||||||||||||||||||
Db          1 GCCATCTTGGCCAGGATTAAA 21
```

RESULT 26
ACC62354/c
ID ACC62354 standard; DNA; 21 BP.
XX
AC ACC62354;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human NOV3 reverse PCR primer SEQ ID NO:229.
XX
KW Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003023001-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028538.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318184P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 14-DEC-2001; 2001US-0341144P.
PR 26-FEB-2002; 2002US-0359599P.
PR 05-MAR-2002; 2002US-0361663P.
PR 03-MAY-2002; 2002US-0377908P.
PR 17-MAY-2002; 2002US-0381483P.
PR 29-MAY-2002; 2002US-0383863P.
PR 02-JUL-2002; 2002US-0393332P.
PR 17-JUL-2002; 2002US-0396412P.
PR 13-AUG-2002; 2002US-0403517P.
PR 06-SEP-2002; 2002US-00236417.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
PI Malyankar UM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M;
PI Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
PI Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong M;
XX
DR WPI; 2003-313241/30.
XX
PT Novel human proteins and nucleic acid encoding the proteins, useful for
PT diagnosis, treatment and prevention of disorders involving the human
PT protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS Example C; Page 289; 460pp; English.
XX
CC The present invention describes isolated human NOVX proteins, where X is
CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
CC antiparkinsonian and antilipaemic activities, and can be used in gene
CC therapy. NOVX proteins are useful for treating or preventing a pathology

CC associated with a NOVX protein in humans and for treating a syndrome
CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human trypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
SQ Sequence 21 BP; 4 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4182 AGATCTGATCAAGAGTCCGGA 4202
||||||||||||||||||||
Db 21 AGATCTGATCAAGAGTCCGGA 1

RESULT 27
ADE27671
ID ADE27671 standard; RNA; 21 BP.
XX
AC ADE27671;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:626.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Disclosure; SEQ ID NO 626; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 3 A; 7 C; 2 G; 2 T; 7 U; 0 Other;

Query Match 0.5%; Score 21; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 3027 CTGAACCACTGCTTCTCTTTT 3047
|:|||||||:||::|:|::||
Db 1 CUGAACCACUGCUUCUCUUTT 21

RESULT 28
ADE27667
ID ADE27667 standard; RNA; 21 BP.
XX
AC ADE27667;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:622.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Disclosure; SEQ ID NO 622; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)

```
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 2 G; 2 T; 7 U; 0 Other;

  Query Match             0.5%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches   14;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3027 CTGAACCACTGCTTCTCTTTT 3047
              |:|||||||:||::|:|::||
Db          1 CUGAACCACUGCUUCUCUUTT 21


RESULT 29
ADE27669
ID   ADE27669 standard; RNA; 21 BP.
XX
AC   ADE27669;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:624.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Disclosure; SEQ ID NO 624; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 2 G; 2 T; 7 U; 0 Other;

  Query Match             0.5%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches   14;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3027 CTGAACCACTGCTTCTCTTTT 3047
              |:|||||||:||::|:|::||
Db          1 CUGAACCACUGCUUCUCUUTT 21


RESULT 30
ADE27644
ID   ADE27644 standard; RNA; 21 BP.
XX
AC   ADE27644;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:588.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 588; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
```

```
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 6 A; 6 C; 5 G; 2 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4774 GACCTACCTCAAAGGGCAGTT 4794
              ||||:|||:|||||||||||||
Db          1 GACCUACCUCAAAGGGCAGTT 21


RESULT 31
ADG30282
ID   ADG30282 standard; RNA; 21 BP.
XX
AC   ADG30282;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 848.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 848; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 6 A; 6 C; 5 G; 2 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4774 GACCTACCTCAAAGGGCAGTT 4794
              ||||:|||:|||||||||||||
Db          1 GACCUACCUCAAAGGGCAGTT 21


RESULT 32
ADG30274
ID   ADG30274 standard; RNA; 23 BP.
XX
AC   ADG30274;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 840.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 840; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
```

```
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 23 BP; 6 A; 6 C; 5 G; 2 T; 2 U; 2 Other;

  Query Match             0.5%;  Score 21;  DB 1;  Length 23;
  Best Local Similarity   90.5%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4774 GACCTACCTCAAAGGGCAGTT 4794
              ||||:|||:|||||||||||||
Db          2 GACCUACCUCAAAGGGCAGTT 22


RESULT 33
AAV54646/c
ID   AAV54646 standard; cDNA; 26 BP.
XX
AC   AAV54646;
XX
DT   27-AUG-2003  (revised)
DT   18-NOV-1998  (first entry)
XX
DE   Mortierella sp. delta9-desaturase PCR primer #2.
XX
KW   Delta9-desaturase; unsaturated fatty acid; arachidonic acid;
KW   dihomo-linoleic acid; gamma-linoleic acid; eicosapentaenic acid;
KW   docohexaenoic acid; PCR primer; ss.
XX
OS   Synthetic.
OS   Mortierella.
XX
FH   Key             Location/Qualifiers
FT   modified_base   18
FT                   /*tag=  a
FT                   /mod_base= i
FT                   /note= "inosine"
FT   modified_base   24
FT                   /*tag=  e
FT                   /mod_base= i
FT                   /note= "inosine"
XX
PN   WO9838314-A1.
XX
PD   03-SEP-1998.
XX
PF   27-FEB-1998;   98WO-JP000819.
XX
PR   27-FEB-1997;   97JP-00044303.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Shimizu S,  Kobayashi M;
XX
DR   WPI; 1998-481209/41.
XX
PT   Mortierella-derived genome DNA and cDNA encoding ~D9-desaturase - giving
PT   transformant e.g. Aspergillus oryzae, for improved productivity of
PT   unsaturated fatty acids including oleic acid.
XX
PS   Example 1; Page 17; 39pp; Japanese.
XX
CC   AAV54645-V54648 are PCR primers used in the isolation of a Delta 9-
CC   desaturase from a microorganism belonging to Mortierella s.p.
CC   mortierella. This sequence can be used in a method for improving the
CC   productivity of unsaturated fatty acids, especially the physiologically
CC   active compounds e.g. arachidonic acid, dihomo- gamma -linoleic acid,
CC   eicosapentaenic acid and docohexaenoic acid. The invention significantly
CC   improves the production of unsaturated fatty acids. (Updated on 27-AUG-
CC   2003 to correct OS field.)
XX
SQ   Sequence 26 BP; 2 A; 5 C; 3 G; 6 T; 0 U; 10 Other;

  Query Match             0.5%;  Score 20.8;  DB 1;  Length 26;
  Best Local Similarity   61.5%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1115 GGTGAGGGCTTCCACAACTACCACCA 1140
              || ||:|| |::||:||:|::||:||
Db         26 GGNGARGGNTWYCAYAAYTWYCAYCA 1


RESULT 34
ADE27653/c
ID   ADE27653 standard; RNA; 22 BP.
XX
AC   ADE27653;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:597.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 597; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
```

CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 8 A; 6 C; 2 G; 2 T; 3 U; 1 Other;

Query Match 0.5%; Score 20.6; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 993 GATATGCTGTGGTGCTTAATG 1013
:||||||||||||||||||||
Db 21 SATATGCTGTGGTGCTTAATG 1

RESULT 35
ADE27661/c
ID ADE27661 standard; RNA; 22 BP.
XX
AC ADE27661;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:605.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 605; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 8 A; 6 C; 2 G; 2 T; 3 U; 1 Other;

Query Match 0.5%; Score 20.6; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 993 GATATGCTGTGGTGCTTAATG 1013
:||||||||||||||||||||
Db 21 SATATGCTGTGGTGCTTAATG 1

RESULT 36
ADC72195
ID ADC72195 standard; RNA; 21 BP.
XX
AC ADC72195;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human stearyl coenzyme A desaturase siRNA SCD2-sense.
XX
KW p53 pathway modulating agent; stearyl coenzyme A desaturase; SCD;
KW p53 gene; cancer; signal integrator; DNA damage; hypoxia;
KW nucleotide deprivation; oncogene activation; cytostatic; gene therapy;
KW defective p53 function; angiogenic; apoptotic;
KW cell proliferative disorder; human; small interfering RNA; siRNA; ss;
KW SCD2-sense.
XX
OS Homo sapiens.
XX
PN WO2003074662-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006087.
XX
PR 01-MAR-2002; 2002US-0361196P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Belvin M, Francis-Lang H, Friedman L, Plowman GD, Heuer TS;
XX
DR WPI; 2003-748276/70.
XX
PT Identifying a candidate p53 pathway-modulating agent as therapeutic
PT targets for disorders related to defective p53 function e.g. cancer by
PT contacting an assay system having SCD polypeptide or nucleic acid, with a
PT test agent.
XX
PS Example 6; SEQ ID NO 21; 44pp; English.
XX
CC This invention relates to a novel method of identifying candidate p53
CC pathway modulating agent which comprises contacting an assay system
CC comprising stearyl coenzyme A desaturase (SCD) polypeptide or nucleic
CC acid, or their functionally active fragment or derivative, with a test
CC agent under conditions where, but for the presence of the test agent, the
CC system provides a reference activity. The p53 gene is mutated in over 50
CC different types of human cancers and is believed to be the most commonly
CC mutated gene in human cancer. The human p53 protein normally functions as
CC a central integrator of signals including DNA damage, hypoxia, nucleotide
CC deprivation and oncogene activation. Modulators of p53 may have
CC cytostatic activity or be useful in gene therapy. The methods of the
CC invention are useful for identifying modulators of the p53 pathway as
CC therapeutic targets for disorders associated with defective p53 function,
CC such as angiogenic, apoptotic or cell proliferative disorders, for

```
CC   example cancer. The modulators are useful as research reagents,
CC   diagnostics and therapeutics. The present sequence (SCD2-sense) is that
CC   of a human Stearoyl-CoA desaturase sequence (see ADC72205) small
CC   interfering RNA (siRNA) used in the exemplification of the invention.
XX
SQ   Sequence 21 BP; 3 A; 5 C; 5 G; 0 T; 6 U; 2 Other;

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   61.9%;  Pred. No. 1.4e+02;
  Matches   13;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 ACAGTGTGTTCGTTGCCACTT 986
              ||||:|:|::||::||||::
Db          1 ACAGUGUGUUCGUUGCCACYY 21


RESULT 37
ADC72198/c
ID   ADC72198 standard; RNA; 21 BP.
XX
AC   ADC72198;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human stearyl coenzyme A desaturase siRNA SCD3-antisense.
XX
KW   p53 pathway modulating agent; stearyl coenzyme A desaturase; SCD;
KW   p53 gene; cancer; signal integrator; DNA damage; hypoxia;
KW   nucleotide deprivation; oncogene activation; cytostatic; gene therapy;
KW   defective p53 function; angiogenic; apoptotic;
KW   cell proliferative disorder; human; small interfering RNA; siRNA; ss;
KW   SCD3-antisense.
XX
OS   Homo sapiens.
XX
PN   WO2003074662-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006087.
XX
PR   01-MAR-2002; 2002US-0361196P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Belvin M,  Francis-Lang H,  Friedman L,  Plowman GD,  Heuer TS;
XX
DR   WPI; 2003-748276/70.
XX
PT   Identifying a candidate p53 pathway-modulating agent as therapeutic
PT   targets for disorders related to defective p53 function e.g. cancer by
PT   contacting an assay system having SCD polypeptide or nucleic acid, with a
PT   test agent.
XX
PS   Example 6; SEQ ID NO 24; 44pp; English.
XX
CC   This invention relates to a novel method of identifying candidate p53
CC   pathway modulating agent which comprises contacting an assay system
CC   comprising stearyl coenzyme A desaturase (SCD) polypeptide or nucleic
CC   acid, or their functionally active fragment or derivative, with a test
CC   agent under conditions where, but for the presence of the test agent, the
CC   system provides a reference activity. The p53 gene is mutated in over 50
CC   different types of human cancers and is believed to be the most commonly
CC   mutated gene in human cancer. The human p53 protein normally functions as
CC   a central integrator of signals including DNA damage, hypoxia, nucleotide
CC   deprivation and oncogene activation. Modulators of p53 may have
CC   cytostatic activity or be useful in gene therapy. The methods of the
CC   invention are useful for identifying modulators of the p53 pathway as
CC   therapeutic targets for disorders associated with defective p53 function,
CC   such as angiogenic, apoptotic or cell proliferative disorders, for
CC   example cancer. The modulators are useful as research reagents,
CC   diagnostics and therapeutics. The present sequence (SCD3-antisense) is
CC   that of a human Stearoyl-CoA desaturase sequence (see ADC72205) small
CC   interfering RNA (siRNA) used in the exemplification of the invention.
XX
SQ   Sequence 21 BP; 3 A; 4 C; 8 G; 0 T; 4 U; 2 Other;

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+02;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1247 AAAGTCTCCAAGGCCGCCATC 1267
              ::|||||||||||||||||||
Db         21 RRAGTCTCCAAGGCCGCCATC 1


RESULT 38
ADC72197
ID   ADC72197 standard; RNA; 21 BP.
XX
AC   ADC72197;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human stearyl coenzyme A desaturase siRNA SCD3-sense.
XX
KW   p53 pathway modulating agent; stearyl coenzyme A desaturase; SCD;
KW   p53 gene; cancer; signal integrator; DNA damage; hypoxia;
KW   nucleotide deprivation; oncogene activation; cytostatic; gene therapy;
KW   defective p53 function; angiogenic; apoptotic;
KW   cell proliferative disorder; human; small interfering RNA; siRNA; ss;
KW   SCD3-sense.
XX
OS   Homo sapiens.
XX
PN   WO2003074662-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006087.
XX
PR   01-MAR-2002; 2002US-0361196P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Belvin M,  Francis-Lang H,  Friedman L,  Plowman GD,  Heuer TS;
XX
DR   WPI; 2003-748276/70.
XX
PT   Identifying a candidate p53 pathway-modulating agent as therapeutic
PT   targets for disorders related to defective p53 function e.g. cancer by
PT   contacting an assay system having SCD polypeptide or nucleic acid, with a
PT   test agent.
XX
PS   Example 6; SEQ ID NO 23; 44pp; English.
XX
CC   This invention relates to a novel method of identifying candidate p53
CC   pathway modulating agent which comprises contacting an assay system
CC   comprising stearyl coenzyme A desaturase (SCD) polypeptide or nucleic
CC   acid, or their functionally active fragment or derivative, with a test
CC   agent under conditions where, but for the presence of the test agent, the
CC   system provides a reference activity. The p53 gene is mutated in over 50
CC   different types of human cancers and is believed to be the most commonly
CC   mutated gene in human cancer. The human p53 protein normally functions as
CC   a central integrator of signals including DNA damage, hypoxia, nucleotide
CC   deprivation and oncogene activation. Modulators of p53 may have
CC   cytostatic activity or be useful in gene therapy. The methods of the
CC   invention are useful for identifying modulators of the p53 pathway as
CC   therapeutic targets for disorders associated with defective p53 function,
CC   such as angiogenic, apoptotic or cell proliferative disorders, for
CC   example cancer. The modulators are useful as research reagents,
CC   diagnostics and therapeutics. The present sequence (SCD3-sense) is that
CC   of a human Stearoyl-CoA desaturase sequence (see ADC72205) small
CC   interfering RNA (siRNA) used in the exemplification of the invention.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 4 G; 0 T; 3 U; 2 Other;
```

```
  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1249 AGTCTCCAAGGCCGCCATCTT 1269
              ||:|:|||||||||||||:|::
Db          1 AGUCUCCAAGGCCGCCAUCYY 21
```

RESULT 39
ADC72196/c
ID ADC72196 standard; RNA; 21 BP.
XX
AC ADC72196;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human stearyl coenzyme A desaturase siRNA SCD2-antisense.
XX
KW p53 pathway modulating agent; stearyl coenzyme A desaturase; SCD;
KW p53 gene; cancer; signal integrator; DNA damage; hypoxia;
KW nucleotide deprivation; oncogene activation; cytostatic; gene therapy;
KW defective p53 function; angiogenic; apoptotic;
KW cell proliferative disorder; human; small interfering RNA; siRNA; ss;
KW SCD2-antisense.
XX
OS Homo sapiens.
XX
PN WO2003074662-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006087.
XX
PR 01-MAR-2002; 2002US-0361196P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Belvin M, Francis-Lang H, Friedman L, Plowman GD, Heuer TS;
XX
DR WPI; 2003-748276/70.
XX
PT Identifying a candidate p53 pathway-modulating agent as therapeutic
PT targets for disorders related to defective p53 function e.g. cancer by
PT contacting an assay system having SCD polypeptide or nucleic acid, with a
PT test agent.
XX
PS Example 6; SEQ ID NO 22; 44pp; English.
XX
CC This invention relates to a novel method of identifying candidate p53
CC pathway modulating agent which comprises contacting an assay system
CC comprising stearyl coenzyme A desaturase (SCD) polypeptide or nucleic
CC acid, or their functionally active fragment or derivative, with a test
CC agent under conditions where, but for the presence of the test agent, the
CC system provides a reference activity. The p53 gene is mutated in over 50
CC different types of human cancers and is believed to be the most commonly
CC mutated gene in human cancer. The human p53 protein normally functions as
CC a central integrator of signals including DNA damage, hypoxia, nucleotide
CC deprivation and oncogene activation. Modulators of p53 may have
CC cytostatic activity or be useful in gene therapy. The methods of the
CC invention are useful for identifying modulators of the p53 pathway as
CC therapeutic targets for disorders associated with defective p53 function,
CC such as angiogenic, apoptotic or cell proliferative disorders, for
CC example cancer. The modulators are useful as research reagents,
CC diagnostics and therapeutics. The present sequence (SCD2-antisense) is
CC that of a human Stearoyl-CoA desaturase sequence (see ADC72205) small
CC interfering RNA (siRNA) used in the exemplification of the invention.
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 0 T; 3 U; 2 Other;

```
  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+02;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        964 AAACAGTGTGTTCGTTGCCAC 984
              ::|||||||||||||||||||
Db         21 RRACAGTGTGTTCGTTGCCAC 1
```

RESULT 40
AAC96203
ID AAC96203 standard; DNA; 25 BP.
XX
AC AAC96203;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #170.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 47; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 6 A; 1 C; 4 G; 14 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 1.8e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTTGGGTTAAAAGATG 4528
              |||||||||||  | |||||||||
Db          1 TTTTTTTTTTTTACGGTAAAAGATG 25
```

RESULT 41
ABT07496/c
ID ABT07496 standard; DNA; 20 BP.
XX
AC ABT07496;
XX
DT 14-NOV-2002 (first entry)
XX
DE Rat protein phosphatase 2 oligo inhibitor SEQ ID No 110.
XX

KW Cytostatic; antidiabetic; antisense therapy; aberrant insulin regulation;
KW protein phosphatase 2 catalytic beta subunit; antisense compound; cancer;
KW hyperproliferative disorder; diabetes; inflammation; tumour; rat; ds.
XX
OS Rattus norvegicus.
XX
PN WO200264737-A2.
XX
PD 22-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-US002805.
XX
PR 09-FEB-2001; 2001US-00780045.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-657588/70.
XX
PT New antisense oligonucleotides targeted to nucleic acid encoding Protein
PT Phosphatase 2 catalytic subunit beta, useful for treating diseases
PT related to Protein Phosphatase 2 catalytic subunit beta expression, such
PT as cancer.
XX
PS Example 16; Page 98; 137pp; English.
XX
CC The invention relates to a novel compound 8-50 nucleotides in length
CC targeted to a nucleic acid molecule encoding a protein phosphatase 2
CC catalytic beta subunit, where the compound specifically hybridises with
CC and inhibits the expression of protein phosphatase 2 catalytic beta
CC subunits, or specifically hybridises with at least an 8-nucleotide
CC portion of an active site on a nucleic acid molecule encoding a protein
CC phosphatase 2 catalytic beta subunit. The antisense compounds are useful
CC for modulating the expression of protein phosphatase 2 catalytic beta
CC subunits and for treating diseases or conditions associated with
CC expression of protein phosphatase 2 catalytic beta subunits, e.g.
CC aberrant insulin regulation or diabetes or a hyperproliferative disorder,
CC particularly cancer. The antisense compounds are also useful for
CC diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay
CC infection, inflammation or tumour formation, as research reagents and
CC kits, and in distinguishing between functions of various members of a
CC biological pathway. This polynucleotide sequence represents an
CC oligonucleotide inhibitor of rat protein phosphatase 2 catalytic beta
CC subunit mRNA levels of the invention. NOTE: This oligonucleotide contains
CC phosphorothioate residues and has 2'- MOE wings with a deoxy gap
XX
SQ Sequence 20 BP; 7 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 AAAATATATATACATATATA 2410
||||||||||||||||||||
Db 20 AAAATATATATACATATATA 1

RESULT 42
ABZ77065/c
ID ABZ77065 standard; DNA; 20 BP.
XX
AC ABZ77065;
XX
DT 07-MAY-2003 (first entry)
XX
DE Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:20.
XX
KW Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW 2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN WO2003012031-A2.
XX
PD 13-FEB-2003.
XX
PF 16-JUL-2002; 2002WO-US022676.
XX
PR 30-JUL-2001; 2001US-00918187.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-248160/24.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding human
PT stearoyl-CoA desaturase, useful for treating diseases associated with the
PT desaturase, e.g. atherosclerosis, and in diagnostic and research
PT applications.
XX
PS Claim 3; Page 94; 117pp; English.
XX
CC The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC desaturase, and which specifically hybridises with and inhibits the
CC expression of human stearoyl-CoA desaturase, or which specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC activities, and can be used in antisense therapy. The antisense compounds
CC (I) can be used for modulating the expression of human stearoyl-CoA
CC desaturase and for treating diseases or conditions associated with
CC expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC antisense compounds (I) can also be used for diagnostics, therapeutics
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC tumour formation, as research reagents and kits, and in distinguishing
CC between functions of various members of a biological pathway. The present
CC sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC phosphorothioate antisense oligonucleotide, which is given in an example
CC from the present invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 ATGCCACCTGGCTGGTGAAC 1030
||||||||||||||||||||
Db 20 ATGCCACCTGGCTGGTGAAC 1

RESULT 43
ABZ77068/c

```
ID   ABZ77068 standard; DNA; 20 BP.
XX
AC   ABZ77068;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:23.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 9 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1307 AGTGGCTGAGTTTGGGGTCC 1326
              ||||||||||||||||||||
Db         20 AGTGGCTGAGTTTGGGGTCC 1


RESULT 44
ABZ77072/c
ID   ABZ77072 standard; DNA; 20 BP.
XX
AC   ABZ77072;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:27.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
```

```
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2241 TCCATGAGCTGCTCATTACA 2260
              ||||||||||||||||||||
Db         20 TCCATGAGCTGCTCATTACA 1


RESULT 45
ABZ77082/c
ID   ABZ77082 standard; DNA; 20 BP.
XX
AC   ABZ77082;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:37.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4101 GTGGGAGTGTGTCTGCTGAG 4120
              ||||||||||||||||||||
Db         20 GTGGGAGTGTGTCTGCTGAG 1


RESULT 46
ABZ77115/c
ID   ABZ77115 standard; DNA; 20 BP.
XX
AC   ABZ77115;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:70.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
```

XX
PF 16-JUL-2002; 2002WO-US022676.
XX
PR 30-JUL-2001; 2001US-00918187.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-248160/24.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding human
PT stearoyl-CoA desaturase, useful for treating diseases associated with the
PT desaturase, e.g. atherosclerosis, and in diagnostic and research
PT applications.
XX
PS Claim 3; Page 95; 117pp; English.
XX
CC The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC desaturase, and which specifically hybridises with and inhibits the
CC expression of human stearoyl-CoA desaturase, or which specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC activities, and can be used in antisense therapy. The antisense compounds
CC (I) can be used for modulating the expression of human stearoyl-CoA
CC desaturase and for treating diseases or conditions associated with
CC expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC antisense compounds (I) can also be used for diagnostics, therapeutics
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC tumour formation, as research reagents and kits, and in distinguishing
CC between functions of various members of a biological pathway. The present
CC sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC phosphorothioate antisense oligonucleotide, which is given in an example
CC from the present invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3051 AGTAGAGCTAGCTGCCACTT 3070
||||||||||||||||||||
Db 20 AGTAGAGCTAGCTGCCACTT 1

RESULT 47
ABZ77116/c
ID ABZ77116 standard; DNA; 20 BP.
XX
AC ABZ77116;
XX
DT 07-MAY-2003 (first entry)
XX
DE Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:71.
XX
KW Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW 2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN WO2003012031-A2.
XX
PD 13-FEB-2003.
XX
PF 16-JUL-2002; 2002WO-US022676.
XX
PR 30-JUL-2001; 2001US-00918187.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-248160/24.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding human
PT stearoyl-CoA desaturase, useful for treating diseases associated with the
PT desaturase, e.g. atherosclerosis, and in diagnostic and research
PT applications.
XX
PS Claim 3; Page 95; 117pp; English.
XX
CC The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC desaturase, and which specifically hybridises with and inhibits the
CC expression of human stearoyl-CoA desaturase, or which specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC activities, and can be used in antisense therapy. The antisense compounds
CC (I) can be used for modulating the expression of human stearoyl-CoA
CC desaturase and for treating diseases or conditions associated with
CC expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC antisense compounds (I) can also be used for diagnostics, therapeutics
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC tumour formation, as research reagents and kits, and in distinguishing
CC between functions of various members of a biological pathway. The present
CC sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC phosphorothioate antisense oligonucleotide, which is given in an example
CC from the present invention
XX
SQ Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3321 CTGCTTACTTGGTGAGGGTG 3340
||||||||||||||||||||
Db 20 CTGCTTACTTGGTGAGGGTG 1

RESULT 48
ABZ77099/c
ID ABZ77099 standard; DNA; 20 BP.
XX
AC ABZ77099;
XX
DT 07-MAY-2003 (first entry)
XX
DE Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:54.
XX

```
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        936 CCTGGTATTTCTGGGGTGAA 955
              ||||||||||||||||||||
Db         20 CCTGGTATTTCTGGGGTGAA 1
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```
RESULT 49
ABZ77102/c
ID   ABZ77102 standard; DNA; 20 BP.
XX
AC   ABZ77102;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:57.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
```

```
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1261 CGCCATCTTGGCCAGGATTA 1280
              ||||||||||||||||||||
Db         20 CGCCATCTTGGCCAGGATTA 1


RESULT 50
ABZ77112/c
ID   ABZ77112 standard; DNA; 20 BP.
XX
AC   ABZ77112;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:67.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2631 ACTGAGTGAGTTATTGGGAG 2650
              ||||||||||||||||||||
Db         20 ACTGAGTGAGTTATTGGGAG 1


RESULT 51
ABZ77124/c
ID   ABZ77124 standard; DNA; 20 BP.
XX
AC   ABZ77124;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:79.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
```

```
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 9 A; 6 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5044 ATGCCTTTTCTGTGATTGGG 5063
              ||||||||||||||||||||
Db         20 ATGCCTTTTCTGTGATTGGG 1


RESULT 52
ABZ77069/c
ID   ABZ77069 standard; DNA; 20 BP.
XX
AC   ABZ77069;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:24.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1581 CCCTTATTGCCTCCCAGGCA 1600
              ||||||||||||||||||||
Db         20 CCCTTATTGCCTCCCAGGCA 1


RESULT 53
ABZ77105/c
ID   ABZ77105 standard; DNA; 20 BP.
XX
AC   ABZ77105;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:60.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
```

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XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1748 ACAGAATCTTCTGGGTAGTC 1767
              ||||||||||||||||||||
Db         20 ACAGAATCTTCTGGGTAGTC 1


RESULT 54
ABZ77120/c
ID   ABZ77120 standard; DNA; 20 BP.
XX
AC   ABZ77120;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:75.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4357 GGGCCTGAGTGGAGGATTAT 4376
              ||||||||||||||||||||
Db         20 GGGCCTGAGTGGAGGATTAT 1


RESULT 55
ABZ77071/c
ID   ABZ77071 standard; DNA; 20 BP.
XX
AC   ABZ77071;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:26.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1941 TGCCTACCTAATGAGGACTT 1960
              ||||||||||||||||||||
Db         20 TGCCTACCTAATGAGGACTT 1


RESULT 56
ABZ77106/c
ID   ABZ77106 standard; DNA; 20 BP.
XX
AC   ABZ77106;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:61.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
```

```
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 9 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1881 GAATGTAAGGATGAGGGAAG 1900
              ||||||||||||||||||||
Db         20 GAATGTAAGGATGAGGGAAG 1


RESULT 57
ABZ77109/c
ID   ABZ77109 standard; DNA; 20 BP.
XX
AC   ABZ77109;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:64.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2281 TGCCATCTTCAGGATATTGG 2300
              ||||||||||||||||||||
Db         20 TGCCATCTTCAGGATATTGG 1


RESULT 58
ABZ77114/c
ID   ABZ77114 standard; DNA; 20 BP.
XX
AC   ABZ77114;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:69.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
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FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2941 CAGGCAGCCTCCTTTGTGTG 2960
              ||||||||||||||||||||
Db         20 CAGGCAGCCTCCTTTGTGTG 1


RESULT 59
ABZ77117/c
ID   ABZ77117 standard; DNA; 20 BP.
XX
AC   ABZ77117;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:72.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3401 GTTCTCACTGGGAAGAAGCA 3420
              ||||||||||||||||||||
Db         20 GTTCTCACTGGGAAGAAGCA 1
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RESULT 60
ABZ77119/c
ID   ABZ77119 standard; DNA; 20 BP.
XX
AC   ABZ77119;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:74.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4052 ATGGCACCTCAGGCTGAGGG 4071
              ||||||||||||||||||||
Db         20 ATGGCACCTCAGGCTGAGGG 1


RESULT 61
ABZ77070/c
ID   ABZ77070 standard; DNA; 20 BP.
XX
AC   ABZ77070;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:25.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
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FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
```

```
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1861 GGGAGAGAGTTAGCATGTAT 1880
              ||||||||||||||||||||
Db         20 GGGAGAGAGTTAGCATGTAT 1


RESULT 62
ABZ77100/c
ID   ABZ77100 standard; DNA; 20 BP.
XX
AC   ABZ77100;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:55.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
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FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1082 CGGGAGAATATCCTGGTTTC 1101
              ||||||||||||||||||||
Db         20 CGGGAGAATATCCTGGTTTC 1


RESULT 63
ABZ77111/c
ID   ABZ77111 standard; DNA; 20 BP.
XX
AC   ABZ77111;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:66.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
```

```
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATCTATA 2560
              ||||||||||||||||||||
Db         20 GCTGAGGGACAGGATCTATA 1


RESULT 64
ABZ77118/c
ID   ABZ77118 standard; DNA; 20 BP.
XX
AC   ABZ77118;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:73.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3941 TCATCAGATGCCTGCTTGAT 3960
              ||||||||||||||||||||
Db         20 TCATCAGATGCCTGCTTGAT 1


RESULT 65
ABZ77121/c
ID   ABZ77121 standard; DNA; 20 BP.
XX
AC   ABZ77121;
XX
DT   07-MAY-2003  (first entry)
XX
```

```
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:76.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 8 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4431 AGGGCTGCTTTTCTTAAGTG 4450
             ||||||||||||||||||||
Db         20 AGGGCTGCTTTTCTTAAGTG 1


RESULT 66
ABZ77076/c
ID   ABZ77076 standard; DNA; 20 BP.
XX
AC   ABZ77076;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:31.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
```

```
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3231 TTGAGCCAGTGGGCCAGCCA 3250
              ||||||||||||||||||||
Db         20 TTGAGCCAGTGGGCCAGCCA 1


RESULT 67
ABZ77081/c
ID   ABZ77081 standard; DNA; 20 BP.
XX
AC   ABZ77081;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:36.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3851 AGGATCTAAGGGAAGATCAC 3870
              ||||||||||||||||||||
Db         20 AGGATCTAAGGGAAGATCAC 1


RESULT 68
ABZ77103/c
ID   ABZ77103 standard; DNA; 20 BP.
XX
AC   ABZ77103;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:58.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
```

```
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1401 CAGGATGCTAAAGATGATGA 1420
              ||||||||||||||||||||
Db         20 CAGGATGCTAAAGATGATGA 1


RESULT 69
ABZ77125/c
ID   ABZ77125 standard; DNA; 20 BP.
XX
AC   ABZ77125;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:80.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 9 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5081 TTATGTGGGATATAGTAGTT 5100
              ||||||||||||||||||||
Db         20 TTATGTGGGATATAGTAGTT 1


RESULT 70
ABZ77074/c
ID   ABZ77074 standard; DNA; 20 BP.
XX
AC   ABZ77074;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:29.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
```

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OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2980 CTTGCTGTCCAGGCAGCTCC 2999
              ||||||||||||||||||||
Db         20 CTTGCTGTCCAGGCAGCTCC 1


RESULT 71
ABZ77075/c
ID   ABZ77075 standard; DNA; 20 BP.
XX
AC   ABZ77075;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:30.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
```

```
  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3011 AGAATGCTCAGGGTCACTGA 3030
              ||||||||||||||||||||
Db         20 AGAATGCTCAGGGTCACTGA 1


RESULT 72
ABZ77088/c
ID   ABZ77088 standard; DNA; 20 BP.
XX
AC   ABZ77088;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:43.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4921 GCTGTCATTAGTCTATATGG 4940
              ||||||||||||||||||||
Db         20 GCTGTCATTAGTCTATATGG 1


RESULT 73
ABZ77067/c
ID   ABZ77067 standard; DNA; 20 BP.
XX
AC   ABZ77067;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:22.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
```

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PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1171 GTACCGCTGGCACATCAACT 1190
              ||||||||||||||||||||
Db         20 GTACCGCTGGCACATCAACT 1


RESULT 74
ABZ77108/c
ID   ABZ77108 standard; DNA; 20 BP.
XX
AC   ABZ77108;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:63.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2102 AGTGGTCTCTGCTGGGGAAG 2121
              ||||||||||||||||||||
Db         20 AGTGGTCTCTGCTGGGGAAG 1


RESULT 75
ABZ77078/c
ID   ABZ77078 standard; DNA; 20 BP.
XX
AC   ABZ77078;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:33.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
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FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCAAAGC 3490
              ||||||||||||||||||||
Db         20 GTCAGGGTGAACTGCAAAGC 1


RESULT 76
ABZ77084/c
ID   ABZ77084 standard; DNA; 20 BP.
XX
AC   ABZ77084;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:39.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4406 GGGCTTCATTCTGGAAACTT 4425
              ||||||||||||||||||||
Db         20 GGGCTTCATTCTGGAAACTT 1
```

```
RESULT 77
ABZ77086/c
ID   ABZ77086 standard; DNA; 20 BP.
XX
AC   ABZ77086;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:41.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTTAACTA 4727
              ||||||||||||||||||||
Db         20 CTGGGCAAGTCACTTAACTA 1


RESULT 78
ABZ77110/c
ID   ABZ77110 standard; DNA; 20 BP.
XX
AC   ABZ77110;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:65.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
```

```
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 10 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2481 GAGAGGAGGAATTAGTTGGG 2500
              ||||||||||||||||||||
Db         20 GAGAGGAGGAATTAGTTGGG 1


RESULT 79
ABZ77083/c
ID   ABZ77083 standard; DNA; 20 BP.
XX
AC   ABZ77083;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:38.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4226 GGGTGTGCTGACAACTTAGC 4245
              ||||||||||||||||||||
Db         20 GGGTGTGCTGACAACTTAGC 1


RESULT 80
ABZ77087/c
ID   ABZ77087 standard; DNA; 20 BP.
XX
AC   ABZ77087;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:42.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
```

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XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4771 ACTGACCTACCTCAAAGGGC 4790
              ||||||||||||||||||||
Db         20 ACTGACCTACCTCAAAGGGC 1


RESULT 81
ABZ77101/c
ID   ABZ77101 standard; DNA; 20 BP.
XX
AC   ABZ77101;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:56.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1151 TATGACTACTCTGCCAGTGA 1170
              ||||||||||||||||||||
Db         20 TATGACTACTCTGCCAGTGA 1


RESULT 82
ABZ77107/c
ID   ABZ77107 standard; DNA; 20 BP.
XX
AC   ABZ77107;
XX
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```
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:62.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 7 A; 5 C; 8 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1985 CCTTTCTCTCCTGGCTCGGG 2004
              ||||||||||||||||||||
Db         20 CCTTTCTCTCCTGGCTCGGG 1


RESULT 83
ABZ77080/c
ID   ABZ77080 standard; DNA; 20 BP.
XX
AC   ABZ77080;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:35.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
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FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
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XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
```

```
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3791 ACAGGGGTTAGCCTGGACTA 3810
              ||||||||||||||||||||
Db         20 ACAGGGGTTAGCCTGGACTA 1


RESULT 84
ABZ77066/c
ID   ABZ77066 standard; DNA; 20 BP.
XX
AC   ABZ77066;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:21.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
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FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
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CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1111 TGTGGGTGAGGGCTTCCACA 1130
              ||||||||||||||||||||
Db         20 TGTGGGTGAGGGCTTCCACA 1


RESULT 85
ABZ77073/c
ID   ABZ77073 standard; DNA; 20 BP.
XX
AC   ABZ77073;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:28.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
```

```
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2616 GGGCTTGAGAAGGTTACTGA 2635
              ||||||||||||||||||||
Db         20 GGGCTTGAGAAGGTTACTGA 1


RESULT 86
ABZ77077/c
ID   ABZ77077 standard; DNA; 20 BP.
XX
AC   ABZ77077;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:32.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3291 GTCAGAACCAGAGGGCATGC 3310
              ||||||||||||||||||||
Db         20 GTCAGAACCAGAGGGCATGC 1


RESULT 87
ABZ77098/c
ID   ABZ77098 standard; DNA; 20 BP.
XX
AC   ABZ77098;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:53.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
```

```
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        901 GCTGCTGATGTGCTTCATCC 920
              ||||||||||||||||||||
Db         20 GCTGCTGATGTGCTTCATCC 1

RESULT 88
ABZ77104/c
ID   ABZ77104 standard; DNA; 20 BP.
XX
AC   ABZ77104;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:59.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
```

```
XX
SQ   Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1601 AGCAGCTGGTCAGTCTTTGC 1620
              ||||||||||||||||||||
Db         20 AGCAGCTGGTCAGTCTTTGC 1


RESULT 89
ABZ77113/c
ID   ABZ77113 standard; DNA; 20 BP.
XX
AC   ABZ77113;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:68.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2826 GGCAGGGTTAGGAATCTCTT 2845
              ||||||||||||||||||||
Db         20 GGCAGGGTTAGGAATCTCTT 1


RESULT 90
ABZ77079/c
ID   ABZ77079 standard; DNA; 20 BP.
XX
AC   ABZ77079;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:34.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
```

```
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3502 CCTGGGATTTGAGATACCAC 3521
              ||||||||||||||||||||
Db         20 CCTGGGATTTGAGATACCAC 1


RESULT 91
ABZ77085/c
ID   ABZ77085 standard; DNA; 20 BP.
XX
AC   ABZ77085;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:40.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 10 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4571 GTATCTTGGGTGTATTCTCT 4590
              ||||||||||||||||||||
Db         20 GTATCTTGGGTGTATTCTCT 1


RESULT 92
ABZ77089/c
ID   ABZ77089 standard; DNA; 20 BP.
XX
AC   ABZ77089;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:44.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
```

```
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5021 ATTGCCACGGAAACATACAG 5040
              ||||||||||||||||||||
Db         20 ATTGCCACGGAAACATACAG 1


RESULT 93
ABZ77122/c
ID   ABZ77122 standard; DNA; 20 BP.
XX
AC   ABZ77122;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:77.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4681 ACTGTGCCACTGACTTGCTG 4700
```

```
                    ||||||||||||||||||||
Db         20 ACTGTGCCACTGACTTGCTG 1


RESULT 94
ABZ77123/c
ID   ABZ77123 standard; DNA; 20 BP.
XX
AC   ABZ77123;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:78.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Claim 3; Page 95; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4971 GAAGCGGTGGATAACTAGCC 4990
                ||||||||||||||||||||
Db         20 GAAGCGGTGGATAACTAGCC 1


RESULT 95
ADE27643
ID   ADE27643 standard; RNA; 21 BP.
XX
AC   ADE27643;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:587.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 587; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

```
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 4 A; 4 C; 8 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3785 GAGGCTACAGGGGTTAGCCT 3804
              |||||:|||||||::|||||
Db          1 GAGGCUACAGGGGUUAGCCT 20


RESULT 96
ADE27674/c
ID   ADE27674 standard; RNA; 21 BP.
XX
AC   ADE27674;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:629.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Disclosure; SEQ ID NO 629; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3026 ACTGAACCACTGCTTCTCTT 3045
              ||||||||||||||||||||
Db         20 ACTGAACCACTGCTTCTCTT 1


RESULT 97
ADE27670/c
ID   ADE27670 standard; RNA; 21 BP.
XX
AC   ADE27670;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:625.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Disclosure; SEQ ID NO 625; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
```

```
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3026 ACTGAACCACTGCTTCTCTT 3045
              ||||||||||||||||||||
Db         20 ACTGAACCACTGCTTCTCTT 1


RESULT 98
ADE27645/c
ID   ADE27645 standard; RNA; 21 BP.
XX
AC   ADE27645;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:589.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 589; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 8 A; 6 C; 2 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        994 ATATGCTGTGGTGCTTAATG 1013
              ||||||||||||||||||||
Db         20 ATATGCTGTGGTGCTTAATG 1


RESULT 99
ADE27672/c
ID   ADE27672 standard; RNA; 21 BP.
XX
AC   ADE27672;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:627.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Disclosure; SEQ ID NO 627; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
```

```
XX
SQ   Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3026 ACTGAACCACTGCTTCTCTT 3045
              ||||||||||||||||||||
Db         20 ACTGAACCACTGCTTCTCTT 1


RESULT 100
ADE27647/c
ID   ADE27647 standard; RNA; 21 BP.
XX
AC   ADE27647;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:591.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 591; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 3 A; 8 C; 4 G; 2 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3784 AGAGGCTACAGGGGTTAGCC 3803
              ||||||||||||||||||||
Db         20 AGAGGCTACAGGGGTTAGCC 1


RESULT 101
ADE27675/c
ID   ADE27675 standard; RNA; 21 BP.
XX
AC   ADE27675;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:630.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Disclosure; SEQ ID NO 630; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;
```

```
  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3026 ACTGAACCACTGCTTCTCTT 3045
              ||||||||||||||||||||
Db         20 ACTGAACCACTGCTTCTCTT 1


RESULT 102
ADG30281
ID   ADG30281 standard; RNA; 21 BP.
XX
AC   ADG30281;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 847.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 847; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 4 A; 4 C; 8 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3785 GAGGCTACAGGGGTTAGCCT 3804
              |||||:|||||||::|||||
Db          1 GAGGCUACAGGGGUUAGCCT 20


RESULT 103
ADG30277/c
ID   ADG30277 standard; RNA; 21 BP.
XX
AC   ADG30277;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 843.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 843; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
```

```
XX
SQ   Sequence 21 BP; 3 A; 8 C; 4 G; 2 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3784 AGAGGCTACAGGGGTTAGCC 3803
              ||||||||||||||||||||
Db         20 AGAGGCTACAGGGGTTAGCC 1


RESULT 104
ADG30275/c
ID   ADG30275 standard; RNA; 21 BP.
XX
AC   ADG30275;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 841.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 841; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 8 A; 6 C; 2 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        994 ATATGCTGTGGTGCTTAATG 1013
              ||||||||||||||||||||
Db         20 ATATGCTGTGGTGCTTAATG 1


RESULT 105
ADG30283/c
ID   ADG30283 standard; RNA; 21 BP.
XX
AC   ADG30283;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 849.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 849; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
```

CC gene therapy applications. The current sequence is that of the siNA DNA-
CC RNA hybrid of the invention.
XX
SQ Sequence 21 BP; 8 A; 6 C; 2 G; 2 T; 3 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 994 ATATGCTGTGGTGCTTAATG 1013
||||||||||||||||||||
Db 20 ATATGCTGTGGTGCTTAATG 1

RESULT 106
ADG30285/c
ID ADG30285 standard; RNA; 21 BP.
XX
AC ADG30285;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD-targeted siNA DNA-RNA hybrid - SEQ ID 851.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX
PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 851; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA DNA-
CC RNA hybrid of the invention.
XX
SQ Sequence 21 BP; 3 A; 8 C; 4 G; 2 T; 4 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3784 AGAGGCTACAGGGGTTAGCC 3803
||||||||||||||||||||
Db 20 AGAGGCTACAGGGGTTAGCC 1

RESULT 107
ADO14557/c
ID ADO14557 standard; RNA; 21 BP.
XX
AC ADO14557;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human interleukin-2-targeted siNA antisense strandSEQ ID NO:303.
XX
KW cytostatic; vasotropic; nephrotropic; cancer; restenosis;
KW polycystic kidney disease; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human; interleukin-2; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .8
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 9
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 10. .11
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 12
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 13. .14
FT /*tag= e
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 15. .17
FT /*tag= f
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 18. .19
FT /*tag= g
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 20. .21
FT /*tag= h
FT /mod_base= OTHER
FT /note= "Deoxyribothimidine. Also, the internucleotide
FT linkage is phosphorothioate or phosphorodithioate.
FT Optionally linked to glyceryl moiety"
XX
PN WO2003070744-A1.
XX

PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004566.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-731546/69.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS Disclosure; SEQ ID NO 303; 138pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human interleukin-2 gene by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA, double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
CC and/or complexes of siRNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of the interleukin-2 gene in cells, tissue
CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
CC transplants for the treatment of a variety of conditions. They may be
CC used for treating cancer, restenosis and polycystic kidney disease. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents a the antisense strand of
CC an exemplary chemically modified human interleukin-2-targeted double-
CC stranded siNA.
XX
SQ Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3026 ACTGAACCACTGCTTCTCTT 3045
||||||||||||||||||||
Db 20 ACTGAACCACTGCTTCTCTT 1

RESULT 108
ADO14559/c
ID ADO14559 standard; RNA; 21 BP.
XX
AC ADO14559;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human interleukin-2-targeted siNA antisense strandSEQ ID NO:305.
XX
KW cytostatic; vasotropic; nephrotropic; cancer; restenosis;
KW polycystic kidney disease; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human; interleukin-2; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .8
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 9
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 10. .11
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 12
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 13. .14
FT /*tag= e
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 15. .17
FT /*tag= f
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 18. .19
FT /*tag= g
FT /mod_base= OTHER
FT /note= "2'-O-methyl base"
FT modified_base 20. .21
FT /*tag= h
FT /mod_base= OTHER
FT /note= "Deoxyribothimidine. Optionally linked to glyceryl
FT moiety"
XX
PN WO2003070744-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004566.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-731546/69.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS Disclosure; SEQ ID NO 305; 138pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human interleukin-2 gene by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA, double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,

```
CC   expressed from a vector or enzymatically synthesised. The invention also
CC   relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
CC   and/or complexes of siRNA; and vectors that express siNA. The siNAs are
CC   used to modulate expression of the interleukin-2 gene in cells, tissue
CC   explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
CC   transplants for the treatment of a variety of conditions. They may be
CC   used for treating cancer, restenosis and polycystic kidney disease. The
CC   siNAs are also useful for drug screening, diagnosis, therapeutic target
CC   identification and validation, genetic engineering, pharmacogenomics,
CC   studying gene function, and gene mapping (e.g., of single nucleotide
CC   polymorphisms). The present sequence represents a the antisense strand of
CC   an exemplary chemically modified human interleukin-2-targeted double-
CC   stranded siNA.
XX
SQ   Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3026 ACTGAACCACTGCTTCTCTT 3045
              ||||||||||||||||||||
Db         20 ACTGAACCACTGCTTCTCTT 1


RESULT 109
ADO14560/c
ID   ADO14560 standard; RNA; 21 BP.
XX
AC   ADO14560;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human interleukin-2-targeted siNA antisense strandSEQ ID NO:306.
XX
KW   cytostatic; vasotropic; nephrotropic; cancer; restenosis;
KW   polycystic kidney disease; RNA interference;
KW   short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW   double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW   expression modulation; gene therapy; drug screening; diagnosis;
KW   therapeutic target identification; pharmacogenomics;
KW   gene function analysis; gene mapping; human; interleukin-2; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .8
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Deoxy base"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoro base"
FT   modified_base   10. .11
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Deoxy base"
FT   modified_base   12
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoro base"
FT   modified_base   13. .14
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "Deoxy base"
FT   modified_base   15. .17
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoro base"
FT   modified_base   18. .19
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "Deoxy base"
FT   modified_base   20. .21
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "Deoxyribothimidine. Also, the internucleotide
FT                   linkage is phosphorothioate or phosphorodithioate.
FT                   Optionally linked to glyceryl moiety"
XX
PN   WO2003070744-A1.
XX
PD   28-AUG-2003.
XX
PF   11-FEB-2003; 2003WO-US004566.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-731546/69.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS   Disclosure; SEQ ID NO 306; 138pp; English.
XX
CC   The invention relates to short interfering nucleic acids (siNA) which
CC   downregulate expression of the human interleukin-2 gene by RNA
CC   interference. The siNAs may or may not comprise ribonucleotides and may
CC   be double or single stranded. They further comprise sense and antisense
CC   regions, or alternatively are assembled from a sense oligonucleotide and
CC   an antisense oligonucleotide. Specifically, the siNAs include short
CC   interfering RNA (siRNA, double-stranded RNA, micro-RNA (miRNA) and short
CC   hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC   can contain deoxyribonucleotides, and can be chemically synthesised,
CC   expressed from a vector or enzymatically synthesised. The invention also
CC   relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
CC   and/or complexes of siRNA; and vectors that express siNA. The siNAs are
CC   used to modulate expression of the interleukin-2 gene in cells, tissue
CC   explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
CC   transplants for the treatment of a variety of conditions. They may be
CC   used for treating cancer, restenosis and polycystic kidney disease. The
CC   siNAs are also useful for drug screening, diagnosis, therapeutic target
CC   identification and validation, genetic engineering, pharmacogenomics,
CC   studying gene function, and gene mapping (e.g., of single nucleotide
CC   polymorphisms). The present sequence represents a the antisense strand of
CC   an exemplary chemically modified human interleukin-2-targeted double-
CC   stranded siNA.
XX
SQ   Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3026 ACTGAACCACTGCTTCTCTT 3045
              ||||||||||||||||||||
Db         20 ACTGAACCACTGCTTCTCTT 1


RESULT 110
ADO14555/c
ID   ADO14555 standard; RNA; 21 BP.
XX
AC   ADO14555;
XX
```

DT 01-JUL-2004 (first entry)
XX
DE Human interleukin-2-targeted siNA antisense strandSEQ ID NO:301.
XX
KW cytostatic; vasotropic; nephrotropic; cancer; restenosis;
KW polycystic kidney disease; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human; interleukin-2; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 9
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 12
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 15. .17
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoro base"
FT modified_base 20. .21
FT /*tag= d
FT /mod_base= OTHER
FT /note= "Deoxyribothimidine. Also, the internucleotide
FT linkage is phosphorothioate or phosphorodithioate.
FT Optionally linked to glyceryl moiety"
XX
PN WO2003070744-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004566.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-731546/69.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS Disclosure; SEQ ID NO 301; 138pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human interleukin-2 gene by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA, double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
CC and/or complexes of siRNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of the interleukin-2 gene in cells, tissue
CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
CC transplants for the treatment of a variety of conditions. They may be
CC used for treating cancer, restenosis and polycystic kidney disease. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents a the antisense strand of
CC an exemplary chemically modified human interleukin-2-targeted double-
CC stranded siNA.
XX
SQ Sequence 21 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3026 ACTGAACCACTGCTTCTCTT 3045
||||||||||||||||||||
Db 20 ACTGAACCACTGCTTCTCTT 1

RESULT 111
ADE27666/c
ID ADE27666 standard; RNA; 22 BP.
XX
AC ADE27666;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:621.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Disclosure; SEQ ID NO 621; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD

CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3026 ACTGAACCACTGCTTCTCTT 3045
||||||||||||||||||||
Db 20 ACTGAACCACTGCTTCTCTT 1

RESULT 112
ADE27655/c
ID ADE27655 standard; RNA; 22 BP.
XX
AC ADE27655;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:599.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 599; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 3 A; 8 C; 4 G; 2 T; 4 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3784 AGAGGCTACAGGGGTTAGCC 3803
||||||||||||||||||||
Db 20 AGAGGCTACAGGGGTTAGCC 1

RESULT 113
ADE27663/c
ID ADE27663 standard; RNA; 22 BP.
XX
AC ADE27663;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:607.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 607; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.

CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 3 A; 8 C; 4 G; 2 T; 4 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3784 AGAGGCTACAGGGGTTAGCC 3803
||||||||||||||||||||
Db 20 AGAGGCTACAGGGGTTAGCC 1

RESULT 114
ADE27668/c
ID ADE27668 standard; RNA; 22 BP.
XX
AC ADE27668;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:623.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Disclosure; SEQ ID NO 623; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 7 A; 2 C; 7 G; 2 T; 3 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3026 ACTGAACCACTGCTTCTCTT 3045
||||||||||||||||||||
Db 20 ACTGAACCACTGCTTCTCTT 1

RESULT 115
ADE27664/c
ID ADE27664 standard; RNA; 22 BP.
XX
AC ADE27664;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:608.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 608; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;

CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 2 A; 5 C; 6 G; 2 T; 6 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4771 ACTGACCTACCTCAAAGGGCAG 4792
|: ||||||||||||||||||||
Db 22 ASAGACCTACCTCAAAGGGCAG 1

RESULT 116
ADE27656/c
ID ADE27656 standard; RNA; 22 BP.
XX
AC ADE27656;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:600.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 600; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 2 A; 5 C; 6 G; 2 T; 6 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4771 ACTGACCTACCTCAAAGGGCAG 4792
|: ||||||||||||||||||||
Db 22 ASAGACCTACCTCAAAGGGCAG 1

RESULT 117
ADE27651
ID ADE27651 standard; RNA; 23 BP.
XX
AC ADE27651;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:595.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 595; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is

```
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 4 A; 4 C; 8 G; 2 T; 3 U; 2 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+02;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3785 GAGGCTACAGGGGTTAGCCT 3804
              |||||:|||||||::|||||
Db          2 GAGGCUACAGGGGUUAGCCT 21


RESULT 118
ADE27659
ID   ADE27659 standard; RNA; 23 BP.
XX
AC   ADE27659;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:603.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 603; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 4 A; 4 C; 8 G; 2 T; 3 U; 2 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+02;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3785 GAGGCTACAGGGGTTAGCCT 3804
              |||||:|||||||::|||||
Db          2 GAGGCUACAGGGGUUAGCCT 21


RESULT 119
ADG30273
ID   ADG30273 standard; RNA; 23 BP.
XX
AC   ADG30273;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 839.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Posnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 839; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
```

```
CC   RNA hybrid of the invention.
XX
SQ   Sequence 23 BP; 4 A; 4 C; 8 G; 2 T; 3 U; 2 Other;

  Query Match             0.5%;  Score 20;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+02;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3785 GAGGCTACAGGGGTTAGCCT 3804
              |||||:|||||||::|||||
Db          2 GAGGCUACAGGGGUUAGCCT 21


RESULT 120
ADG75988
ID   ADG75988 standard; DNA; 24 BP.
XX
AC   ADG75988;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Immunostimulatory non-CpG oligonucleotide IMT 037 SeqID 100.
XX
KW   ss; non-CpG; immunostimulatory; non-palindromic; immune response;
KW   proliferation; differentiation; cytokine; antibody production; B-cell;
KW   plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW   chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
KW   renal cell carcinoma.
XX
OS   Synthetic.
XX
PN   WO2003101375-A2.
XX
PD   11-DEC-2003.
XX
PF   30-MAY-2003; 2003WO-EP005691.
XX
PR   30-MAY-2002; 2002CA-02388049.
XX
PA   (IMMU-) IMMUNOTECH SA.
XX
PI   Lopez RA;
XX
DR   WPI; 2004-053333/05.
XX
PT   New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT   acid sequence motif, useful for inducing B-cell activation, treating,
PT   preventing or ameliorating immune system disorder or tumoral disease e.g.
PT   melanoma.
XX
PS   Disclosure; Fig 3; 139pp; English.
XX
CC   This invention relates to novel immunostimulatory oligonucleotides that
CC   contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC   oligonucleotides (without a CpG motif), which can stimulate an immune
CC   response in animals of the order of primate, including humans. The immune
CC   response is characterised by the proliferation, differentiation, cytokine
CC   and antibody production in B-cells, as well as cell differentiation and
CC   cytokine production in plasmacytoid dendritic cells. The present
CC   invention describes immunomodulator compositions that also comprise an
CC   antigen selected from, for example, viruses, bacteria, parasites, tumour
CC   cells and glycolipids. As such, these DNA oligos can be used in gene
CC   therapy for inducing B-cell activation, treating, preventing or
CC   ameliorating an immune system disorder or a tumoural disease including
CC   chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC   carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG
CC   variant DNA oligo, used in an exemplification of the invention.
XX
SQ   Sequence 24 BP; 0 A; 3 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 19.8;  DB 1;  Length 24;
  Best Local Similarity   91.3%;  Pred. No. 2e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2121 GGGTTTTCTTTTCTTTTTTTCTT 2143
              |||| || |||||||||||||||
Db          2 GGGTCTTTTTTTCTTTTTTTCTT 24


RESULT 121
AAZ77065/c
ID   AAZ77065 standard; DNA; 21 BP.
XX
AC   AAZ77065;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:11421.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 9; Page 2665; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 21 BP; 7 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 2e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4688 CACTGACTTGCTGTGTGACCC 4708
              || ||||||||||||||||||
Db         21 CATTGACTTGCTGTGTGACCC 1


RESULT 122
ADE27646/c
```

```
ID   ADE27646 standard; RNA; 21 BP.
XX
AC   ADE27646;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:590.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 590; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 2e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2518 ACTGCTGGACATGAGATGGAG 2538
              | ||||||||||||||||||||
Db         21 AATGCTGGACATGAGATGGAG 1


RESULT 123
ADG30284/c
ID   ADG30284 standard; RNA; 21 BP.
XX
AC   ADG30284;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 850.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 850; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 2e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2518 ACTGCTGGACATGAGATGGAG 2538
              | ||||||||||||||||||||
Db         21 AATGCTGGACATGAGATGGAG 1


RESULT 124
ADG30276/c
```

```
ID   ADG30276 standard; RNA; 21 BP.
XX
AC   ADG30276;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 842.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 842; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 2e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2518 ACTGCTGGACATGAGATGGAG 2538
              | ||||||||||||||||||||
Db         21 AATGCTGGACATGAGATGGAG 1


RESULT 125
ADE27658
ID   ADE27658 standard; RNA; 23 BP.
XX
AC   ADE27658;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:602.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 602; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 2 Other;

  Query Match             0.4%;  Score 19.2;  DB 1;  Length 23;
  Best Local Similarity   75.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2519 CTGCTGGACATGAGATGGAG 2538
              ::||:|||||:||||:||||
Db          1 BUGCUGGACAUGAGAUGGAG 20


RESULT 126
ADE27650
```

```
ID   ADE27650 standard; RNA; 23 BP.
XX
AC   ADE27650;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:594.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 594; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 23 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 2 Other;

  Query Match             0.4%;  Score 19.2;  DB 1;  Length 23;
  Best Local Similarity   75.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2519 CTGCTGGACATGAGATGGAG 2538
              ::||:|||||:||||:||||
Db          1 BUGCUGGACAUGAGAUGGAG 20


RESULT 127
ADE27114
ID   ADE27114 standard; RNA; 19 BP.
XX
AC   ADE27114;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:58.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 58; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 ACAGTGCTGCCCACCTCTT 1047
              ||||:||:|||||||:|::
Db          1 ACAGUGCUGCCCACCUCUU 19


RESULT 128
ADE27154
ID   ADE27154 standard; RNA; 19 BP.
XX
```

```
AC   ADE27154;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:98.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 98; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1749 CAGAATCTTCTGGGTAGTC 1767
              |||||:|::|:|||:||:|
Db          1 CAGAAUCUUCUGGGUAGUC 19


RESULT 129
ADE27158
ID   ADE27158 standard; RNA; 19 BP.
XX
AC   ADE27158;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:102.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 102; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 4 C; 2 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1821 TTCATTTGACACAAAGCTT 1839
              ::||:::||||||||||::
Db          1 UUCAUUUGACACAAAGCUU 19


RESULT 130
ADE27166
ID   ADE27166 standard; RNA; 19 BP.
XX
AC   ADE27166;
XX
```

DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:110.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 110; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 9 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1965 CCCCACCACATAGCATGCT 1983
||||||||||:||||:||:
Db 1 CCCCACCACAUAGCAUGCU 19

RESULT 131
ADE27186
ID ADE27186 standard; RNA; 19 BP.
XX
AC ADE27186;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:130.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 130; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2325 GGCTGTGGCATTTCCAAAC 2343
|||:|:||||:::||||||
Db 1 GGCUGUGGCAUUUCCAAAC 19

RESULT 132
ADE27188
ID ADE27188 standard; RNA; 19 BP.
XX
AC ADE27188;
XX
DT 29-JAN-2004 (first entry)
XX

DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:132.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 132; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 1 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2361 GATTTAAGGAGGTGAAGTC 2379
              ||:::|||||||:||||:|
Db          1 GAUUUAAGGAGGUGAAGUC 19
```

RESULT 133
ADE27216
ID ADE27216 standard; RNA; 19 BP.
XX
AC ADE27216;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:160.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 160; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 8 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2865 TCCTGGCTCTACCCTGTCT 2883
              :||:|||:|:||||:|:|:
Db          1 UCCUGGCUCUACCCUGUCU 19
```

RESULT 134
ADE27252
ID ADE27252 standard; RNA; 19 BP.
XX
AC ADE27252;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:196.
XX

```
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 196; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 7 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3513 AGATACCACAAACCCTGCT 3531
              |||:|||||||||||:||:
Db          1 AGAUACCACAAACCCUGCU 19


RESULT 135
ADE27266
ID   ADE27266 standard; RNA; 19 BP.
XX
AC   ADE27266;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:210.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 210; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 3 C; 4 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3765 TCTTCTGTGTTAATTGCGT 3783
              :|::|:|:|::||::|||:
Db          1 UCUUCUGUGUUAAUUGCGU 19


RESULT 136
ADE27267
ID   ADE27267 standard; RNA; 19 BP.
XX
AC   ADE27267;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:211.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
```

```
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 211; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 2 C; 8 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3783 TAGAGGCTACAGGGGTTAG 3801
              :||||||:|||||||::||
Db          1 UAGAGGCUACAGGGGUUAG 19


RESULT 137
ADE27275
ID   ADE27275 standard; RNA; 19 BP.
XX
AC   ADE27275;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:219.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 219; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3927 TCTAATTCCACAGGTCATC 3945
              :|:||::|||||||:||:|
Db          1 UCUAAUUCCACAGGUCAUC 19


RESULT 138
ADE27285
ID   ADE27285 standard; RNA; 19 BP.
XX
AC   ADE27285;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:229.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
```

KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 229; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 2 C; 8 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4107 GTGTGTCTGCTGAGTAAGG 4125
              |:|:|:|:||:|||:||||
Db          1 GUGUGUCUGCUGAGUAAGG 19
```

RESULT 139
ADE27297
ID ADE27297 standard; RNA; 19 BP.
XX
AC ADE27297;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:241.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 241; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4323 CCTGAGACCCTACTGAAGT 4341
              ||:|||||||:||:||||:
Db          1 CCUGAGACCCUACUGAAGU 19
```

RESULT 140
ADE27303
ID ADE27303 standard; RNA; 19 BP.
XX
AC ADE27303;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:247.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX

OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 247; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 3 C; 5 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4431 AGGGCTGCTTTTCTTAAGT 4449
              |||||:||::::|::|||:
Db          1 AGGGCUGCUUUUCUUAAGU 19
```

RESULT 141
ADE27398/c
ID ADE27398 standard; RNA; 19 BP.
XX
AC ADE27398;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:342.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 342; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 8 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        921 TGCCCACGCTTGTGCCCTG 939
              |||||||||||||||||||
Db         19 TGCCCACGCTTGTGCCCTG 1
```

RESULT 142
ADE27405/c
ID ADE27405 standard; RNA; 19 BP.
XX
AC ADE27405;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:349.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX

PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 349; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 4 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 TCGGATATCGTCCTTATGA 1065
||||||||||||||||||||
Db 19 TCGGATATCGTCCTTATGA 1

RESULT 143
ADE27409/c
ID ADE27409 standard; RNA; 19 BP.
XX
AC ADE27409;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:353.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 353; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 3 C; 7 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1119 AGGGCTTCCACAACTACCA 1137
||||||||||||||||||||
Db 19 AGGGCTTCCACAACTACCA 1

RESULT 144
ADE27414/c
ID ADE27414 standard; RNA; 19 BP.
XX
AC ADE27414;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:358.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX

PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 358; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1209 ATTGCATGGCCGCCCTCGG 1227
||||||||||||||||||||
Db 19 ATTGCATGGCCGCCCTCGG 1

RESULT 145
ADE27417/c
ID ADE27417 standard; RNA; 19 BP.
XX
AC ADE27417;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:361.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 361; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1263 CCATCTTGGCCAGGATTAA 1281
||||||||||||||||||||
Db 19 CCATCTTGGCCAGGATTAA 1

RESULT 146
ADE27424/c
ID ADE27424 standard; RNA; 19 BP.
XX
AC ADE27424;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:368.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX

PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 368; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1389 GAATAATGCTACCAGGATG 1407
||||||||||||||||||
Db 19 GAATAATGCTACCAGGATG 1

RESULT 147
ADE27436/c
ID ADE27436 standard; RNA; 19 BP.
XX
AC ADE27436;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:380.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 380; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 5 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1605 GCTGGTCAGTCTTTGCTCA 1623
||||||||||||||||||
Db 19 GCTGGTCAGTCTTTGCTCA 1

RESULT 148
ADE27502/c
ID ADE27502 standard; RNA; 19 BP.
XX
AC ADE27502;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:446.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 446; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 2 C; 4 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2793 AACATCTAGCCTAAAGTAT 2811
||||||||||||||||||
Db 19 AACATCTAGCCTAAAGTAT 1

RESULT 149
ADE27504/c
ID ADE27504 standard; RNA; 19 BP.
XX
AC ADE27504;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:448.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 448; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2829 AGGGTTAGGAATCTCTTCA 2847
||||||||||||||||||
Db 19 AGGGTTAGGAATCTCTTCA 1

RESULT 150
ADE27544/c
ID ADE27544 standard; RNA; 19 BP.
XX
AC ADE27544;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:488.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 488; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 2 C; 6 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3549 AGCAAACTAACCAGCATTC 3567
||||||||||||||||||||
Db 19 AGCAAACTAACCAGCATTC 1

RESULT 151
ADE27570/c
ID ADE27570 standard; RNA; 19 BP.
XX
AC ADE27570;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:514.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 514; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4017 GATCTGATCTGTACCATGA 4035
||||||||||||||||||||
Db 19 GATCTGATCTGTACCATGA 1

RESULT 152
ADE27580/c
ID ADE27580 standard; RNA; 19 BP.
XX
AC ADE27580;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:524.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 524; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4197 TCCGGATTTCTAACAGTCC 4215
||||||||||||||||||
Db 19 TCCGGATTTCTAACAGTCC 1

RESULT 153
ADE27587/c
ID ADE27587 standard; RNA; 19 BP.
XX
AC ADE27587;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:531.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 531; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4323 CCTGAGACCCTACTGAAGT 4341
||||||||||||||||||
Db 19 CCTGAGACCCTACTGAAGT 1

RESULT 154
ADE27595/c
ID ADE27595 standard; RNA; 19 BP.
XX
AC ADE27595;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:539.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 539; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 0 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4467 GGTGGAAATAATTTGAATG 4485
||||||||||||||||||||
Db 19 GGTGGAAATAATTTGAATG 1

RESULT 155
ADE27605/c
ID ADE27605 standard; RNA; 19 BP.
XX
AC ADE27605;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:549.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 549; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 7 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4647 TATGCTGGTGGTTAAGGCC 4665
||||||||||||||||||||
Db 19 TATGCTGGTGGTTAAGGCC 1

RESULT 156
ADE27612/c
ID ADE27612 standard; RNA; 19 BP.
XX
AC ADE27612;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:556.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 556; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4773 TGACCTACCTCAAAGGGCA 4791
||||||||||||||||||
Db 19 TGACCTACCTCAAAGGGCA 1

RESULT 157
ADE27615/c
ID ADE27615 standard; RNA; 19 BP.
XX
AC ADE27615;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:559.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 559; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4827 TTTGGGATCCTTCAGCACA 4845
||||||||||||||||||
Db 19 TTTGGGATCCTTCAGCACA 1

RESULT 158
ADE27619/c
ID ADE27619 standard; RNA; 19 BP.
XX
AC ADE27619;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:563.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.

```
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 563; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 6 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4899 GATACGTCCGTGTGTCCCA 4917
              ||||||||||||||||||
Db         19 GATACGTCCGTGTGTCCCA 1


RESULT 159
ADE27106
ID   ADE27106 standard; RNA; 19 BP.
XX
AC   ADE27106;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:50.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 50; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        885 ACTACAAACCTGGCTTGCT 903
              ||:|||||||:|||::||:
Db          1 ACUACAAACCUGGCUUGCU 19


RESULT 160
ADE27109
ID   ADE27109 standard; RNA; 19 BP.
XX
AC   ADE27109;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:53.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

```
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 53; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 2 C; 7 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        939 GGTATTTCTGGGGTGAAAC 957
              ||:|:::|:||||:|||||
Db          1 GGUAUUUCUGGGGUGAAAC 19


RESULT 161
ADE27124
ID   ADE27124 standard; RNA; 19 BP.
XX
AC   ADE27124;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:68.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 68; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 7 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1209 ATTGCATGGCCGCCCTCGG 1227
              |::|||:|||||||:|||
Db          1 AUUGCAUGGCCGCCCUCGG 19


RESULT 162
ADE27152
ID   ADE27152 standard; RNA; 19 BP.
XX
AC   ADE27152;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:96.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
```

```
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 96; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 2 C; 8 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1713 GAGCTTTGAAGTAGGTGGC 1731
              ||||:::||||:|||:|||
Db          1 GAGCUUUGAAGUAGGUGGC 19


RESULT 163
ADE27156
ID   ADE27156 standard; RNA; 19 BP.
XX
AC   ADE27156;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:100.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 100; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1785 AGCCCAGGCTTTTGCTAGA 1803
              |||||||||::::||:|||
Db          1 AGCCCAGGCUUUUGCUAGA 19


RESULT 164
ADE27168
ID   ADE27168 standard; RNA; 19 BP.
XX
AC   ADE27168;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:112.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
```

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 112; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2001 CGGGGTAAAAAGTGGCTGC 2019
||||:||||||:|||:||
Db 1 CGGGGUAAAAAGUGGCUGC 19

RESULT 165
ADE27178
ID ADE27178 standard; RNA; 19 BP.
XX
AC ADE27178;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:122.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 122; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 2181 GTCTTGAAGTTGGGTGTTT 2199
|:|::||||::|||:|:::
Db 1 GUCUUGAAGUUGGGUGUUU 19

RESULT 166
ADE27190
ID ADE27190 standard; RNA; 19 BP.
XX
AC ADE27190;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:134.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

XX
PS Example 3; SEQ ID NO 134; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 2 C; 1 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2397 TATATACATATATACATTG 2415
:|:|:|||:|:|:|||::|
Db 1 UAUAUACAUAUAUACAUUG 19

RESULT 167
ADE27196
ID ADE27196 standard; RNA; 19 BP.
XX
AC ADE27196;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:140.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 140; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 8 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 2505 CAATTTCCTCTCCACTGCT 2523
|||:::||:|:||||:||:
Db 1 CAAUUUCCUCUCCACUGCU 19

RESULT 168
ADE27200
ID ADE27200 standard; RNA; 19 BP.
XX
AC ADE27200;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:144.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 144; 139pp; English.

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 3 C; 6 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2577 GAACTTCACATAGGAAGGG 2595
              ||||::||||:||||||||
Db          1 GAACUUCACAUAGGAAGGG 19


RESULT 169
ADE27207
ID   ADE27207 standard; RNA; 19 BP.
XX
AC   ADE27207;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:151.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 151; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2703 CTCCTTGAAATGAGTAAAA 2721
              |:||::||||:|||:||||
Db          1 CUCCUUGAAAUGAGUAAAA 19


RESULT 170
ADE27219
ID   ADE27219 standard; RNA; 19 BP.
XX
AC   ADE27219;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:163.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 163; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
```

```
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 6 C; 1 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2919 AACGTTTTCTTCTTTCCCT 2937
              ||||::::|::|:::|||:
Db          1 AACGUUUUCUUCUUUCCCU 19


RESULT 171
ADE27234
ID   ADE27234 standard; RNA; 19 BP.
XX
AC   ADE27234;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:178.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 178; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 9 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3189 CCCTCCCTCTCTCATGAGG 3207
              |||:|||:|:|:||:||||
Db          1 CCCUCCCUCUCUCAUGAGG 19


RESULT 172
ADE27241
ID   ADE27241 standard; RNA; 19 BP.
XX
AC   ADE27241;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:185.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 185; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
```

```
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 7 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 TGCCCCCTGCTTACTTGGT 3333
              :||||||:||::||::||:
Db          1 UGCCCCCUGCUUACUUGGU 19


RESULT 173
ADE27269
ID   ADE27269 standard; RNA; 19 BP.
XX
AC   ADE27269;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:213.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 213; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 4 C; 3 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3819 CTTGTCTTTTGAGCTATTC 3837
              |::|:|::::||||:|::|
Db          1 CUUGUCUUUUGAGCUAUUC 19


RESULT 174
ADE27274
ID   ADE27274 standard; RNA; 19 BP.
XX
AC   ADE27274;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:218.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 218; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
```

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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 15:35:28 ; Search time 35 Seconds
(without alignments)
3.669 Million cell updates/sec

Title: US-10-619-253-3
Perfect score: 4324
Sequence: 1 gtactacaaacctggcttgc.....aataaaagtgaagtgaatct 4324

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 782 seqs, 14851 residues

Total number of hits satisfying chosen parameters: 1564

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 895 summaries

Database : rnpb.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	0.7	30	1	US-10-236-417-228	Sequence 228, App
	2	25	0.6	25	1	US-11-036-317-535842	Sequence 535842,
	3	25	0.6	25	1	US-11-036-317-537139	Sequence 537139,
	4	25	0.6	25	1	US-11-036-317-573632	Sequence 573632,
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	6	25	0.6	25	1	US-11-036-317-727767	Sequence 727767,
	7	24	0.6	24	1	US-10-758-783-3	Sequence 3, Appli
	8	23.8	0.6	27	1	US-10-038-854-327	Sequence 327, App
	9	23.8	0.6	27	1	US-10-038-854-330	Sequence 330, App
	10	23.8	0.6	27	1	US-10-708-204-4431	Sequence 4431, Ap
	11	23.4	0.5	25	1	US-11-036-317-535843	Sequence 535843,
	12	23.4	0.5	25	1	US-11-036-317-537138	Sequence 537138,
	13	23.4	0.5	25	1	US-11-036-317-573633	Sequence 573633,
	14	23.4	0.5	25	1	US-11-036-317-659531	Sequence 659531,
	15	23.4	0.5	25	1	US-11-036-317-727766	Sequence 727766,
	16	23	0.5	23	1	US-10-377-133-14	Sequence 14, Appl
	17	23	0.5	23	1	US-10-377-133-15	Sequence 15, Appl
	18	22	0.5	22	1	US-10-236-417-227	Sequence 227, App
	19	21.8	0.5	25	1	US-10-719-900-766668	Sequence 766668,
	20	21.8	0.5	25	1	US-10-719-900-766669	Sequence 766669,
	21	21.8	0.5	25	1	US-11-060-756-177454	Sequence 177454,
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	24	20.8	0.5	25	1	US-10-719-900-927417	Sequence 927417,
	25	20.8	0.5	25	1	US-11-060-756-141375	Sequence 141375,
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	29	20.2	0.5	21	1	US-10-377-133-23	Sequence 23, Appl
c	30	20.2	0.5	21	1	US-10-377-133-24	Sequence 24, Appl
	31	20.2	0.5	25	1	US-10-719-900-54411	Sequence 54411, A
	32	20.2	0.5	25	1	US-10-719-900-143534	Sequence 143534,
	33	20.2	0.5	25	1	US-10-719-900-352484	Sequence 352484,
	34	20.2	0.5	25	1	US-10-956-157-64768	Sequence 64768, A
	35	20.2	0.5	25	1	US-10-956-157-265721	Sequence 265721,
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c	38	20.2	0.5	25	1	US-10-719-956-160951	Sequence 160951,
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	40	20.2	0.5	25	1	US-11-036-317-723353	Sequence 723353,
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c 209	20	0.5	20	1	US-10-619-253-105	Sequence 105, App
c 210	20	0.5	20	1	US-10-619-253-106	Sequence 106, App
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c 222	20	0.5	20	1	US-10-619-253-118	Sequence 118, App
c 223	20	0.5	20	1	US-10-619-253-119	Sequence 119, App
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c 258	20	0.5	20	1	US-10-619-253-154	Sequence 154, App
c 259	20	0.5	20	1	US-10-619-253-155	Sequence 155, App
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c 261	20	0.5	20	1	US-10-619-253-157	Sequence 157, App
c 262	20	0.5	20	1	US-10-619-253-158	Sequence 158, App
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c 268	20	0.5	20	1	US-10-619-253-164	Sequence 164, App
c 269	20	0.5	20	1	US-10-619-253-165	Sequence 165, App
c 270	20	0.5	20	1	US-10-619-253-166	Sequence 166, App
c 271	20	0.5	20	1	US-10-619-253-167	Sequence 167, App
c 272	20	0.5	20	1	US-10-619-253-168	Sequence 168, App
c 273	20	0.5	20	1	US-10-619-253-169	Sequence 169, App
c 274	20	0.5	20	1	US-10-619-253-170	Sequence 170, App
c 275	20	0.5	20	1	US-10-619-253-171	Sequence 171, App
c 276	20	0.5	20	1	US-10-619-253-172	Sequence 172, App
c 277	20	0.5	20	1	US-10-619-253-173	Sequence 173, App
c 278	20	0.5	20	1	US-10-619-253-174	Sequence 174, App
c 279	20	0.5	20	1	US-10-619-253-175	Sequence 175, App
c 280	20	0.5	20	1	US-10-619-253-176	Sequence 176, App
c 281	20	0.5	20	1	US-10-619-253-177	Sequence 177, App
c 282	20	0.5	20	1	US-10-619-253-178	Sequence 178, App
c 283	20	0.5	20	1	US-10-619-253-179	Sequence 179, App
c 284	20	0.5	20	1	US-10-619-253-180	Sequence 180, App
c 285	20	0.5	20	1	US-10-619-253-181	Sequence 181, App
c 286	20	0.5	20	1	US-10-619-253-182	Sequence 182, App
c 287	20	0.5	20	1	US-10-619-253-183	Sequence 183, App
c 288	20	0.5	20	1	US-10-619-253-184	Sequence 184, App
c 289	20	0.5	20	1	US-10-619-253-185	Sequence 185, App
c 290	20	0.5	20	1	US-10-619-253-186	Sequence 186, App
c 291	20	0.5	20	1	US-10-619-253-187	Sequence 187, App
c 292	20	0.5	20	1	US-10-619-253-188	Sequence 188, App
c 293	20	0.5	20	1	US-10-619-253-189	Sequence 189, App
c 294	20	0.5	20	1	US-10-619-253-190	Sequence 190, App
c 295	20	0.5	20	1	US-10-619-253-191	Sequence 191, App
c 296	20	0.5	20	1	US-10-619-253-192	Sequence 192, App
c 297	20	0.5	20	1	US-10-619-253-193	Sequence 193, App
c 298	20	0.5	20	1	US-10-619-253-194	Sequence 194, App
c 299	20	0.5	20	1	US-10-619-253-195	Sequence 195, App
c 300	20	0.5	20	1	US-10-619-253-196	Sequence 196, App
c 301	20	0.5	20	1	US-10-619-253-197	Sequence 197, App
c 302	20	0.5	20	1	US-10-619-253-251	Sequence 251, App
c 303	20	0.5	20	1	US-10-619-253-252	Sequence 252, App
c 304	20	0.5	20	1	US-10-619-253-383	Sequence 383, App
c 305	20	0.5	20	1	US-10-619-253-384	Sequence 384, App
c 306	20	0.5	20	1	US-10-619-253-389	Sequence 389, App
c 307	20	0.5	20	1	US-10-619-253-392	Sequence 392, App
c 308	20	0.5	20	1	US-10-619-253-393	Sequence 393, App
c 309	20	0.5	20	1	US-10-619-253-394	Sequence 394, App
c 310	20	0.5	20	1	US-10-619-253-395	Sequence 395, App
c 311	20	0.5	20	1	US-10-619-253-396	Sequence 396, App
c 312	20	0.5	20	1	US-10-619-253-397	Sequence 397, App
c 313	19.4	0.4	21	1	US-10-349-143-11421	Sequence 11421, A
c 314	19	0.4	20	1	US-10-619-253-391	Sequence 391, App
c 315	18.8	0.4	22	1	US-10-708-204-928	Sequence 928, App
c 316	18.8	0.4	22	1	US-10-708-204-1661	Sequence 1661, Ap
c 317	18.8	0.4	22	1	US-10-708-204-2379	Sequence 2379, Ap
c 318	18.4	0.4	20	1	US-10-619-253-249	Sequence 249, App
c 319	18.4	0.4	20	1	US-10-619-253-390	Sequence 390, App
c 320	18.4	0.4	20	1	US-10-619-253-398	Sequence 398, App
c 321	18.4	0.4	21	1	US-10-108-732-42	Sequence 42, Appl
c 322	18	0.4	22	1	US-10-270-839-75	Sequence 75, Appl
323	17.8	0.4	22	1	US-09-776-479-908	Sequence 908, App
324	17.8	0.4	22	1	US-09-776-479-908	Sequence 908, App
325	17.8	0.4	22	1	US-10-112-653-877	Sequence 877, App
326	17.8	0.4	22	1	US-10-017-995-908	Sequence 908, App
327	17.8	0.4	22	1	US-10-314-578-908	Sequence 908, App
c 328	17.8	0.4	22	1	US-10-766-590-4	Sequence 4, Appli
329	17.8	0.4	22	1	US-10-831-778-908	Sequence 908, App
c 330	17.4	0.4	19	1	US-10-893-010-239	Sequence 239, App
331	17.4	0.4	19	1	US-10-893-010-478	Sequence 478, App
c 332	17.4	0.4	20	1	US-09-263-959-849	Sequence 849, App
333	17.4	0.4	20	1	US-10-006-191-136	Sequence 136, App
334	17.4	0.4	20	1	US-10-160-807-80	Sequence 80, Appl
c 335	17.4	0.4	20	1	US-10-160-807-225	Sequence 225, App
336	17.4	0.4	20	1	US-10-655-847-80	Sequence 80, Appl
c 337	17.4	0.4	20	1	US-10-655-847-225	Sequence 225, App
c 338	17.4	0.4	20	1	US-10-619-253-250	Sequence 250, App
c 339	17.4	0.4	20	1	US-10-619-253-340	Sequence 340, App
c 340	17.4	0.4	20	1	US-10-619-253-385	Sequence 385, App
341	17.4	0.4	20	1	US-10-946-914-136	Sequence 136, App
c 342	17.4	0.4	21	1	US-10-957-432-758	Sequence 758, App
343	17	0.4	17	1	US-09-788-362-3	Sequence 3, Appli
344	17	0.4	17	1	US-09-090-672B-106	Sequence 106, App
345	17	0.4	17	1	US-09-788-338-3	Sequence 3, Appli
346	17	0.4	17	1	US-09-730-559B-108	Sequence 108, App
347	17	0.4	17	1	US-10-220-373-9	Sequence 9, Appli
348	17	0.4	17	1	US-10-339-793-185	Sequence 185, App
349	17	0.4	17	1	US-10-291-808-64	Sequence 64, Appl
350	17	0.4	17	1	US-10-380-255-8	Sequence 8, Appli
351	17	0.4	17	1	US-10-380-254-5	Sequence 5, Appli
352	17	0.4	17	1	US-10-398-885A-4	Sequence 4, Appli
353	17	0.4	17	1	US-10-398-877-20	Sequence 20, Appl
354	17	0.4	17	1	US-10-239-734-5	Sequence 5, Appli
355	17	0.4	17	1	US-10-608-863-5	Sequence 5, Appli
356	17	0.4	20	1	US-09-005-243-32	Sequence 32, Appl
357	17	0.4	20	1	US-09-224-683-32	Sequence 32, Appl
c 358	17	0.4	20	1	US-10-164-915-1	Sequence 1, Appli
c 359	17	0.4	20	1	US-10-374-686-2	Sequence 2, Appli
360	17	0.4	20	1	US-10-671-395-558	Sequence 558, App
361	17	0.4	20	1	US-10-671-395-616	Sequence 616, App
362	17	0.4	20	1	US-10-671-395-654	Sequence 654, App
363	17	0.4	20	1	US-10-671-395-990	Sequence 990, App
364	17	0.4	20	1	US-10-175-608-32	Sequence 32, Appl
365	17	0.4	20	1	US-10-620-642-32	Sequence 32, Appl
c 366	17	0.4	21	1	US-10-374-686-3	Sequence 3, Appli
c 367	16.8	0.4	20	1	US-09-725-265-31	Sequence 31, Appl
368	16.8	0.4	20	1	US-09-752-639-40	Sequence 40, Appl
c 369	16.8	0.4	20	1	US-09-891-517-31	Sequence 31, Appl
370	16.8	0.4	20	1	US-09-891-517-42	Sequence 42, Appl
371	16.8	0.4	20	1	US-09-984-198-40	Sequence 40, Appl
c 372	16.8	0.4	20	1	US-09-909-595-56	Sequence 56, Appl
c 373	16.8	0.4	20	1	US-10-077-383-29	Sequence 29, Appl
c 374	16.8	0.4	20	1	US-10-209-608-31	Sequence 31, Appl
375	16.8	0.4	20	1	US-10-301-844-26	Sequence 26, Appl
c 376	16.8	0.4	20	1	US-10-301-844-26	Sequence 26, Appl
c 377	16.8	0.4	20	1	US-10-683-386-31	Sequence 31, Appl
378	16.8	0.4	20	1	US-10-671-395-707	Sequence 707, App
379	16.8	0.4	20	1	US-10-728-399-87	Sequence 87, Appl
380	16.8	0.4	20	1	US-10-728-399-141	Sequence 141, App
381	16.8	0.4	20	1	US-10-728-399-199	Sequence 199, App
382	16.8	0.4	20	1	US-10-728-399-273	Sequence 273, App
c 383	16.8	0.4	20	1	US-10-661-088-17	Sequence 17, Appl
384	16.8	0.4	20	1	US-10-661-088-18	Sequence 18, Appl
c 385	16.8	0.4	20	1	US-10-661-097-17	Sequence 17, Appl
386	16.8	0.4	20	1	US-10-661-097-18	Sequence 18, Appl
c 387	16.8	0.4	20	1	US-10-661-355-17	Sequence 17, Appl
388	16.8	0.4	20	1	US-10-661-355-18	Sequence 18, Appl
c 389	16.8	0.4	20	1	US-10-661-099-17	Sequence 17, Appl
390	16.8	0.4	20	1	US-10-661-099-18	Sequence 18, Appl
391	16.8	0.4	20	1	US-10-476-962-56	Sequence 56, Appl
392	16.8	0.4	20	1	US-10-741-853A-6	Sequence 6, Appli
c 393	16.8	0.4	20	1	US-10-661-415-17	Sequence 17, Appl
394	16.8	0.4	20	1	US-10-661-415-18	Sequence 18, Appl
c 395	16.8	0.4	20	1	US-10-484-007-56	Sequence 56, Appl
396	16.8	0.4	20	1	US-10-646-270-2	Sequence 2, Appli
c 397	16.8	0.4	20	1	US-10-619-253-242	Sequence 242, App
c 398	16.8	0.4	20	1	US-10-619-253-245	Sequence 245, App

c 399	16.8	0.4	20	1	US-10-619-253-400	Sequence 400, App
c 400	16.8	0.4	20	1	US-10-643-801-113	Sequence 113, App
401	16.8	0.4	20	1	US-10-967-092-40	Sequence 40, Appl
c 402	16.8	0.4	20	1	US-10-661-402-17	Sequence 17, Appl
403	16.8	0.4	20	1	US-10-661-402-18	Sequence 18, Appl
c 404	16.8	0.4	20	1	US-10-661-403-17	Sequence 17, Appl
405	16.8	0.4	20	1	US-10-661-403-18	Sequence 18, Appl
c 406	16.8	0.4	20	1	US-10-969-812A-16	Sequence 16, Appl
407	16.8	0.4	20	1	US-10-969-812A-17	Sequence 17, Appl
408	16.8	0.4	20	1	US-11-011-500-40	Sequence 40, Appl
409	16.8	0.4	20	1	US-11-012-047-40	Sequence 40, Appl
410	16.8	0.4	21	1	US-09-263-959-807	Sequence 807, App
c 411	16.8	0.4	21	1	US-09-263-959-1158	Sequence 1158, Ap
c 412	16.8	0.4	21	1	US-10-270-839-76	Sequence 76, Appl
c 413	16.8	0.4	21	1	US-10-606-133-127	Sequence 127, App
414	16.8	0.4	21	1	US-10-751-736-19427	Sequence 19427, A
c 415	16.8	0.4	21	1	US-10-751-736-33961	Sequence 33961, A
c 416	16.8	0.4	21	1	US-10-847-918-9238	Sequence 9238, Ap
c 417	16.8	0.4	21	1	US-10-847-918-9239	Sequence 9239, Ap
418	16.8	0.4	21	1	US-10-847-918-9240	Sequence 9240, Ap
419	16.4	0.4	18	1	US-09-725-265-16	Sequence 16, Appl
420	16.4	0.4	18	1	US-09-891-517-16	Sequence 16, Appl
c 421	16.4	0.4	18	1	US-09-775-479-8	Sequence 8, Appli
422	16.4	0.4	18	1	US-10-209-608-16	Sequence 16, Appl
423	16.4	0.4	18	1	US-10-683-386-16	Sequence 16, Appl
c 424	16.4	0.4	19	1	US-10-863-973-877	Sequence 877, App
425	16.4	0.4	19	1	US-10-863-973-1100	Sequence 1100, Ap
c 426	16.4	0.4	19	1	US-10-922-675-877	Sequence 877, App
427	16.4	0.4	19	1	US-10-922-675-1100	Sequence 1100, Ap
c 428	16.4	0.4	19	1	US-11-014-373-192	Sequence 192, App
429	16.4	0.4	19	1	US-11-014-373-469	Sequence 469, App
c 430	16.4	0.4	20	1	US-10-002-491-55	Sequence 55, Appl
c 431	16.4	0.4	20	1	US-10-257-158A-7871	Sequence 7871, Ap
c 432	16	0.4	16	1	US-09-263-959-544	Sequence 544, App
433	16	0.4	17	1	US-09-090-672B-105	Sequence 105, App
434	16	0.4	17	1	US-09-090-672B-107	Sequence 107, App
435	16	0.4	17	1	US-09-730-559B-107	Sequence 107, App
436	16	0.4	17	1	US-09-730-559B-109	Sequence 109, App
437	16	0.4	17	1	US-10-309-152A-3	Sequence 3, Appli
438	16	0.4	17	1	US-10-220-373-7	Sequence 7, Appli
439	16	0.4	17	1	US-10-220-373-8	Sequence 8, Appli
440	16	0.4	17	1	US-10-408-025-5	Sequence 5, Appli
441	16	0.4	17	1	US-10-380-255-6	Sequence 6, Appli
442	16	0.4	17	1	US-10-380-255-7	Sequence 7, Appli
443	16	0.4	17	1	US-10-380-254-3	Sequence 3, Appli
444	16	0.4	17	1	US-10-380-254-4	Sequence 4, Appli
445	16	0.4	17	1	US-10-398-885A-2	Sequence 2, Appli
446	16	0.4	17	1	US-10-398-885A-3	Sequence 3, Appli
447	16	0.4	17	1	US-10-398-877-18	Sequence 18, Appl
448	16	0.4	17	1	US-10-398-877-19	Sequence 19, Appl
449	16	0.4	17	1	US-10-239-734-3	Sequence 3, Appli
450	16	0.4	17	1	US-10-239-734-4	Sequence 4, Appli
451	16	0.4	17	1	US-10-735-592-12	Sequence 12, Appl
452	16	0.4	17	1	US-10-608-863-3	Sequence 3, Appli
453	16	0.4	17	1	US-10-608-863-4	Sequence 4, Appli
454	16	0.4	18	1	US-09-904-744-2	Sequence 2, Appli
455	16	0.4	18	1	US-09-994-311-5	Sequence 5, Appli
456	16	0.4	18	1	US-09-994-311-6	Sequence 6, Appli
457	16	0.4	18	1	US-10-872-984-5	Sequence 5, Appli
458	16	0.4	18	1	US-10-872-984-6	Sequence 6, Appli
459	16	0.4	18	1	US-10-669-962-29	Sequence 29, Appl
c 460	16	0.4	19	1	US-10-205-309-325	Sequence 325, App
461	16	0.4	19	1	US-10-205-309-650	Sequence 650, App
c 462	16	0.4	19	1	US-10-670-011-18	Sequence 18, Appl
463	16	0.4	19	1	US-10-670-011-114	Sequence 114, App
c 464	16	0.4	19	1	US-10-764-957-18	Sequence 18, Appl
465	16	0.4	19	1	US-10-764-957-114	Sequence 114, App
c 466	16	0.4	19	1	US-10-871-222-404	Sequence 404, App
467	16	0.4	19	1	US-10-871-222-508	Sequence 508, App
c 468	16	0.4	19	1	US-10-962-898-2014	Sequence 2014, Ap
469	16	0.4	19	1	US-10-962-898-2110	Sequence 2110, Ap
c 470	16	0.4	20	1	US-09-953-047-91	Sequence 91, Appl
471	16	0.4	20	1	US-10-181-177-55	Sequence 55, Appl
c 472	16	0.4	20	1	US-10-630-401-91	Sequence 91, Appl
473	16	0.4	20	1	US-10-275-080A-5	Sequence 5, Appli
474	16	0.4	20	1	US-10-275-080A-6	Sequence 6, Appli
475	16	0.4	20	1	US-10-671-395-433	Sequence 433, App
476	16	0.4	20	1	US-10-671-395-938	Sequence 938, App
c 477	16	0.4	20	1	US-10-728-078-14	Sequence 14, Appl
478	16	0.4	20	1	US-10-644-052A-376	Sequence 376, App
479	16	0.4	20	1	US-10-644-052A-377	Sequence 377, App
480	16	0.4	20	1	US-10-831-901A-29727	Sequence 29727, A
481	16	0.4	20	1	US-10-831-901A-29728	Sequence 29728, A
482	16	0.4	20	1	US-10-831-901A-29729	Sequence 29729, A
483	16	0.4	20	1	US-10-831-901A-29730	Sequence 29730, A
484	16	0.4	20	1	US-10-831-901A-29731	Sequence 29731, A
485	15.8	0.4	19	1	US-09-969-373-4453	Sequence 4453, Ap
486	15.8	0.4	19	1	US-09-263-959-643	Sequence 643, App
c 487	15.8	0.4	19	1	US-09-263-959-761	Sequence 761, App
488	15.8	0.4	19	1	US-09-263-959-836	Sequence 836, App
c 489	15.8	0.4	19	1	US-10-272-552-2	Sequence 2, Appli
c 490	15.8	0.4	19	1	US-10-291-342-2	Sequence 2, Appli
491	15.8	0.4	19	1	US-10-665-951-390	Sequence 390, App
c 492	15.8	0.4	19	1	US-10-665-951-817	Sequence 817, App
493	15.8	0.4	19	1	US-10-683-990-97	Sequence 97, Appl
c 494	15.8	0.4	19	1	US-10-683-990-194	Sequence 194, App
c 495	15.8	0.4	19	1	US-10-826-573-4	Sequence 4, Appli
496	15.8	0.4	19	1	US-10-758-155-390	Sequence 390, App
c 497	15.8	0.4	19	1	US-10-758-155-817	Sequence 817, App
498	15.8	0.4	19	1	US-10-831-620-390	Sequence 390, App
c 499	15.8	0.4	19	1	US-10-831-620-817	Sequence 817, App
500	15.8	0.4	19	1	US-10-844-076-390	Sequence 390, App
c 501	15.8	0.4	19	1	US-10-844-076-817	Sequence 817, App
c 502	15.8	0.4	19	1	US-10-877-889-723	Sequence 723, App
503	15.8	0.4	19	1	US-10-877-889-1048	Sequence 1048, Ap
504	15.8	0.4	19	1	US-10-962-898-390	Sequence 390, App
c 505	15.8	0.4	19	1	US-10-962-898-817	Sequence 817, App
506	15.6	0.4	17	1	US-10-146-474-17	Sequence 17, Appl
507	15.6	0.4	17	1	US-10-301-764-17	Sequence 17, Appl
508	15.4	0.4	17	1	US-10-238-700-1260	Sequence 1260, Ap
509	15.4	0.4	17	1	US-10-138-674-1073	Sequence 1073, Ap
c 510	15.4	0.4	17	1	US-10-138-674-7622	Sequence 7622, Ap
511	15.4	0.4	17	1	US-10-287-949A-1073	Sequence 1073, Ap
c 512	15.4	0.4	17	1	US-10-287-949A-7622	Sequence 7622, Ap
513	15.4	0.4	17	1	US-10-735-592-11	Sequence 11, Appl
514	15.4	0.4	17	1	US-10-735-592-14	Sequence 14, Appl
c 515	15.4	0.4	17	1	US-10-712-633-664	Sequence 664, App
516	15.4	0.4	17	1	US-10-724-270-1260	Sequence 1260, Ap
517	15.4	0.4	17	1	US-10-951-303-1073	Sequence 1073, Ap
518	15.4	0.4	18	1	US-09-725-265-17	Sequence 17, Appl
519	15.4	0.4	18	1	US-09-725-265-20	Sequence 20, Appl
520	15.4	0.4	18	1	US-09-891-517-17	Sequence 17, Appl
521	15.4	0.4	18	1	US-09-891-517-20	Sequence 20, Appl
522	15.4	0.4	18	1	US-09-888-326-85	Sequence 85, Appl
c 523	15.4	0.4	18	1	US-09-888-326-85	Sequence 85, Appl
524	15.4	0.4	18	1	US-09-823-887C-5	Sequence 5, Appli
525	15.4	0.4	18	1	US-09-823-887C-6	Sequence 6, Appli
526	15.4	0.4	18	1	US-09-823-887C-7	Sequence 7, Appli
527	15.4	0.4	18	1	US-10-209-608-17	Sequence 17, Appl
528	15.4	0.4	18	1	US-10-209-608-20	Sequence 20, Appl
c 529	15.4	0.4	18	1	US-10-272-970-18	Sequence 18, Appl
530	15.4	0.4	18	1	US-10-106-799-1	Sequence 1, Appli
531	15.4	0.4	18	1	US-10-106-799-2	Sequence 2, Appli
532	15.4	0.4	18	1	US-10-106-799-3	Sequence 3, Appli
533	15.4	0.4	18	1	US-10-333-461-18	Sequence 18, Appl
534	15.4	0.4	18	1	US-10-352-253A-18	Sequence 18, Appl
535	15.4	0.4	18	1	US-10-109-363-16	Sequence 16, Appl
536	15.4	0.4	18	1	US-10-109-363-17	Sequence 17, Appl
537	15.4	0.4	18	1	US-10-109-363-18	Sequence 18, Appl
538	15.4	0.4	18	1	US-10-352-255A-18	Sequence 18, Appl
c 539	15.4	0.4	18	1	US-10-297-068-878	Sequence 878, App
c 540	15.4	0.4	18	1	US-10-108-260A-5080	Sequence 5080, Ap
c 541	15.4	0.4	18	1	US-10-627-929-10	Sequence 10, Appl
542	15.4	0.4	18	1	US-10-683-386-17	Sequence 17, Appl
543	15.4	0.4	18	1	US-10-683-386-20	Sequence 20, Appl
c 544	15.4	0.4	19	1	US-09-917-138-2	Sequence 2, Appli

c 545	15.4	0.4	19	1	US-09-750-373-40	Sequence 40, Appl
c 546	15.4	0.4	19	1	US-09-923-327-224	Sequence 224, App
c 547	15.4	0.4	19	1	US-10-665-951-939	Sequence 939, App
548	15.4	0.4	19	1	US-10-665-951-1263	Sequence 1263, Ap
549	15.4	0.4	19	1	US-10-800-487-162	Sequence 162, App
c 550	15.4	0.4	19	1	US-10-800-487-328	Sequence 328, App
c 551	15.4	0.4	19	1	US-10-758-155-939	Sequence 939, App
552	15.4	0.4	19	1	US-10-758-155-1263	Sequence 1263, Ap
c 553	15.4	0.4	19	1	US-10-831-620-939	Sequence 939, App
554	15.4	0.4	19	1	US-10-831-620-1263	Sequence 1263, Ap
c 555	15.4	0.4	19	1	US-10-844-076-939	Sequence 939, App
556	15.4	0.4	19	1	US-10-844-076-1263	Sequence 1263, Ap
557	15.4	0.4	19	1	US-10-923-181-162	Sequence 162, App
c 558	15.4	0.4	19	1	US-10-923-181-328	Sequence 328, App
559	15.4	0.4	19	1	US-10-708-204-3039	Sequence 3039, Ap
c 560	15.4	0.4	19	1	US-10-962-898-939	Sequence 939, App
561	15.4	0.4	19	1	US-10-962-898-1263	Sequence 1263, Ap
562	15.2	0.4	17	1	US-10-015-593-2	Sequence 2, Appli
563	15.2	0.4	17	1	US-10-380-596A-5	Sequence 5, Appli
564	15.2	0.4	17	1	US-10-872-645-29	Sequence 29, Appl
565	15.2	0.4	18	1	US-09-981-397A-1	Sequence 1, Appli
566	15.2	0.4	19	1	US-09-371-307-85	Sequence 85, Appl
c 567	15.2	0.4	19	1	US-10-103-614A-4	Sequence 4, Appli
568	15.2	0.4	19	1	US-10-176-884-44	Sequence 44, Appl
569	15.2	0.4	19	1	US-10-177-478-1	Sequence 1, Appli
570	15.2	0.4	19	1	US-10-182-230-196	Sequence 196, App
571	15.2	0.4	19	1	US-10-401-321-85	Sequence 85, Appl
572	15.2	0.4	19	1	US-10-965-470-1	Sequence 1, Appli
573	15.2	0.4	19	1	US-10-950-095-73	Sequence 73, Appl
574	15.2	0.4	19	1	US-10-950-321-1	Sequence 1, Appli
575	15.2	0.4	19	1	US-11-051-456-44	Sequence 44, Appl
576	15	0.3	15	1	US-09-504-231A-22	Sequence 22, Appl
577	15	0.3	15	1	US-09-930-218-5	Sequence 5, Appli
578	15	0.3	15	1	US-09-274-553D-22	Sequence 22, Appl
579	15	0.3	15	1	US-09-776-874A-5	Sequence 5, Appli
580	15	0.3	15	1	US-09-955-410-17	Sequence 17, Appl
c 581	15	0.3	15	1	US-09-955-410-18	Sequence 18, Appl
c 582	15	0.3	15	1	US-09-263-959-543	Sequence 543, App
c 583	15	0.3	15	1	US-09-263-959-545	Sequence 545, App
584	15	0.3	15	1	US-09-805-296D-10	Sequence 10, Appl
585	15	0.3	15	1	US-09-983-210-19	Sequence 19, Appl
c 586	15	0.3	15	1	US-09-983-210-20	Sequence 20, Appl
587	15	0.3	15	1	US-09-850-982B-4	Sequence 4, Appli
588	15	0.3	15	1	US-09-988-113-5	Sequence 5, Appli
589	15	0.3	15	1	US-09-793-146-54	Sequence 54, Appl
590	15	0.3	15	1	US-09-793-146-55	Sequence 55, Appl
c 591	15	0.3	15	1	US-10-208-357-21	Sequence 21, Appl
c 592	15	0.3	15	1	US-10-176-055-9	Sequence 9, Appli
593	15	0.3	15	1	US-10-202-189-9	Sequence 9, Appli
594	15	0.3	15	1	US-10-072-975-10	Sequence 10, Appl
595	15	0.3	15	1	US-10-227-001-23	Sequence 23, Appl
596	15	0.3	15	1	US-10-341-582-5	Sequence 5, Appli
597	15	0.3	15	1	US-10-106-749-1	Sequence 1, Appli
598	15	0.3	15	1	US-10-106-749-5	Sequence 5, Appli
599	15	0.3	15	1	US-10-384-451-5	Sequence 5, Appli
600	15	0.3	15	1	US-10-269-031A-54	Sequence 54, Appl
601	15	0.3	15	1	US-10-352-704-10	Sequence 10, Appl
c 602	15	0.3	15	1	US-10-352-704-16	Sequence 16, Appl
603	15	0.3	15	1	US-10-154-890-17	Sequence 17, Appl
c 604	15	0.3	15	1	US-10-154-890-18	Sequence 18, Appl
605	15	0.3	15	1	US-10-431-438-5	Sequence 5, Appli
606	15	0.3	15	1	US-10-091-231-2	Sequence 2, Appli
607	15	0.3	15	1	US-10-384-450-5	Sequence 5, Appli
c 608	15	0.3	15	1	US-10-440-850-323	Sequence 323, App
609	15	0.3	15	1	US-10-371-218A-5	Sequence 5, Appli
610	15	0.3	15	1	US-10-291-808-68	Sequence 68, Appl
611	15	0.3	15	1	US-10-045-674-622	Sequence 622, App
612	15	0.3	15	1	US-10-456-573-5	Sequence 5, Appli
613	15	0.3	15	1	US-10-360-275-10	Sequence 10, Appl
614	15	0.3	15	1	US-10-637-935-9	Sequence 9, Appli
615	15	0.3	15	1	US-10-239-655A-4	Sequence 4, Appli
616	15	0.3	15	1	US-10-433-005-4	Sequence 4, Appli
617	15	0.3	15	1	US-10-344-092-2	Sequence 2, Appli
618	15	0.3	15	1	US-10-785-116-5	Sequence 5, Appli
619	15	0.3	15	1	US-10-737-059-2	Sequence 2, Appli
620	15	0.3	15	1	US-10-830-484-4	Sequence 4, Appli
621	15	0.3	15	1	US-10-755-118-3	Sequence 3, Appli
622	15	0.3	15	1	US-10-755-118-4	Sequence 4, Appli
623	15	0.3	15	1	US-10-755-118-31	Sequence 31, Appl
c 624	15	0.3	15	1	US-10-755-118-32	Sequence 32, Appl
625	15	0.3	15	1	US-10-755-118-36	Sequence 36, Appl
626	15	0.3	15	1	US-10-755-118-38	Sequence 38, Appl
627	15	0.3	15	1	US-10-755-118-39	Sequence 39, Appl
628	15	0.3	15	1	US-10-755-118-40	Sequence 40, Appl
629	15	0.3	15	1	US-10-755-118-43	Sequence 43, Appl
630	15	0.3	15	1	US-10-755-118-44	Sequence 44, Appl
631	15	0.3	15	1	US-10-755-118-45	Sequence 45, Appl
632	15	0.3	15	1	US-10-755-118-48	Sequence 48, Appl
633	15	0.3	15	1	US-10-755-118-49	Sequence 49, Appl
634	15	0.3	15	1	US-10-770-989-9	Sequence 9, Appli
635	15	0.3	15	1	US-10-833-502-9	Sequence 9, Appli
636	15	0.3	15	1	US-10-939-214-54	Sequence 54, Appl
637	15	0.3	15	1	US-10-939-214-55	Sequence 55, Appl
638	15	0.3	15	1	US-10-601-140A-5	Sequence 5, Appli
639	15	0.3	15	1	US-10-601-140A-16	Sequence 16, Appl
640	15	0.3	15	1	US-10-601-140A-19	Sequence 19, Appl
641	15	0.3	15	1	US-10-239-919A-4	Sequence 4, Appli
642	15	0.3	15	1	US-10-938-661A-22	Sequence 22, Appl
643	15	0.3	15	1	US-10-781-758-5	Sequence 5, Appli
644	15	0.3	15	1	US-10-824-175-3	Sequence 3, Appli
c 645	15	0.3	15	1	US-10-866-388A-9	Sequence 9, Appli
646	15	0.3	15	1	US-10-601-497B-469	Sequence 469, App
647	15	0.3	16	1	US-09-739-928-2	Sequence 2, Appli
648	15	0.3	16	1	US-09-739-928-3	Sequence 3, Appli
649	15	0.3	16	1	US-09-739-928-4	Sequence 4, Appli
650	15	0.3	16	1	US-09-739-928-5	Sequence 5, Appli
651	15	0.3	16	1	US-09-739-928-6	Sequence 6, Appli
652	15	0.3	16	1	US-09-739-928-7	Sequence 7, Appli
653	15	0.3	16	1	US-09-739-928-8	Sequence 8, Appli
654	15	0.3	16	1	US-09-152-059-70	Sequence 70, Appl
655	15	0.3	16	1	US-09-895-585-9	Sequence 9, Appli
656	15	0.3	16	1	US-09-805-296D-9	Sequence 9, Appli
c 657	15	0.3	16	1	US-09-843-676-131	Sequence 131, App
c 658	15	0.3	16	1	US-09-766-253-131	Sequence 131, App
c 659	15	0.3	16	1	US-09-438-486-131	Sequence 131, App
c 660	15	0.3	16	1	US-10-208-357-22	Sequence 22, Appl
c 661	15	0.3	16	1	US-10-053-758-131	Sequence 131, App
c 662	15	0.3	16	1	US-10-054-295-131	Sequence 131, App
c 663	15	0.3	16	1	US-10-054-611-131	Sequence 131, App
664	15	0.3	16	1	US-10-072-975-9	Sequence 9, Appli
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666	15	0.3	16	1	US-10-227-001-21	Sequence 21, Appl
667	15	0.3	16	1	US-10-008-029-70	Sequence 70, Appl
668	15	0.3	16	1	US-10-208-650-70	Sequence 70, Appl
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670	15	0.3	16	1	US-10-203-780-9	Sequence 9, Appli
671	15	0.3	16	1	US-10-360-275-9	Sequence 9, Appli
672	15	0.3	16	1	US-10-432-803-4	Sequence 4, Appli
673	15	0.3	16	1	US-10-776-099-9	Sequence 9, Appli
c 674	15	0.3	16	1	US-10-398-483-10	Sequence 10, Appl
675	15	0.3	16	1	US-10-755-118-94	Sequence 94, Appl
c 676	15	0.3	16	1	US-10-121-641D-1	Sequence 1, Appli
677	15	0.3	17	1	US-09-726-096A-5	Sequence 5, Appli
678	15	0.3	17	1	US-09-843-676-132	Sequence 132, App
679	15	0.3	17	1	US-09-766-253-132	Sequence 132, App
680	15	0.3	17	1	US-09-438-486-132	Sequence 132, App
c 681	15	0.3	17	1	US-10-208-357-23	Sequence 23, Appl
682	15	0.3	17	1	US-10-053-758-132	Sequence 132, App
683	15	0.3	17	1	US-10-054-295-132	Sequence 132, App
684	15	0.3	17	1	US-10-117-267-5	Sequence 5, Appli
685	15	0.3	17	1	US-10-054-611-132	Sequence 132, App
686	15	0.3	17	1	US-10-333-461-24	Sequence 24, Appl
687	15	0.3	17	1	US-10-352-253A-24	Sequence 24, Appl
688	15	0.3	17	1	US-10-352-255A-24	Sequence 24, Appl
689	15	0.3	17	1	US-10-291-808-63	Sequence 63, Appl
690	15	0.3	17	1	US-10-138-674-1074	Sequence 1074, Ap

	691	15	0.3	17	1	US-10-138-674-1075	Sequence 1075, Ap
	692	15	0.3	17	1	US-10-138-674-1076	Sequence 1076, Ap
c	693	15	0.3	17	1	US-10-138-674-2532	Sequence 2532, Ap
c	694	15	0.3	17	1	US-10-324-409B-16	Sequence 16, Appl
	695	15	0.3	17	1	US-10-287-949A-1074	Sequence 1074, Ap
	696	15	0.3	17	1	US-10-287-949A-1075	Sequence 1075, Ap
	697	15	0.3	17	1	US-10-287-949A-1076	Sequence 1076, Ap
c	698	15	0.3	17	1	US-10-287-949A-2532	Sequence 2532, Ap
	699	15	0.3	17	1	US-10-735-592-2	Sequence 2, Appli
	700	15	0.3	17	1	US-10-735-592-8	Sequence 8, Appli
	701	15	0.3	17	1	US-10-735-592-15	Sequence 15, Appl
	702	15	0.3	17	1	US-10-735-592-16	Sequence 16, Appl
	703	15	0.3	17	1	US-10-735-592-17	Sequence 17, Appl
	704	15	0.3	17	1	US-10-735-592-25	Sequence 25, Appl
	705	15	0.3	17	1	US-10-735-592-48	Sequence 48, Appl
	706	15	0.3	17	1	US-10-735-592-49	Sequence 49, Appl
	707	15	0.3	17	1	US-10-735-592-54	Sequence 54, Appl
	708	15	0.3	17	1	US-10-735-592-55	Sequence 55, Appl
	709	15	0.3	17	1	US-10-735-592-56	Sequence 56, Appl
	710	15	0.3	17	1	US-10-477-173-865	Sequence 865, App
	711	15	0.3	17	1	US-10-951-549-3	Sequence 3, Appli
	712	15	0.3	17	1	US-10-951-303-1074	Sequence 1074, Ap
	713	15	0.3	17	1	US-10-951-303-1075	Sequence 1075, Ap
	714	15	0.3	17	1	US-10-951-303-1076	Sequence 1076, Ap
c	715	15	0.3	17	1	US-10-951-303-2532	Sequence 2532, Ap
	716	15	0.3	18	1	US-09-809-545A-84	Sequence 84, Appl
c	717	15	0.3	18	1	US-09-904-744-1	Sequence 1, Appli
	718	15	0.3	18	1	US-09-888-326-837	Sequence 837, App
	719	15	0.3	18	1	US-09-994-311-7	Sequence 7, Appli
	720	15	0.3	18	1	US-09-776-479-913	Sequence 913, App
	721	15	0.3	18	1	US-09-776-479-913	Sequence 913, App
	722	15	0.3	18	1	US-09-776-479-939	Sequence 939, App
	723	15	0.3	18	1	US-09-776-479-939	Sequence 939, App
	724	15	0.3	18	1	US-09-370-541-14	Sequence 14, Appl
	725	15	0.3	18	1	US-09-775-479-9	Sequence 9, Appli
	726	15	0.3	18	1	US-09-979-275A-7	Sequence 7, Appli
	727	15	0.3	18	1	US-10-125-295-9	Sequence 9, Appli
c	728	15	0.3	18	1	US-10-208-357-24	Sequence 24, Appl
	729	15	0.3	18	1	US-10-112-653-882	Sequence 882, App
	730	15	0.3	18	1	US-10-017-995-913	Sequence 913, App
	731	15	0.3	18	1	US-10-017-995-939	Sequence 939, App
	732	15	0.3	18	1	US-10-206-613-4	Sequence 4, Appli
	733	15	0.3	18	1	US-10-056-479A-15	Sequence 15, Appl
	734	15	0.3	18	1	US-10-352-704-12	Sequence 12, Appl
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	736	15	0.3	18	1	US-10-075-335-9	Sequence 9, Appli
	737	15	0.3	18	1	US-10-292-088-144	Sequence 144, App
	738	15	0.3	18	1	US-10-314-578-913	Sequence 913, App
	739	15	0.3	18	1	US-10-314-578-939	Sequence 939, App
	740	15	0.3	18	1	US-10-328-578-142	Sequence 142, App
	741	15	0.3	18	1	US-10-389-155-97	Sequence 97, Appl
c	742	15	0.3	18	1	US-10-271-602B-84	Sequence 84, Appl
	743	15	0.3	18	1	US-10-334-143-204	Sequence 204, App
	744	15	0.3	18	1	US-10-389-417-97	Sequence 97, Appl
	745	15	0.3	18	1	US-10-653-416-26	Sequence 26, Appl
	746	15	0.3	18	1	US-10-623-371-142	Sequence 142, App
	747	15	0.3	18	1	US-10-785-744-15	Sequence 15, Appl
	748	15	0.3	18	1	US-10-735-592-1	Sequence 1, Appli
c	749	15	0.3	18	1	US-10-628-525-30	Sequence 30, Appl
c	750	15	0.3	18	1	US-10-849-072-21	Sequence 21, Appl
	751	15	0.3	18	1	US-10-849-072-23	Sequence 23, Appl
	752	15	0.3	18	1	US-10-831-778-913	Sequence 913, App
	753	15	0.3	18	1	US-10-831-778-939	Sequence 939, App
	754	15	0.3	18	1	US-10-776-933-150	Sequence 150, App
	755	15	0.3	18	1	US-10-674-159A-112	Sequence 112, App
	756	15	0.3	18	1	US-10-776-917-141	Sequence 141, App
	757	15	0.3	18	1	US-10-766-096-9	Sequence 9, Appli
	758	15	0.3	18	1	US-10-872-984-7	Sequence 7, Appli
	759	15	0.3	18	1	US-10-638-141-10	Sequence 10, Appl
	760	15	0.3	18	1	US-10-776-934-741	Sequence 741, App
c	761	15	0.3	18	1	US-10-741-600-73428	Sequence 73428, A
	762	15	0.3	18	1	US-10-601-140A-24	Sequence 24, Appl
	763	15	0.3	18	1	US-10-884-617-2	Sequence 2, Appli
	764	15	0.3	18	1	US-10-669-962-27	Sequence 27, Appl
	765	15	0.3	18	1	US-10-669-962-28	Sequence 28, Appl
	766	15	0.3	18	1	US-10-503-120-1	Sequence 1, Appli
	767	15	0.3	18	1	US-10-503-120-8	Sequence 8, Appli
	768	15	0.3	18	1	US-10-503-120-9	Sequence 9, Appli
	769	15	0.3	18	1	US-10-503-120-10	Sequence 10, Appl
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	771	15	0.3	18	1	US-10-775-973-10	Sequence 10, Appl
	772	15	0.3	18	1	US-10-959-440-84	Sequence 84, Appl
	773	15	0.3	18	1	US-11-024-428-7	Sequence 7, Appli
	774	15	0.3	20	1	US-10-619-253-146	Sequence 146, App
c	775	14.8	0.3	18	1	US-09-263-959-515	Sequence 515, App
c	776	14.8	0.3	18	1	US-09-263-959-873	Sequence 873, App
	777	14.8	0.3	18	1	US-09-789-210-13	Sequence 13, Appl
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	779	14.8	0.3	18	1	US-10-011-204-4	Sequence 4, Appli
c	780	14.8	0.3	18	1	US-10-077-383-31	Sequence 31, Appl
	781	14.8	0.3	18	1	US-10-077-383-32	Sequence 32, Appl
c	782	14.8	0.3	18	1	US-10-746-547-107	Sequence 107, App
	783	14.8	0.3	18	1	US-10-473-126-650	Sequence 650, App
	784	14.8	0.3	18	1	US-10-473-126-826	Sequence 826, App
	785	14.8	0.3	18	1	US-10-473-126-1242	Sequence 1242, Ap
c	786	14.8	0.3	20	1	US-10-006-191-136	Sequence 136, App
c	787	14.8	0.3	20	1	US-10-946-914-136	Sequence 136, App
	788	14.8	0.3	20	1	US-09-953-047-91	Sequence 91, Appl
	789	14.8	0.3	20	1	US-10-630-401-91	Sequence 91, Appl
	790	14.8	0.3	25	1	US-10-719-956-160951	Sequence 160951,
c	791	14.2	0.3	19	1	US-09-263-959-836	Sequence 836, App
	792	14.2	0.3	19	1	US-09-917-138-2	Sequence 2, Appli
	793	14.2	0.3	20	1	US-09-725-265-31	Sequence 31, Appl
	794	14.2	0.3	20	1	US-09-891-517-31	Sequence 31, Appl
c	795	14.2	0.3	20	1	US-09-891-517-42	Sequence 42, Appl
	796	14.2	0.3	20	1	US-10-209-608-31	Sequence 31, Appl
	797	14.2	0.3	20	1	US-10-683-386-31	Sequence 31, Appl
c	798	13.8	0.3	17	1	US-10-138-674-1076	Sequence 1076, Ap
c	799	13.8	0.3	17	1	US-10-287-949A-1076	Sequence 1076, Ap
c	800	13.8	0.3	17	1	US-10-735-592-55	Sequence 55, Appl
c	801	13.8	0.3	17	1	US-10-951-303-1076	Sequence 1076, Ap
c	802	13.8	0.3	18	1	US-09-725-265-17	Sequence 17, Appl
c	803	13.8	0.3	18	1	US-09-891-517-17	Sequence 17, Appl
c	804	13.8	0.3	18	1	US-10-209-608-17	Sequence 17, Appl
c	805	13.8	0.3	18	1	US-10-683-386-17	Sequence 17, Appl
	806	13.8	0.3	18	1	US-09-904-744-1	Sequence 1, Appli
	807	13.8	0.3	20	1	US-09-918-187-27	Sequence 27, Appl
	808	13.8	0.3	20	1	US-10-484-442-27	Sequence 27, Appl
	809	13.8	0.3	20	1	US-10-619-253-27	Sequence 27, Appl
	810	13.6	0.3	20	1	US-10-467-008-110	Sequence 110, App
c	811	13.6	0.3	20	1	US-10-671-395-938	Sequence 938, App
c	812	13.4	0.3	17	1	US-10-735-592-17	Sequence 17, Appl
c	813	13.4	0.3	17	1	US-10-735-592-56	Sequence 56, Appl
c	814	13.4	0.3	19	1	US-09-371-307-85	Sequence 85, Appl
c	815	13.4	0.3	19	1	US-10-176-884-44	Sequence 44, Appl
c	816	13.4	0.3	19	1	US-10-177-478-1	Sequence 1, Appli
c	817	13.4	0.3	19	1	US-10-182-230-196	Sequence 196, App
c	818	13.4	0.3	19	1	US-10-401-321-85	Sequence 85, Appl
c	819	13.4	0.3	19	1	US-10-965-470-1	Sequence 1, Appli
c	820	13.4	0.3	19	1	US-10-950-095-73	Sequence 73, Appl
c	821	13.4	0.3	19	1	US-10-950-321-1	Sequence 1, Appli
c	822	13.4	0.3	19	1	US-11-051-456-44	Sequence 44, Appl
	823	13.2	0.3	18	1	US-09-775-479-8	Sequence 8, Appli
c	824	13.2	0.3	18	1	US-09-809-545A-84	Sequence 84, Appl
c	825	13.2	0.3	18	1	US-09-888-326-837	Sequence 837, App
c	826	13.2	0.3	18	1	US-09-994-311-7	Sequence 7, Appli
c	827	13.2	0.3	18	1	US-09-776-479-913	Sequence 913, App
c	828	13.2	0.3	18	1	US-09-776-479-913	Sequence 913, App
c	829	13.2	0.3	18	1	US-09-776-479-939	Sequence 939, App
c	830	13.2	0.3	18	1	US-09-776-479-939	Sequence 939, App
c	831	13.2	0.3	18	1	US-09-370-541-14	Sequence 14, Appl
c	832	13.2	0.3	18	1	US-09-979-275A-7	Sequence 7, Appli
c	833	13.2	0.3	18	1	US-10-125-295-9	Sequence 9, Appli
	834	13.2	0.3	18	1	US-10-208-357-24	Sequence 24, Appl
c	835	13.2	0.3	18	1	US-10-112-653-882	Sequence 882, App
c	836	13.2	0.3	18	1	US-10-017-995-913	Sequence 913, App

c 837	13.2	0.3	18	1	US-10-017-995-939	Sequence 939, App
c 838	13.2	0.3	18	1	US-10-206-613-4	Sequence 4, Appli
c 839	13.2	0.3	18	1	US-10-056-479A-15	Sequence 15, Appl
c 840	13.2	0.3	18	1	US-10-352-704-12	Sequence 12, Appl
841	13.2	0.3	18	1	US-10-352-704-18	Sequence 18, Appl
c 842	13.2	0.3	18	1	US-10-075-335-9	Sequence 9, Appli
c 843	13.2	0.3	18	1	US-10-292-088-144	Sequence 144, App
c 844	13.2	0.3	18	1	US-10-314-578-913	Sequence 913, App
c 845	13.2	0.3	18	1	US-10-314-578-939	Sequence 939, App
c 846	13.2	0.3	18	1	US-10-389-155-97	Sequence 97, Appl
847	13.2	0.3	18	1	US-10-271-602B-84	Sequence 84, Appl
c 848	13.2	0.3	18	1	US-10-334-143-204	Sequence 204, App
c 849	13.2	0.3	18	1	US-10-389-417-97	Sequence 97, Appl
c 850	13.2	0.3	18	1	US-10-653-416-26	Sequence 26, Appl
c 851	13.2	0.3	18	1	US-10-785-744-15	Sequence 15, Appl
c 852	13.2	0.3	18	1	US-10-735-592-1	Sequence 1, Appli
853	13.2	0.3	18	1	US-10-628-525-30	Sequence 30, Appl
854	13.2	0.3	18	1	US-10-849-072-21	Sequence 21, Appl
c 855	13.2	0.3	18	1	US-10-849-072-23	Sequence 23, Appl
c 856	13.2	0.3	18	1	US-10-831-778-913	Sequence 913, App
c 857	13.2	0.3	18	1	US-10-831-778-939	Sequence 939, App
c 858	13.2	0.3	18	1	US-10-776-933-150	Sequence 150, App
c 859	13.2	0.3	18	1	US-10-674-159A-112	Sequence 112, App
c 860	13.2	0.3	18	1	US-10-776-917-141	Sequence 141, App
c 861	13.2	0.3	18	1	US-10-766-096-9	Sequence 9, Appli
c 862	13.2	0.3	18	1	US-10-872-984-7	Sequence 7, Appli
c 863	13.2	0.3	18	1	US-10-638-141-10	Sequence 10, Appl
c 864	13.2	0.3	18	1	US-10-776-934-741	Sequence 741, App
c 865	13.2	0.3	18	1	US-10-601-140A-24	Sequence 24, Appl
c 866	13.2	0.3	18	1	US-10-884-617-2	Sequence 2, Appli
c 867	13.2	0.3	18	1	US-10-669-962-28	Sequence 28, Appl
c 868	13.2	0.3	18	1	US-10-503-120-1	Sequence 1, Appli
c 869	13.2	0.3	18	1	US-10-503-120-8	Sequence 8, Appli
c 870	13.2	0.3	18	1	US-10-503-120-9	Sequence 9, Appli
c 871	13.2	0.3	18	1	US-10-503-120-10	Sequence 10, Appl
872	13.2	0.3	18	1	US-10-503-120-21	Sequence 21, Appl
c 873	13.2	0.3	18	1	US-10-775-973-10	Sequence 10, Appl
c 874	13.2	0.3	18	1	US-10-959-440-84	Sequence 84, Appl
c 875	13.2	0.3	18	1	US-11-024-428-7	Sequence 7, Appli
876	13.2	0.3	19	1	US-11-014-373-192	Sequence 192, App
c 877	13.2	0.3	19	1	US-11-014-373-469	Sequence 469, App
878	13.2	0.3	19	1	US-10-205-309-325	Sequence 325, App
c 879	13.2	0.3	19	1	US-10-205-309-650	Sequence 650, App
880	13.2	0.3	20	1	US-10-619-253-151	Sequence 151, App
881	13.2	0.3	20	1	US-09-263-959-849	Sequence 849, App
c 882	13.2	0.3	20	1	US-09-005-243-32	Sequence 32, Appl
c 883	13.2	0.3	20	1	US-09-224-683-32	Sequence 32, Appl
c 884	13.2	0.3	20	1	US-10-671-395-654	Sequence 654, App
c 885	13.2	0.3	20	1	US-10-175-608-32	Sequence 32, Appl
c 886	13.2	0.3	20	1	US-10-620-642-32	Sequence 32, Appl
c 887	13.2	0.3	20	1	US-10-728-399-273	Sequence 273, App
c 888	13.2	0.3	20	1	US-10-671-395-433	Sequence 433, App
889	13.2	0.3	20	1	US-10-728-078-14	Sequence 14, Appl
c 890	13.2	0.3	20	1	US-10-831-901A-29730	Sequence 29730, A
c 891	13.2	0.3	20	1	US-10-831-901A-29731	Sequence 29731, A
c 892	13	0.3	19	1	US-10-683-990-97	Sequence 97, Appl
893	13	0.3	19	1	US-10-683-990-194	Sequence 194, App
894	12.8	0.3	16	1	US-09-263-959-544	Sequence 544, App
895	12.8	0.3	16	1	US-10-164-915-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-10-236-417-228
; Sequence 228, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442C
;  CURRENT APPLICATION NUMBER: US/10/236,417
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-01
;  PRIOR APPLICATION NUMBER: US60/318,430
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: US60/322,781
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/318,184
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/361,663
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US60/396,412
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US60/322,636
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/322,817
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/322,816
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/323,519
;  PRIOR FILING DATE: 2001-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 341
;  SOFTWARE: Custom
; SEQ ID NO 228
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: probe
US-10-236-417-228

  Query Match             0.7%;  Score 30;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.76;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4136 TCAAGATTCTAAAGCTCAATTCAAGTGACA 4165
             ||||||||||||||||||||||||||||||
Db          1 TCAAGATTCTAAAGCTCAATTCAAGTGACA 30


RESULT 2
US-11-036-317-535842
; Sequence 535842, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 535842
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-535842

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1170 AGTACCGCTGGCACATCAACTTCAC 1194
             |||||||||||||||||||||||||
Db          1 AGTACCGCTGGCACATCAACTTCAC 25


RESULT 3
US-11-036-317-537139
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; Sequence 537139, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 537139
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-537139

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1166 AGTGAGTACCGCTGGCACATCAACT 1190
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Db          1 AGTGAGTACCGCTGGCACATCAACT 25


RESULT 4
US-11-036-317-573632
; Sequence 573632, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 573632
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-573632

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1165 CAGTGAGTACCGCTGGCACATCAAC 1189
             |||||||||||||||||||||||||
Db          1 CAGTGAGTACCGCTGGCACATCAAC 25


RESULT 5
US-11-036-317-659530
; Sequence 659530, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 659530
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-659530

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1169 GAGTACCGCTGGCACATCAACTTCA 1193
             |||||||||||||||||||||||||
Db          1 GAGTACCGCTGGCACATCAACTTCA 25


RESULT 6
US-11-036-317-727767
; Sequence 727767, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 727767
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-727767

  Query Match             0.6%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1167 GTGAGTACCGCTGGCACATCAACTT 1191
             |||||||||||||||||||||||||
Db          1 GTGAGTACCGCTGGCACATCAACTT 25


RESULT 7
US-10-758-783-3
; Sequence 3, Application US/10758783
; Publication No. US20040142868A1
; GENERAL INFORMATION:
;  APPLICANT: Sleeman, Mark W.
;  TITLE OF INVENTION: Method of Treating Liver Steatosis in a
;  TITLE OF INVENTION:  Mammal
;  FILE REFERENCE: REG 145A
;  CURRENT APPLICATION NUMBER: US/10/758,783
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: 60/441,464
;  PRIOR FILING DATE: 2003-01-21
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-758-783-3

  Query Match             0.6%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        903 TGCTGATGTGCTTCATCCTGCCCA 926
              ||||||||||||||||||||||||
Db          1 TGCTGATGTGCTTCATCCTGCCCA 24
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RESULT 8
US-10-038-854-327
; Sequence 327, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Eisen, Andrew J
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Guo, Xiaojia S
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  MacDougall, John R
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-230
;  CURRENT APPLICATION NUMBER: US/10/038,854
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/258,928
;  PRIOR FILING DATE: 2000-12-29
;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 327
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: chemically
;   OTHER INFORMATION: synthesized
US-10-038-854-327

  Query Match             0.6%;  Score 23.8;  DB 1;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 13;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1143 CCTTTCCCTATGACTACTCTGCCAGTG 1169
                ||||||||| |||||||||||| ||||
Db          1 CCTTTCCCTTTGACTACTCTGCGAGTG 27


RESULT 9
US-10-038-854-330
; Sequence 330, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Eisen, Andrew J
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Guo, Xiaojia S
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  MacDougall, John R
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-230
;  CURRENT APPLICATION NUMBER: US/10/038,854
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/258,928
;  PRIOR FILING DATE: 2000-12-29
;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 330
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: chemically
;   OTHER INFORMATION: synthesized
US-10-038-854-330
```

```
  Query Match             0.6%;  Score 23.8;  DB 1;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 13;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1143 CCTTTCCCTATGACTACTCTGCCAGTG 1169
              ||||||||| |||||||||||| ||||
Db          1 CCTTTCCCTTTGACTACTCTGCGAGTG 27


RESULT 10
US-10-708-204-4431
; Sequence 4431, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4431
;   LENGTH: 27
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-708-204-4431

  Query Match             0.6%;  Score 23.8;  DB 1;  Length 27;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   18;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4698 CTGTGTGACCCTGGGCAAGTCACTTAA 4724
              |:|:|:|||| :|||||||:|||:: |
Db          1 CUGUGUGACCUUGGGCAAGUCACUUCA 27


RESULT 11
US-11-036-317-535843
; Sequence 535843, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 535843
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-535843

  Query Match             0.5%;  Score 23.4;  DB 1;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 14;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1170 AGTACCGCTGGCACATCAACTTCAC 1194
              |||||||||||| ||||||||||||
Db          1 AGTACCGCTGGCTCATCAACTTCAC 25


RESULT 12
US-11-036-317-537138
; Sequence 537138, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 537138
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-537138

  Query Match             0.5%;  Score 23.4;  DB 1;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 14;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1166 AGTGAGTACCGCTGGCACATCAACT 1190
              ||||||||||||| ||||||||||||
Db          1 AGTGAGTACCGCAGGCACATCAACT 25


RESULT 13
US-11-036-317-573633
; Sequence 573633, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 573633
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-573633

  Query Match             0.5%;  Score 23.4;  DB 1;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 14;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1165 CAGTGAGTACCGCTGGCACATCAAC 1189
              ||||||||||||| ||||||||||||
Db          1 CAGTGAGTACCGGTGGCACATCAAC 25


RESULT 14
US-11-036-317-659531
; Sequence 659531, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 659531
;   LENGTH: 25
```

```
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-659531

  Query Match             0.5%;  Score 23.4;  DB 1;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 14;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1169 GAGTACCGCTGGCACATCAACTTCA 1193
              ||||||||||||| ||||||||||||
Db          1 GAGTACCGCTGGGACATCAACTTCA 25


RESULT 15
US-11-036-317-727766
; Sequence 727766, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 727766
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-727766

  Query Match             0.5%;  Score 23.4;  DB 1;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 14;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1167 GTGAGTACCGCTGGCACATCAACTT 1191
              ||||||||||||| ||||||||||||
Db          1 GTGAGTACCGCTCGCACATCAACTT 25


RESULT 16
US-10-377-133-14
; Sequence 14, Application US/10377133
; Publication No. US20030219795A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: SCDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX03-015C
;  CURRENT APPLICATION NUMBER: US/10/377,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US60/361,196
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-377-133-14

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        964 AAACAGTGTGTTCGTTGCCACTT 986
              |||||||||||||||||||||||
Db          1 AAACAGTGTGTTCGTTGCCACTT 23


RESULT 17
US-10-377-133-15
; Sequence 15, Application US/10377133
; Publication No. US20030219795A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: SCDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX03-015C
;  CURRENT APPLICATION NUMBER: US/10/377,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US60/361,196
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-377-133-15

  Query Match             0.5%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1247 AAAGTCTCCAAGGCCGCCATCTT 1269
              |||||||||||||||||||||||
Db          1 AAAGTCTCCAAGGCCGCCATCTT 23


RESULT 18
US-10-236-417-227
; Sequence 227, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442C
;  CURRENT APPLICATION NUMBER: US/10/236,417
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-01
;  PRIOR APPLICATION NUMBER: US60/318,430
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: US60/322,781
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/318,184
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/361,663
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US60/396,412
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US60/322,636
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/322,817
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/322,816
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/323,519
;  PRIOR FILING DATE: 2001-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 341
;  SOFTWARE: Custom
; SEQ ID NO 227
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-417-227

  Query Match             0.5%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4112 TCTGCTGAGTAAGGAACACGAT 4133
             ||||||||||||||||||||||
Db          1 TCTGCTGAGTAAGGAACACGAT 22


RESULT 19
US-10-719-900-766668
; Sequence 766668, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 766668
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-766668

  Query Match             0.5%;  Score 21.8;  DB 1;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 30;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5160 TACTAATCTGAGATTGTGTTTGTTC 5184
             |||| ||||||| ||||||||||||
Db          1 TACTCATCTGAGCTTGTGTTTGTTC 25


RESULT 20
US-10-719-900-766669
; Sequence 766669, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 766669
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-766669

  Query Match             0.5%;  Score 21.8;  DB 1;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 30;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5160 TACTAATCTGAGATTGTGTTTGTTC 5184
             |||| ||||||| ||||||||||||
Db          1 TACTCATCTGAGGTTGTGTTTGTTC 25


RESULT 21
US-11-060-756-177454
; Sequence 177454, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 177454
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: probe
US-11-060-756-177454

  Query Match             0.5%;  Score 21.8;  DB 1;  Length 25;
  Best Local Similarity   92.0%;  Pred. No. 30;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4682 CTGTGCCACTGACTTGCTGTGTGAC 4706
             || | ||||||||||||||||||||||
Db          1 CTCTTCCACTGACTTGCTGTGTGAC 25


RESULT 22
US-10-236-417-229/c
; Sequence 229, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442C
;  CURRENT APPLICATION NUMBER: US/10/236,417
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-01
;  PRIOR APPLICATION NUMBER: US60/318,430
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: US60/322,781
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/318,184
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/361,663
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US60/396,412
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US60/322,636
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/322,817
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/322,816
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US60/323,519
;  PRIOR FILING DATE: 2001-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 341
;  SOFTWARE: Custom
; SEQ ID NO 229
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer
US-10-236-417-229

  Query Match             0.5%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCGGA 4202
             |||||||||||||||||||||
Db         21 AGATCTGATCAAGAGTCCGGA 1


RESULT 23
US-10-719-900-187154/c
; Sequence 187154, Application US/10719900
; Publication No. US20050026164A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 187154
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-187154

  Query Match             0.5%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2803 CTAAAGTATACAACTGCCTGG 2823
             |||||||||||||||||||||
Db         25 CTAAAGTATACAACTGCCTGG 5


RESULT 24
US-10-719-900-927417
; Sequence 927417, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 927417
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-927417

  Query Match             0.5%;  Score 20.8;  DB 1;  Length 25;
  Best Local Similarity   91.7%;  Pred. No. 48;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1777 TTATCTTCAGCCCAGGCTTTTGCT 1800
             |||| | ||||||||||||||||||
Db          1 TTATTTCCAGCCCAGGCTTTTGCT 24


RESULT 25
US-11-060-756-141375
; Sequence 141375, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141375
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: probe
US-11-060-756-141375

  Query Match             0.5%;  Score 20.8;  DB 1;  Length 25;
  Best Local Similarity   91.7%;  Pred. No. 48;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4689 ACTGACTTGCTGTGTGACCCTGGG 4712
             |||||||||||||||||| | ||
Db          1 ACTGACTTGCTGTGTGACCTTAGG 24


RESULT 26
US-10-681-773-79988
; Sequence 79988, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
;  APPLICANT: Matsuzaki, Hajime
;  APPLICANT:  Mei, Rui
;  APPLICANT:  Shen, Mei-Mei
;  APPLICANT:  Kennedy, Giulia
;  TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
;  FILE REFERENCE: 3522.2
;  CURRENT APPLICATION NUMBER: US/10/681,773
;  CURRENT FILING DATE:  2003-10-07
;  PRIOR APPLICATION NUMBER: 60/470,475
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 60/417,190
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 124031
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79988
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-681-773-79988

  Query Match             0.5%;  Score 20.4;  DB 1;  Length 25;
  Best Local Similarity   95.5%;  Pred. No. 58;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4696 TGCTGTGTGACCCTGGGCAAGT 4717
             |||||||||| ||||||||||
Db          3 TGCTGTGTGATCCTGGGCAAGT 24


RESULT 27
US-10-377-133-21
; Sequence 21, Application US/10377133
; Publication No. US20030219795A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: SCDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX03-015C
;  CURRENT APPLICATION NUMBER: US/10/377,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US60/361,196
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(21)
;   OTHER INFORMATION: YY is deoxyribonucleotide dTdT
US-10-377-133-21

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   61.9%;  Pred. No. 52;
  Matches   13;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        966 ACAGTGTGTTCGTTGCCACTT 986
              ||||:|:|::||::|||||::
Db          1 ACAGUGUGUUCGUUGCCACYY 21


RESULT 28
US-10-377-133-22/c
; Sequence 22, Application US/10377133
; Publication No. US20030219795A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: SCDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX03-015C
;  CURRENT APPLICATION NUMBER: US/10/377,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US60/361,196
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(21)
;   OTHER INFORMATION: YY is deoxyribonucleotide dTdT
US-10-377-133-22

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 52;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        964 AAACAGTGTGTTCGTTGCCAC 984
              ::|||||||||||||||||||
Db         21 RRACAGTGTGTTCGTTGCCAC 1


RESULT 29
US-10-377-133-23
; Sequence 23, Application US/10377133
; Publication No. US20030219795A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: SCDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX03-015C
;  CURRENT APPLICATION NUMBER: US/10/377,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US60/361,196
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(21)
;   OTHER INFORMATION: YY is deoxyribonucleotide dTdT
US-10-377-133-23

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 52;
  Matches   16;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1249 AGTCTCCAAGGCCGCCATCTT 1269
              ||:|:|||||||||||:|::
Db          1 AGUCUCCAAGGCCGCCAUCYY 21


RESULT 30
US-10-377-133-24/c
; Sequence 24, Application US/10377133
; Publication No. US20030219795A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: SCDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX03-015C
;  CURRENT APPLICATION NUMBER: US/10/377,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US60/361,196
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(21)
;   OTHER INFORMATION: YY is deoxyribonucleotide dTdT
US-10-377-133-24

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 52;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1247 AAAGTCTCCAAGGCCGCCATC 1267
              ::|||||||||||||||||||
Db         21 RRAGTCTCCAAGGCCGCCATC 1


RESULT 31
US-10-719-900-54411
; Sequence 54411, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 54411
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-54411

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        890 AAACCTGGCTTGCTGCTGATGTGCT 914
              || |||||| | ||||||||||||
Db          1 AAGCCTGGCATTCTGCTGATGTGCT 25


RESULT 32
US-10-719-900-143534
; Sequence 143534, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
```

```
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 143534
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-143534

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1086 AGAATATCCTGGTTTCACTTGGAGC 1110
              ||||||||||||||| || || ||
Db          1 AGAATATCCTGGTTTCCCTGGGTGC 25


RESULT 33
US-10-719-900-352484
; Sequence 352484, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 352484
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-352484

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1427 CCCATTCCAGTACAGTATTCTTTTA 1451
              || ||||| |||||||||||||| ||
Db          1 CCTATTCCGGTACAGTATTCTTATA 25


RESULT 34
US-10-956-157-64768
; Sequence 64768, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64768
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Probe Sequence
US-10-956-157-64768

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1511 TCTTCTCTTATCCTCTCTCTCTTCT 1535
              |||||||||||| ||| ||| ||||
Db          1 TCTTCTCTTATCTTCTGTCTGTTCT 25


RESULT 35
US-10-956-157-265721
; Sequence 265721, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 265721
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Probe Sequence
US-10-956-157-265721

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4758 TGGGGATAATAATACTGACCTACCT 4782
              ||||  |||||||||| ||||||||
Db          1 TGGGATTAATAATACTTACCTACCT 25


RESULT 36
US-10-956-157-274624/c
; Sequence 274624, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274624
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Probe Sequence
US-10-956-157-274624

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1198 ATTCTTCATTGATTGCATGGCCGCC 1222
              |||||| ||||| |||||||| |||
Db         25 ATTCTTTATTGAGTGCATGGCGGCC 1


RESULT 37
US-10-719-956-124413/c
; Sequence 124413, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
```

```
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 124413
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-124413

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4954 TGAATGAATCCATTGGAGAAGCGGT 4978
                ||||||  ||||||||||||||| | |
Db         25 TGAATGCATCCATTGGAGAAGTGCT 1


RESULT 38
US-10-719-956-160951/c
; Sequence 160951, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 160951
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-160951

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4697 GCTGTGTGACCCTGGGCAAGTCACT 4721
                | ||||||||||||| |||| |||||
Db         25 GTTGTGTGACCCTGAGCAAATCACT 1


RESULT 39
US-10-719-956-699166/c
; Sequence 699166, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 699166
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-699166

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4453 CACATTTGATGGAGGGTGGAAATAA 4477
                ||||||||||||| || |||| ||
Db         25 CACATTTGATGGAGAGTTGAAAAAA 1


RESULT 40
US-11-036-317-723353
; Sequence 723353, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 723353
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-723353

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        883 GTACTACAAACCTGGCTTGCTGCTG 907
                |||||||||  ||||||  | ||||||
Db          1 GTACTACAAGCCTGGCATTCTGCTG 25


RESULT 41
US-11-036-317-871787/c
; Sequence 871787, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 871787
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-871787

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3142 CTGGCAAACCCTCCCAGAAACATCT 3166
                ||||||  |||||||  ||||  |||||
Db         25 CTGGCAGACCCTCCGAGAAGCATCT 1


RESULT 42
US-11-060-756-43423
; Sequence 43423, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
```

```
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43423
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: probe
US-11-060-756-43423

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4690 CTGACTTGCTGTGTGACCCTGGGCA 4714
             |||||||||||||||||| | || |
Db          1 CTGACTTGCTGTGTGACCTTAGGAA 25


RESULT 43
US-11-060-756-261851/c
; Sequence 261851, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 261851
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: probe
US-11-060-756-261851

  Query Match             0.5%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 63;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1198 ATTCTTCATTGATTGCATGGCCGCC 1222
             |||||| ||||| |||||||| |||
Db         25 ATTCTTTATTGAGTGCATGGCGGCC 1


RESULT 44
US-09-918-187-20/c
; Sequence 20, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-20

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1011 ATGCCACCTGGCTGGTGAAC 1030
             ||||||||||||||||||||
Db         20 ATGCCACCTGGCTGGTGAAC 1


RESULT 45
US-09-918-187-21/c
; Sequence 21, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-21

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1111 TGTGGGTGAGGGCTTCCACA 1130
             ||||||||||||||||||||
Db         20 TGTGGGTGAGGGCTTCCACA 1


RESULT 46
US-09-918-187-22/c
; Sequence 22, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-22

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1171 GTACCGCTGGCACATCAACT 1190
             ||||||||||||||||||||
Db         20 GTACCGCTGGCACATCAACT 1


RESULT 47
US-09-918-187-23/c
; Sequence 23, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
```

```
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-23

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1307 AGTGGCTGAGTTTGGGGTCC 1326
             ||||||||||||||||||||
Db         20 AGTGGCTGAGTTTGGGGTCC 1


RESULT 48
US-09-918-187-24/c
; Sequence 24, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-24

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1581 CCCTTATTGCCTCCCAGGCA 1600
             ||||||||||||||||||||
Db         20 CCCTTATTGCCTCCCAGGCA 1


RESULT 49
US-09-918-187-25/c
; Sequence 25, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-25

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1861 GGGAGAGAGTTAGCATGTAT 1880
             ||||||||||||||||||||
Db         20 GGGAGAGAGTTAGCATGTAT 1


RESULT 50
US-09-918-187-26/c
; Sequence 26, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-26

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1941 TGCCTACCTAATGAGGACTT 1960
             ||||||||||||||||||||
Db         20 TGCCTACCTAATGAGGACTT 1


RESULT 51
US-09-918-187-27/c
; Sequence 27, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-27

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2241 TCCATGAGCTGCTCATTACA 2260
             ||||||||||||||||||||
Db         20 TCCATGAGCTGCTCATTACA 1


RESULT 52
US-09-918-187-28/c
; Sequence 28, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
```

```
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-28

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2616 GGGCTTGAGAAGGTTACTGA 2635
              ||||||||||||||||||||
Db         20 GGGCTTGAGAAGGTTACTGA 1


RESULT 53
US-09-918-187-29/c
; Sequence 29, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-29

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2980 CTTGCTGTCCAGGCAGCTCC 2999
              ||||||||||||||||||||
Db         20 CTTGCTGTCCAGGCAGCTCC 1


RESULT 54
US-09-918-187-30/c
; Sequence 30, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 30
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-30

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3011 AGAATGCTCAGGGTCACTGA 3030
              ||||||||||||||||||||
Db         20 AGAATGCTCAGGGTCACTGA 1


RESULT 55
US-09-918-187-31/c
; Sequence 31, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-31

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3231 TTGAGCCAGTGGGCCAGCCA 3250
              ||||||||||||||||||||
Db         20 TTGAGCCAGTGGGCCAGCCA 1


RESULT 56
US-09-918-187-32/c
; Sequence 32, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 32
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-32

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3291 GTCAGAACCAGAGGGCATGC 3310
              ||||||||||||||||||||
Db         20 GTCAGAACCAGAGGGCATGC 1


RESULT 57
US-09-918-187-33/c
; Sequence 33, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
```

```
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-33

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCAAAGC 3490
              ||||||||||||||||||||
Db         20 GTCAGGGTGAACTGCAAAGC 1


RESULT 58
US-09-918-187-34/c
; Sequence 34, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-34

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3502 CCTGGGATTTGAGATACCAC 3521
              ||||||||||||||||||||
Db         20 CCTGGGATTTGAGATACCAC 1


RESULT 59
US-09-918-187-35/c
; Sequence 35, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-35

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3791 ACAGGGGTTAGCCTGGACTA 3810
              ||||||||||||||||||||
Db         20 ACAGGGGTTAGCCTGGACTA 1


RESULT 60
US-09-918-187-36/c
; Sequence 36, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-36

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3851 AGGATCTAAGGGAAGATCAC 3870
              ||||||||||||||||||||
Db         20 AGGATCTAAGGGAAGATCAC 1


RESULT 61
US-09-918-187-37/c
; Sequence 37, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-37

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4101 GTGGGAGTGTGTCTGCTGAG 4120
              ||||||||||||||||||||
Db         20 GTGGGAGTGTGTCTGCTGAG 1


RESULT 62
US-09-918-187-38/c
; Sequence 38, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
```

```
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-38

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4226 GGGTGTGCTGACAACTTAGC 4245
             ||||||||||||||||||||
Db         20 GGGTGTGCTGACAACTTAGC 1


RESULT 63
US-09-918-187-39/c
; Sequence 39, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-39

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4406 GGGCTTCATTCTGGAAACTT 4425
             ||||||||||||||||||||
Db         20 GGGCTTCATTCTGGAAACTT 1


RESULT 64
US-09-918-187-40/c
; Sequence 40, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-40

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4571 GTATCTTGGGTGTATTCTCT 4590
             ||||||||||||||||||||
Db         20 GTATCTTGGGTGTATTCTCT 1


RESULT 65
US-09-918-187-41/c
; Sequence 41, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-41

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTTAACTA 4727
             ||||||||||||||||||||
Db         20 CTGGGCAAGTCACTTAACTA 1


RESULT 66
US-09-918-187-42/c
; Sequence 42, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-42

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4771 ACTGACCTACCTCAAAGGGC 4790
             ||||||||||||||||||||
Db         20 ACTGACCTACCTCAAAGGGC 1


RESULT 67
US-09-918-187-43/c
; Sequence 43, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
```

```
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-43

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4921 GCTGTCATTAGTCTATATGG 4940
              ||||||||||||||||||||
Db         20 GCTGTCATTAGTCTATATGG 1


RESULT 68
US-09-918-187-44/c
; Sequence 44, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-44

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5021 ATTGCCACGGAAACATACAG 5040
              ||||||||||||||||||||
Db         20 ATTGCCACGGAAACATACAG 1


RESULT 69
US-09-918-187-53/c
; Sequence 53, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 53
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-53

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        901 GCTGCTGATGTGCTTCATCC 920
              ||||||||||||||||||||
Db         20 GCTGCTGATGTGCTTCATCC 1


RESULT 70
US-09-918-187-54/c
; Sequence 54, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-54

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        936 CCTGGTATTTCTGGGGTGAA 955
              ||||||||||||||||||||
Db         20 CCTGGTATTTCTGGGGTGAA 1


RESULT 71
US-09-918-187-55/c
; Sequence 55, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-55

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1082 CGGGAGAATATCCTGGTTTC 1101
              ||||||||||||||||||||
Db         20 CGGGAGAATATCCTGGTTTC 1


RESULT 72
US-09-918-187-56/c
; Sequence 56, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
```

```
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-56

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1151 TATGACTACTCTGCCAGTGA 1170
             ||||||||||||||||||||
Db         20 TATGACTACTCTGCCAGTGA 1


RESULT 73
US-09-918-187-57/c
; Sequence 57, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-57

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1261 CGCCATCTTGGCCAGGATTA 1280
             ||||||||||||||||||||
Db         20 CGCCATCTTGGCCAGGATTA 1


RESULT 74
US-09-918-187-58/c
; Sequence 58, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-58

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1401 CAGGATGCTAAAGATGATGA 1420
             ||||||||||||||||||||
Db         20 CAGGATGCTAAAGATGATGA 1


RESULT 75
US-09-918-187-59/c
; Sequence 59, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-59

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1601 AGCAGCTGGTCAGTCTTTGC 1620
             ||||||||||||||||||||
Db         20 AGCAGCTGGTCAGTCTTTGC 1


RESULT 76
US-09-918-187-60/c
; Sequence 60, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 60
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-60

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1748 ACAGAATCTTCTGGGTAGTC 1767
             ||||||||||||||||||||
Db         20 ACAGAATCTTCTGGGTAGTC 1


RESULT 77
US-09-918-187-61/c
; Sequence 61, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-61

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1881 GAATGTAAGGATGAGGGAAG 1900
              ||||||||||||||||||||
Db         20 GAATGTAAGGATGAGGGAAG 1


RESULT 78
US-09-918-187-62/c
; Sequence 62, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-62

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1985 CCTTTCTCTCCTGGCTCGGG 2004
              ||||||||||||||||||||
Db         20 CCTTTCTCTCCTGGCTCGGG 1


RESULT 79
US-09-918-187-63/c
; Sequence 63, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 63
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-63

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2102 AGTGGTCTCTGCTGGGGAAG 2121
              ||||||||||||||||||||
Db         20 AGTGGTCTCTGCTGGGGAAG 1


RESULT 80
US-09-918-187-64/c
; Sequence 64, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-64

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2281 TGCCATCTTCAGGATATTGG 2300
              ||||||||||||||||||||
Db         20 TGCCATCTTCAGGATATTGG 1


RESULT 81
US-09-918-187-65/c
; Sequence 65, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-65

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2481 GAGAGGAGGAATTAGTTGGG 2500
              ||||||||||||||||||||
Db         20 GAGAGGAGGAATTAGTTGGG 1


RESULT 82
US-09-918-187-66/c
; Sequence 66, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 66
;   LENGTH: 20
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-66

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATCTATA 2560
              ||||||||||||||||||||
Db         20 GCTGAGGGACAGGATCTATA 1


RESULT 83
US-09-918-187-67/c
; Sequence 67, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-67

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2631 ACTGAGTGAGTTATTGGGAG 2650
              ||||||||||||||||||||
Db         20 ACTGAGTGAGTTATTGGGAG 1


RESULT 84
US-09-918-187-68/c
; Sequence 68, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 68
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-68

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2826 GGCAGGGTTAGGAATCTCTT 2845
              ||||||||||||||||||||
Db         20 GGCAGGGTTAGGAATCTCTT 1


RESULT 85
US-09-918-187-69/c
; Sequence 69, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 69
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-69

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2941 CAGGCAGCCTCCTTTGTGTG 2960
              ||||||||||||||||||||
Db         20 CAGGCAGCCTCCTTTGTGTG 1


RESULT 86
US-09-918-187-70/c
; Sequence 70, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-70

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3051 AGTAGAGCTAGCTGCCACTT 3070
              ||||||||||||||||||||
Db         20 AGTAGAGCTAGCTGCCACTT 1


RESULT 87
US-09-918-187-71/c
; Sequence 71, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 71
;   LENGTH: 20
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-71

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3321 CTGCTTACTTGGTGAGGGTG 3340
              ||||||||||||||||||||
Db         20 CTGCTTACTTGGTGAGGGTG 1


RESULT 88
US-09-918-187-72/c
; Sequence 72, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 72
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-72

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3401 GTTCTCACTGGGAAGAAGCA 3420
              ||||||||||||||||||||
Db         20 GTTCTCACTGGGAAGAAGCA 1


RESULT 89
US-09-918-187-73/c
; Sequence 73, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 73
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-73

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3941 TCATCAGATGCCTGCTTGAT 3960
              ||||||||||||||||||||
Db         20 TCATCAGATGCCTGCTTGAT 1


RESULT 90
US-09-918-187-74/c
; Sequence 74, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 74
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-74

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4052 ATGGCACCTCAGGCTGAGGG 4071
              ||||||||||||||||||||
Db         20 ATGGCACCTCAGGCTGAGGG 1


RESULT 91
US-09-918-187-75/c
; Sequence 75, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-75

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4357 GGGCCTGAGTGGAGGATTAT 4376
              ||||||||||||||||||||
Db         20 GGGCCTGAGTGGAGGATTAT 1


RESULT 92
US-09-918-187-76/c
; Sequence 76, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 76
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-76

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4431 AGGGCTGCTTTTCTTAAGTG 4450
              ||||||||||||||||||||
Db         20 AGGGCTGCTTTTCTTAAGTG 1


RESULT 93
US-09-918-187-77/c
; Sequence 77, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 77
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-77

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4681 ACTGTGCCACTGACTTGCTG 4700
              ||||||||||||||||||||
Db         20 ACTGTGCCACTGACTTGCTG 1


RESULT 94
US-09-918-187-78/c
; Sequence 78, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 78
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-78

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4971 GAAGCGGTGGATAACTAGCC 4990
              ||||||||||||||||||||
Db         20 GAAGCGGTGGATAACTAGCC 1


RESULT 95
US-09-918-187-79/c
; Sequence 79, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-79

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5044 ATGCCTTTTCTGTGATTGGG 5063
              ||||||||||||||||||||
Db         20 ATGCCTTTTCTGTGATTGGG 1


RESULT 96
US-09-918-187-80/c
; Sequence 80, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-80

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5081 TTATGTGGGATATAGTAGTT 5100
              ||||||||||||||||||||
Db         20 TTATGTGGGATATAGTAGTT 1


RESULT 97
US-10-467-008-110/c
; Sequence 110, Application US/10467008
; Publication No. US20040116366A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT B
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: ISPH-0746
;  CURRENT APPLICATION NUMBER: US/10/467,008
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: PCT/US02/02805
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: US 09/780,045
;  PRIOR FILING DATE: 2001-02-09
```

```
;  NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-467-008-110

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATATA 2410
             ||||||||||||||||||||
Db         20 AAAATATATATACATATATA 1


RESULT 98
US-10-484-442-20/c
; Sequence 20, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-20

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1011 ATGCCACCTGGCTGGTGAAC 1030
             ||||||||||||||||||||
Db         20 ATGCCACCTGGCTGGTGAAC 1


RESULT 99
US-10-484-442-21/c
; Sequence 21, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-21

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1111 TGTGGGTGAGGGCTTCCACA 1130
             ||||||||||||||||||||
Db         20 TGTGGGTGAGGGCTTCCACA 1


RESULT 100
US-10-484-442-22/c
; Sequence 22, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-22

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1171 GTACCGCTGGCACATCAACT 1190
             ||||||||||||||||||||
Db         20 GTACCGCTGGCACATCAACT 1


RESULT 101
US-10-484-442-23/c
; Sequence 23, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-23

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1307 AGTGGCTGAGTTTGGGGTCC 1326
             ||||||||||||||||||||
Db         20 AGTGGCTGAGTTTGGGGTCC 1
```

```
RESULT 102
US-10-484-442-24/c
; Sequence 24, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-24

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1581 CCCTTATTGCCTCCCAGGCA 1600
              ||||||||||||||||||||
Db         20 CCCTTATTGCCTCCCAGGCA 1


RESULT 103
US-10-484-442-25/c
; Sequence 25, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-25

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1861 GGGAGAGAGTTAGCATGTAT 1880
              ||||||||||||||||||||
Db         20 GGGAGAGAGTTAGCATGTAT 1


RESULT 104
US-10-484-442-26/c
; Sequence 26, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-26

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1941 TGCCTACCTAATGAGGACTT 1960
              ||||||||||||||||||||
Db         20 TGCCTACCTAATGAGGACTT 1


RESULT 105
US-10-484-442-27/c
; Sequence 27, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-27

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2241 TCCATGAGCTGCTCATTACA 2260
              ||||||||||||||||||||
Db         20 TCCATGAGCTGCTCATTACA 1


RESULT 106
US-10-484-442-28/c
; Sequence 28, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-28

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2616 GGGCTTGAGAAGGTTACTGA 2635
              ||||||||||||||||||||
Db         20 GGGCTTGAGAAGGTTACTGA 1


RESULT 107
US-10-484-442-29/c
; Sequence 29, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-29

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2980 CTTGCTGTCCAGGCAGCTCC 2999
              ||||||||||||||||||||
Db         20 CTTGCTGTCCAGGCAGCTCC 1


RESULT 108
US-10-484-442-30/c
; Sequence 30, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 30
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-30

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3011 AGAATGCTCAGGGTCACTGA 3030
              ||||||||||||||||||||
Db         20 AGAATGCTCAGGGTCACTGA 1


RESULT 109
US-10-484-442-31/c
; Sequence 31, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-31

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3231 TTGAGCCAGTGGGCCAGCCA 3250
              ||||||||||||||||||||
Db         20 TTGAGCCAGTGGGCCAGCCA 1


RESULT 110
US-10-484-442-32/c
; Sequence 32, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 32
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-32

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3291 GTCAGAACCAGAGGGCATGC 3310
              ||||||||||||||||||||
Db         20 GTCAGAACCAGAGGGCATGC 1


RESULT 111
US-10-484-442-33/c
; Sequence 33, Application US/10484442
; Publication No. US20040254359A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-33

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCAAAGC 3490
              ||||||||||||||||||||
Db         20 GTCAGGGTGAACTGCAAAGC 1


RESULT 112
US-10-484-442-34/c
; Sequence 34, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-34

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3502 CCTGGGATTTGAGATACCAC 3521
              ||||||||||||||||||||
Db         20 CCTGGGATTTGAGATACCAC 1


RESULT 113
US-10-484-442-35/c
; Sequence 35, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-35

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3791 ACAGGGGTTAGCCTGGACTA 3810
              ||||||||||||||||||||
Db         20 ACAGGGGTTAGCCTGGACTA 1


RESULT 114
US-10-484-442-36/c
; Sequence 36, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-36

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3851 AGGATCTAAGGGAAGATCAC 3870
              ||||||||||||||||||||
Db         20 AGGATCTAAGGGAAGATCAC 1


RESULT 115
US-10-484-442-37/c
; Sequence 37, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-37
```

```
  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4101 GTGGGAGTGTGTCTGCTGAG 4120
              ||||||||||||||||||||
Db         20 GTGGGAGTGTGTCTGCTGAG 1


RESULT 116
US-10-484-442-38/c
; Sequence 38, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-38

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4226 GGGTGTGCTGACAACTTAGC 4245
              ||||||||||||||||||||
Db         20 GGGTGTGCTGACAACTTAGC 1


RESULT 117
US-10-484-442-39/c
; Sequence 39, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-39

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4406 GGGCTTCATTCTGGAAACTT 4425
              ||||||||||||||||||||
Db         20 GGGCTTCATTCTGGAAACTT 1


RESULT 118
US-10-484-442-40/c
; Sequence 40, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-40

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4571 GTATCTTGGGTGTATTCTCT 4590
              ||||||||||||||||||||
Db         20 GTATCTTGGGTGTATTCTCT 1


RESULT 119
US-10-484-442-41/c
; Sequence 41, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-41

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTTAACTA 4727
              ||||||||||||||||||||
Db         20 CTGGGCAAGTCACTTAACTA 1


RESULT 120
US-10-484-442-42/c
; Sequence 42, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
```

```
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-42

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4771 ACTGACCTACCTCAAAGGGC 4790
              ||||||||||||||||||||
Db         20 ACTGACCTACCTCAAAGGGC 1


RESULT 121
US-10-484-442-43/c
; Sequence 43, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-43

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4921 GCTGTCATTAGTCTATATGG 4940
              ||||||||||||||||||||
Db         20 GCTGTCATTAGTCTATATGG 1


RESULT 122
US-10-484-442-44/c
; Sequence 44, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-44

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5021 ATTGCCACGGAAACATACAG 5040
              ||||||||||||||||||||
Db         20 ATTGCCACGGAAACATACAG 1


RESULT 123
US-10-484-442-53/c
; Sequence 53, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 53
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-53

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        901 GCTGCTGATGTGCTTCATCC 920
              ||||||||||||||||||||
Db         20 GCTGCTGATGTGCTTCATCC 1


RESULT 124
US-10-484-442-54/c
; Sequence 54, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-54

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        936 CCTGGTATTTCTGGGGTGAA 955
              ||||||||||||||||||||
Db         20 CCTGGTATTTCTGGGGTGAA 1


RESULT 125
US-10-484-442-55/c
; Sequence 55, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-55

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1082 CGGGAGAATATCCTGGTTTC 1101
              ||||||||||||||||||||
Db         20 CGGGAGAATATCCTGGTTTC 1


RESULT 126
US-10-484-442-56/c
; Sequence 56, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-56

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1151 TATGACTACTCTGCCAGTGA 1170
              ||||||||||||||||||||
Db         20 TATGACTACTCTGCCAGTGA 1


RESULT 127
US-10-484-442-57/c
; Sequence 57, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-57

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1261 CGCCATCTTGGCCAGGATTA 1280
              ||||||||||||||||||||
Db         20 CGCCATCTTGGCCAGGATTA 1


RESULT 128
US-10-484-442-58/c
; Sequence 58, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-58

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1401 CAGGATGCTAAAGATGATGA 1420
              ||||||||||||||||||||
Db         20 CAGGATGCTAAAGATGATGA 1


RESULT 129
US-10-484-442-59/c
; Sequence 59, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
```

; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-59

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1601 AGCAGCTGGTCAGTCTTTGC 1620
||||||||||||||||||||
Db 20 AGCAGCTGGTCAGTCTTTGC 1

RESULT 130
US-10-484-442-60/c
; Sequence 60, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-60

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1748 ACAGAATCTTCTGGGTAGTC 1767
||||||||||||||||||||
Db 20 ACAGAATCTTCTGGGTAGTC 1

RESULT 131
US-10-484-442-61/c
; Sequence 61, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-61

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1881 GAATGTAAGGATGAGGGAAG 1900
||||||||||||||||||||
Db 20 GAATGTAAGGATGAGGGAAG 1

RESULT 132
US-10-484-442-62/c
; Sequence 62, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-62

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1985 CCTTTCTCTCCTGGCTCGGG 2004
||||||||||||||||||||
Db 20 CCTTTCTCTCCTGGCTCGGG 1

RESULT 133
US-10-484-442-63/c
; Sequence 63, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-63

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2102 AGTGGTCTCTGCTGGGGAAG 2121
||||||||||||||||||||
Db 20 AGTGGTCTCTGCTGGGGAAG 1

```
RESULT 134
US-10-484-442-64/c
; Sequence 64, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-64

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2281 TGCCATCTTCAGGATATTGG 2300
             ||||||||||||||||||||
Db         20 TGCCATCTTCAGGATATTGG 1


RESULT 135
US-10-484-442-65/c
; Sequence 65, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-65

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2481 GAGAGGAGGAATTAGTTGGG 2500
             ||||||||||||||||||||
Db         20 GAGAGGAGGAATTAGTTGGG 1


RESULT 136
US-10-484-442-66/c
; Sequence 66, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 66
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-66

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATCTATA 2560
             ||||||||||||||||||||
Db         20 GCTGAGGGACAGGATCTATA 1


RESULT 137
US-10-484-442-67/c
; Sequence 67, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-67

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2631 ACTGAGTGAGTTATTGGGAG 2650
             ||||||||||||||||||||
Db         20 ACTGAGTGAGTTATTGGGAG 1


RESULT 138
US-10-484-442-68/c
; Sequence 68, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 68
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-68

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2826 GGCAGGGTTAGGAATCTCTT 2845
              ||||||||||||||||||||
Db         20 GGCAGGGTTAGGAATCTCTT 1


RESULT 139
US-10-484-442-69/c
; Sequence 69, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 69
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-69

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2941 CAGGCAGCCTCCTTTGTGTG 2960
              ||||||||||||||||||||
Db         20 CAGGCAGCCTCCTTTGTGTG 1


RESULT 140
US-10-484-442-70/c
; Sequence 70, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-70

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3051 AGTAGAGCTAGCTGCCACTT 3070
              ||||||||||||||||||||
Db         20 AGTAGAGCTAGCTGCCACTT 1


RESULT 141
US-10-484-442-71/c
; Sequence 71, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 71
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-71

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3321 CTGCTTACTTGGTGAGGGTG 3340
              ||||||||||||||||||||
Db         20 CTGCTTACTTGGTGAGGGTG 1


RESULT 142
US-10-484-442-72/c
; Sequence 72, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 72
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-72

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3401 GTTCTCACTGGGAAGAAGCA 3420
              ||||||||||||||||||||
Db         20 GTTCTCACTGGGAAGAAGCA 1


RESULT 143
US-10-484-442-73/c
```

; Sequence 73, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-73

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3941 TCATCAGATGCCTGCTTGAT 3960
||||||||||||||||||||
Db 20 TCATCAGATGCCTGCTTGAT 1

RESULT 144
US-10-484-442-74/c
; Sequence 74, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-74

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4052 ATGGCACCTCAGGCTGAGGG 4071
||||||||||||||||||||
Db 20 ATGGCACCTCAGGCTGAGGG 1

RESULT 145
US-10-484-442-75/c
; Sequence 75, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-75

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4357 GGGCCTGAGTGGAGGATTAT 4376
||||||||||||||||||||
Db 20 GGGCCTGAGTGGAGGATTAT 1

RESULT 146
US-10-484-442-76/c
; Sequence 76, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-76

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4431 AGGGCTGCTTTTCTTAAGTG 4450
||||||||||||||||||||
Db 20 AGGGCTGCTTTTCTTAAGTG 1

RESULT 147
US-10-484-442-77/c
; Sequence 77, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 77
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-77

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4681 ACTGTGCCACTGACTTGCTG 4700
              ||||||||||||||||||||
Db         20 ACTGTGCCACTGACTTGCTG 1


RESULT 148
US-10-484-442-78/c
; Sequence 78, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 78
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-78

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4971 GAAGCGGTGGATAACTAGCC 4990
              ||||||||||||||||||||
Db         20 GAAGCGGTGGATAACTAGCC 1


RESULT 149
US-10-484-442-79/c
; Sequence 79, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-79

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5044 ATGCCTTTTCTGTGATTGGG 5063
              ||||||||||||||||||||
Db         20 ATGCCTTTTCTGTGATTGGG 1


RESULT 150
US-10-484-442-80/c
; Sequence 80, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-80

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5081 TTATGTGGGATATAGTAGTT 5100
              ||||||||||||||||||||
Db         20 TTATGTGGGATATAGTAGTT 1


RESULT 151
US-10-619-253-20/c
; Sequence 20, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-20

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1011 ATGCCACCTGGCTGGTGAAC 1030
              ||||||||||||||||||||
Db         20 ATGCCACCTGGCTGGTGAAC 1


RESULT 152
US-10-619-253-21/c
; Sequence 21, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
```

```
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-21

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1111 TGTGGGTGAGGGCTTCCACA 1130
              ||||||||||||||||||||
Db         20 TGTGGGTGAGGGCTTCCACA 1


RESULT 153
US-10-619-253-22/c
; Sequence 22, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-22

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1171 GTACCGCTGGCACATCAACT 1190
              ||||||||||||||||||||
Db         20 GTACCGCTGGCACATCAACT 1


RESULT 154
US-10-619-253-23/c
; Sequence 23, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-23

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1307 AGTGGCTGAGTTTGGGGTCC 1326
              ||||||||||||||||||||
Db         20 AGTGGCTGAGTTTGGGGTCC 1


RESULT 155
US-10-619-253-24/c
; Sequence 24, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-24

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1581 CCCTTATTGCCTCCCAGGCA 1600
              ||||||||||||||||||||
Db         20 CCCTTATTGCCTCCCAGGCA 1


RESULT 156
US-10-619-253-25/c
; Sequence 25, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-25

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1861 GGGAGAGAGTTAGCATGTAT 1880
              ||||||||||||||||||||
Db         20 GGGAGAGAGTTAGCATGTAT 1
```

```
RESULT 157
US-10-619-253-26/c
; Sequence 26, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-26

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1941 TGCCTACCTAATGAGGACTT 1960
              ||||||||||||||||||||
Db         20 TGCCTACCTAATGAGGACTT 1


RESULT 158
US-10-619-253-27/c
; Sequence 27, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-27

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2241 TCCATGAGCTGCTCATTACA 2260
              ||||||||||||||||||||
Db         20 TCCATGAGCTGCTCATTACA 1


RESULT 159
US-10-619-253-28/c
; Sequence 28, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-28

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2616 GGGCTTGAGAAGGTTACTGA 2635
              ||||||||||||||||||||
Db         20 GGGCTTGAGAAGGTTACTGA 1


RESULT 160
US-10-619-253-29/c
; Sequence 29, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-29

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2980 CTTGCTGTCCAGGCAGCTCC 2999
              ||||||||||||||||||||
Db         20 CTTGCTGTCCAGGCAGCTCC 1


RESULT 161
US-10-619-253-30/c
; Sequence 30, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 30
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
```

US-10-619-253-30

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3011 AGAATGCTCAGGGTCACTGA 3030
||||||||||||||||||||
Db 20 AGAATGCTCAGGGTCACTGA 1

RESULT 162
US-10-619-253-31/c
; Sequence 31, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-31

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3231 TTGAGCCAGTGGGCCAGCCA 3250
||||||||||||||||||||
Db 20 TTGAGCCAGTGGGCCAGCCA 1

RESULT 163
US-10-619-253-32/c
; Sequence 32, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-32

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3291 GTCAGAACCAGAGGGCATGC 3310
||||||||||||||||||||
Db 20 GTCAGAACCAGAGGGCATGC 1

RESULT 164
US-10-619-253-33/c
; Sequence 33, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-33

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3471 GTCAGGGTGAACTGCAAAGC 3490
||||||||||||||||||||
Db 20 GTCAGGGTGAACTGCAAAGC 1

RESULT 165
US-10-619-253-34/c
; Sequence 34, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-34

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3502 CCTGGGATTTGAGATACCAC 3521
||||||||||||||||||||
Db 20 CCTGGGATTTGAGATACCAC 1

RESULT 166
US-10-619-253-35/c
; Sequence 35, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15

```
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-35

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3791 ACAGGGGTTAGCCTGGACTA 3810
              ||||||||||||||||||||
Db         20 ACAGGGGTTAGCCTGGACTA 1


RESULT 167
US-10-619-253-36/c
; Sequence 36, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-36

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3851 AGGATCTAAGGGAAGATCAC 3870
              ||||||||||||||||||||
Db         20 AGGATCTAAGGGAAGATCAC 1


RESULT 168
US-10-619-253-37/c
; Sequence 37, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-37

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4101 GTGGGAGTGTGTCTGCTGAG 4120
              ||||||||||||||||||||
Db         20 GTGGGAGTGTGTCTGCTGAG 1


RESULT 169
US-10-619-253-38/c
; Sequence 38, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-38

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4226 GGGTGTGCTGACAACTTAGC 4245
              ||||||||||||||||||||
Db         20 GGGTGTGCTGACAACTTAGC 1


RESULT 170
US-10-619-253-39/c
; Sequence 39, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-39

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4406 GGGCTTCATTCTGGAAACTT 4425
              ||||||||||||||||||||
Db         20 GGGCTTCATTCTGGAAACTT 1


RESULT 171
US-10-619-253-40/c
```

```
; Sequence 40, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-40

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4571 GTATCTTGGGTGTATTCTCT 4590
              ||||||||||||||||||||
Db         20 GTATCTTGGGTGTATTCTCT 1


RESULT 172
US-10-619-253-41/c
; Sequence 41, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-41

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTTAACTA 4727
              ||||||||||||||||||||
Db         20 CTGGGCAAGTCACTTAACTA 1


RESULT 173
US-10-619-253-42/c
; Sequence 42, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-42

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4771 ACTGACCTACCTCAAAGGGC 4790
              ||||||||||||||||||||
Db         20 ACTGACCTACCTCAAAGGGC 1


RESULT 174
US-10-619-253-43/c
; Sequence 43, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-43

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4921 GCTGTCATTAGTCTATATGG 4940
              ||||||||||||||||||||
Db         20 GCTGTCATTAGTCTATATGG 1


RESULT 175
US-10-619-253-44/c
; Sequence 44, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-44

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5021 ATTGCCACGGAAACATACAG 5040
              ||||||||||||||||||||
Db         20 ATTGCCACGGAAACATACAG 1


RESULT 176
US-10-619-253-53/c
; Sequence 53, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 53
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-53

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        901 GCTGCTGATGTGCTTCATCC 920
              ||||||||||||||||||||
Db         20 GCTGCTGATGTGCTTCATCC 1


RESULT 177
US-10-619-253-54/c
; Sequence 54, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-54

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        936 CCTGGTATTTCTGGGGTGAA 955
              ||||||||||||||||||||
Db         20 CCTGGTATTTCTGGGGTGAA 1


RESULT 178
US-10-619-253-55/c
; Sequence 55, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-55

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1082 CGGGAGAATATCCTGGTTTC 1101
              ||||||||||||||||||||
Db         20 CGGGAGAATATCCTGGTTTC 1


RESULT 179
US-10-619-253-56/c
; Sequence 56, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-56

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1151 TATGACTACTCTGCCAGTGA 1170
              ||||||||||||||||||||
Db         20 TATGACTACTCTGCCAGTGA 1


RESULT 180
US-10-619-253-57/c
; Sequence 57, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 57
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-57

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1261 CGCCATCTTGGCCAGGATTA 1280
              ||||||||||||||||||||
Db         20 CGCCATCTTGGCCAGGATTA 1


RESULT 181
US-10-619-253-58/c
; Sequence 58, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-58

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1401 CAGGATGCTAAAGATGATGA 1420
              ||||||||||||||||||||
Db         20 CAGGATGCTAAAGATGATGA 1


RESULT 182
US-10-619-253-59/c
; Sequence 59, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-59

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1601 AGCAGCTGGTCAGTCTTTGC 1620
              ||||||||||||||||||||
Db         20 AGCAGCTGGTCAGTCTTTGC 1


RESULT 183
US-10-619-253-60/c
; Sequence 60, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 60
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-60

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1748 ACAGAATCTTCTGGGTAGTC 1767
              ||||||||||||||||||||
Db         20 ACAGAATCTTCTGGGTAGTC 1


RESULT 184
US-10-619-253-61/c
; Sequence 61, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-61

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1881 GAATGTAAGGATGAGGGAAG 1900
              ||||||||||||||||||||
Db         20 GAATGTAAGGATGAGGGAAG 1


RESULT 185
US-10-619-253-62/c
; Sequence 62, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
```

```
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-62

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1985 CCTTTCTCTCCTGGCTCGGG 2004
              ||||||||||||||||||||
Db         20 CCTTTCTCTCCTGGCTCGGG 1


RESULT 186
US-10-619-253-63/c
; Sequence 63, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 63
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-63

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2102 AGTGGTCTCTGCTGGGGAAG 2121
              ||||||||||||||||||||
Db         20 AGTGGTCTCTGCTGGGGAAG 1


RESULT 187
US-10-619-253-64/c
; Sequence 64, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-64

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2281 TGCCATCTTCAGGATATTGG 2300
              ||||||||||||||||||||
Db         20 TGCCATCTTCAGGATATTGG 1


RESULT 188
US-10-619-253-65/c
; Sequence 65, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-65

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2481 GAGAGGAGGAATTAGTTGGG 2500
              ||||||||||||||||||||
Db         20 GAGAGGAGGAATTAGTTGGG 1


RESULT 189
US-10-619-253-66/c
; Sequence 66, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 66
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-66

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATCTATA 2560
              ||||||||||||||||||||
```

```
Db         20 GCTGAGGGACAGGATCTATA 1


RESULT 190
US-10-619-253-67/c
; Sequence 67, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-67

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2631 ACTGAGTGAGTTATTGGGAG 2650
             ||||||||||||||||||||
Db         20 ACTGAGTGAGTTATTGGGAG 1


RESULT 191
US-10-619-253-68/c
; Sequence 68, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 68
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-68

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2826 GGCAGGGTTAGGAATCTCTT 2845
             ||||||||||||||||||||
Db         20 GGCAGGGTTAGGAATCTCTT 1


RESULT 192
US-10-619-253-69/c
; Sequence 69, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 69
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-69

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2941 CAGGCAGCCTCCTTTGTGTG 2960
             ||||||||||||||||||||
Db         20 CAGGCAGCCTCCTTTGTGTG 1


RESULT 193
US-10-619-253-70/c
; Sequence 70, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-70

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3051 AGTAGAGCTAGCTGCCACTT 3070
             ||||||||||||||||||||
Db         20 AGTAGAGCTAGCTGCCACTT 1


RESULT 194
US-10-619-253-71/c
; Sequence 71, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 71
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-71

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3321 CTGCTTACTTGGTGAGGGTG 3340
              ||||||||||||||||||||
Db         20 CTGCTTACTTGGTGAGGGTG 1
```

```
RESULT 195
US-10-619-253-72/c
; Sequence 72, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 72
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-72

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3401 GTTCTCACTGGGAAGAAGCA 3420
              ||||||||||||||||||||
Db         20 GTTCTCACTGGGAAGAAGCA 1
```

```
RESULT 196
US-10-619-253-73/c
; Sequence 73, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 73
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-73

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3941 TCATCAGATGCCTGCTTGAT 3960
              ||||||||||||||||||||
Db         20 TCATCAGATGCCTGCTTGAT 1
```

```
RESULT 197
US-10-619-253-74/c
; Sequence 74, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 74
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-74

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4052 ATGGCACCTCAGGCTGAGGG 4071
              ||||||||||||||||||||
Db         20 ATGGCACCTCAGGCTGAGGG 1
```

```
RESULT 198
US-10-619-253-75/c
; Sequence 75, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-75

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4357 GGGCCTGAGTGGAGGATTAT 4376
              ||||||||||||||||||||
Db         20 GGGCCTGAGTGGAGGATTAT 1
```

```
RESULT 199
US-10-619-253-76/c
; Sequence 76, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
```

```
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 76
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-76

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4431 AGGGCTGCTTTTCTTAAGTG 4450
              ||||||||||||||||||||
Db         20 AGGGCTGCTTTTCTTAAGTG 1


RESULT 200
US-10-619-253-77/c
; Sequence 77, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 77
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-77

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4681 ACTGTGCCACTGACTTGCTG 4700
              ||||||||||||||||||||
Db         20 ACTGTGCCACTGACTTGCTG 1


RESULT 201
US-10-619-253-78/c
; Sequence 78, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 78
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-78

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4971 GAAGCGGTGGATAACTAGCC 4990
              ||||||||||||||||||||
Db         20 GAAGCGGTGGATAACTAGCC 1


RESULT 202
US-10-619-253-79/c
; Sequence 79, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-79

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5044 ATGCCTTTTCTGTGATTGGG 5063
              ||||||||||||||||||||
Db         20 ATGCCTTTTCTGTGATTGGG 1


RESULT 203
US-10-619-253-80/c
; Sequence 80, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-80

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5081 TTATGTGGGATATAGTAGTT 5100
              ||||||||||||||||||||
Db         20 TTATGTGGGATATAGTAGTT 1


RESULT 204
```

US-10-619-253-100/c
; Sequence 100, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-100

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1045 CTTCGGATATCGTCCTTATG 1064
||||||||||||||||||||
Db 20 CTTCGGATATCGTCCTTATG 1

RESULT 205
US-10-619-253-101/c
; Sequence 101, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-101

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CAAGAGTGGCTGAGTTTGGG 1322
||||||||||||||||||||
Db 20 CAAGAGTGGCTGAGTTTGGG 1

RESULT 206
US-10-619-253-102/c
; Sequence 102, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-102

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1347 AACCAGCCAGGCAGAGGTTT 1366
||||||||||||||||||||
Db 20 AACCAGCCAGGCAGAGGTTT 1

RESULT 207
US-10-619-253-103/c
; Sequence 103, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 103
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-103

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 TAACTACTGAATAATGCTAC 1400
||||||||||||||||||||
Db 20 TAACTACTGAATAATGCTAC 1

RESULT 208
US-10-619-253-104/c
; Sequence 104, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 104
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-104

Query Match 0.5%; Score 20; DB 1; Length 20;

```
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1419 GATGTTAACCCATTCCAGTA 1438
              ||||||||||||||||||||
Db         20 GATGTTAACCCATTCCAGTA 1


RESULT 209
US-10-619-253-105/c
; Sequence 105, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 105
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-105

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1484 CCTTTATGATGCTAAGCTGA 1503
              ||||||||||||||||||||
Db         20 CCTTTATGATGCTAAGCTGA 1


RESULT 210
US-10-619-253-106/c
; Sequence 106, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 106
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-106

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1597 GGCAAGCAGCTGGTCAGTCT 1616
              ||||||||||||||||||||
Db         20 GGCAAGCAGCTGGTCAGTCT 1


RESULT 211
US-10-619-253-107/c
; Sequence 107, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 107
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-107

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1613 GTCTTTGCTCAGTGTCCAGC 1632
              ||||||||||||||||||||
Db         20 GTCTTTGCTCAGTGTCCAGC 1


RESULT 212
US-10-619-253-108/c
; Sequence 108, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 108
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-108

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1620 CTCAGTGTCCAGCTTCCAAA 1639
              ||||||||||||||||||||
Db         20 CTCAGTGTCCAGCTTCCAAA 1


RESULT 213
US-10-619-253-109/c
; Sequence 109, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
```

```
; SEQ ID NO 109
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-109

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1668 CGAATGGTCTTTGCTCCAGA 1687
              ||||||||||||||||||||
Db         20 CGAATGGTCTTTGCTCCAGA 1


RESULT 214
US-10-619-253-110/c
; Sequence 110, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-110

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1704 AGCTGTTGTGAGCTTTGAAG 1723
              ||||||||||||||||||||
Db         20 AGCTGTTGTGAGCTTTGAAG 1


RESULT 215
US-10-619-253-111/c
; Sequence 111, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 111
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-111

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1711 GTGAGCTTTGAAGTAGGTGG 1730
              ||||||||||||||||||||
Db         20 GTGAGCTTTGAAGTAGGTGG 1


RESULT 216
US-10-619-253-112/c
; Sequence 112, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 112
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-112

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1716 CTTTGAAGTAGGTGGCTTGA 1735
              ||||||||||||||||||||
Db         20 CTTTGAAGTAGGTGGCTTGA 1


RESULT 217
US-10-619-253-113/c
; Sequence 113, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 113
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-113

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1723 GTAGGTGGCTTGAGCTAGAG 1742
              ||||||||||||||||||||
Db         20 GTAGGTGGCTTGAGCTAGAG 1


RESULT 218
US-10-619-253-114/c
; Sequence 114, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
```

; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-114

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1814 AAGCAACTTCATTTGACACA 1833
||||||||||||||||||||
Db 20 AAGCAACTTCATTTGACACA 1

RESULT 219
US-10-619-253-115/c
; Sequence 115, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-115

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1842 AAAGCAGGTAAATTGTCGGG 1861
||||||||||||||||||||
Db 20 AAAGCAGGTAAATTGTCGGG 1

RESULT 220
US-10-619-253-116/c
; Sequence 116, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-116

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1869 GTTAGCATGTATGAATGTAA 1888
||||||||||||||||||||
Db 20 GTTAGCATGTATGAATGTAA 1

RESULT 221
US-10-619-253-117/c
; Sequence 117, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 117
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-117

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1915 CCTCTCGCCATGATCAGACA 1934
||||||||||||||||||||
Db 20 CCTCTCGCCATGATCAGACA 1

RESULT 222
US-10-619-253-118/c
; Sequence 118, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-118

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1969 ACCACATAGCATGCTTCCTT 1988

```
                    ||||||||||||||||||||
Db          20 ACCACATAGCATGCTTCCTT 1


RESULT 223
US-10-619-253-119/c
; Sequence 119, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 119
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-119

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1976 AGCATGCTTCCTTTCTCTCC 1995
                ||||||||||||||||||||
Db          20 AGCATGCTTCCTTTCTCTCC 1


RESULT 224
US-10-619-253-120/c
; Sequence 120, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 120
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-120

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2040 CAATGCCGCAACATATAGTT 2059
                ||||||||||||||||||||
Db          20 CAATGCCGCAACATATAGTT 1


RESULT 225
US-10-619-253-121/c
; Sequence 121, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 121
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-121

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2781 GGGGTCTCTGTTAACATCTA 2800
                ||||||||||||||||||||
Db          20 GGGGTCTCTGTTAACATCTA 1


RESULT 226
US-10-619-253-122/c
; Sequence 122, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 122
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-122

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2839 ATCTCTTCACTACCCTGATT 2858
                ||||||||||||||||||||
Db          20 ATCTCTTCACTACCCTGATT 1


RESULT 227
US-10-619-253-123/c
; Sequence 123, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 123
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-123

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2859 CTTGATTCCTGGCTCTACCC 2878
              ||||||||||||||||||||
Db         20 CTTGATTCCTGGCTCTACCC 1


RESULT 228
US-10-619-253-124/c
; Sequence 124, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 124
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-124

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3020 AGGGTCACTGAACCACTGCT 3039
              ||||||||||||||||||||
Db         20 AGGGTCACTGAACCACTGCT 1


RESULT 229
US-10-619-253-125/c
; Sequence 125, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 125
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-125

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAAGTA 3054
              ||||||||||||||||||||
Db         20 CTGCTTCTCTTTTGAAAGTA 1


RESULT 230
US-10-619-253-126/c
; Sequence 126, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 126
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-126

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3056 AGCTAGCTGCCACTTTCACG 3075
              ||||||||||||||||||||
Db         20 AGCTAGCTGCCACTTTCACG 1


RESULT 231
US-10-619-253-127/c
; Sequence 127, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 127
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-127

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3122 ACTGATGGCTCAAGACAAGG 3141
              ||||||||||||||||||||
Db         20 ACTGATGGCTCAAGACAAGG 1


RESULT 232
US-10-619-253-128/c
; Sequence 128, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
```

```
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 128
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-128

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3132 CAAGACAAGGCTGGCAAACC 3151
             ||||||||||||||||||||
Db         20 CAAGACAAGGCTGGCAAACC 1


RESULT 233
US-10-619-253-129/c
; Sequence 129, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 129
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-129

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3222 GCGCTCATGTTGAGCCAGTG 3241
             ||||||||||||||||||||
Db         20 GCGCTCATGTTGAGCCAGTG 1


RESULT 234
US-10-619-253-130/c
; Sequence 130, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 130
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-130

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3238 AGTGGGCCAGCCACAGAGCA 3257
             ||||||||||||||||||||
Db         20 AGTGGGCCAGCCACAGAGCA 1


RESULT 235
US-10-619-253-131/c
; Sequence 131, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 131
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-131

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3252 AGAGCAAAAGAGGGTTTATT 3271
             ||||||||||||||||||||
Db         20 AGAGCAAAAGAGGGTTTATT 1


RESULT 236
US-10-619-253-132/c
; Sequence 132, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 132
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-132

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3259 AAGAGGGTTTATTTTCAGTC 3278
             ||||||||||||||||||||
Db         20 AAGAGGGTTTATTTTCAGTC 1
```

RESULT 237
US-10-619-253-133/c
; Sequence 133, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-133

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3342 CCCGCCTGAGTCAGTGCTCT 3361
||||||||||||||||||||
Db 20 CCCGCCTGAGTCAGTGCTCT 1

RESULT 238
US-10-619-253-134/c
; Sequence 134, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 134
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-134

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3357 GCTCTCAGCTGGCAGTGCAA 3376
||||||||||||||||||||
Db 20 GCTCTCAGCTGGCAGTGCAA 1

RESULT 239
US-10-619-253-135/c
; Sequence 135, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-135

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3371 GTGCAATGCTTGTAGAAGTA 3390
||||||||||||||||||||
Db 20 GTGCAATGCTTGTAGAAGTA 1

RESULT 240
US-10-619-253-136/c
; Sequence 136, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-136

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3383 TAGAAGTAGGAGGAAACAGT 3402
||||||||||||||||||||
Db 20 TAGAAGTAGGAGGAAACAGT 1

RESULT 241
US-10-619-253-137/c
; Sequence 137, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-137

```
  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3409 TGGGAAGAAGCAAGGGCAAG 3428
              ||||||||||||||||||||
Db         20 TGGGAAGAAGCAAGGGCAAG 1


RESULT 242
US-10-619-253-138/c
; Sequence 138, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 138
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-138

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3432 CCAAGTGCCTCACCTCGAAA 3451
              ||||||||||||||||||||
Db         20 CCAAGTGCCTCACCTCGAAA 1


RESULT 243
US-10-619-253-139/c
; Sequence 139, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 139
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-139

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3480 AACTGCAAAGCTTTGGCTGA 3499
              ||||||||||||||||||||
Db         20 AACTGCAAAGCTTTGGCTGA 1


RESULT 244
US-10-619-253-140/c
; Sequence 140, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 140
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-140

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3655 GCTCAGTCATCAAAGCAGAA 3674
              ||||||||||||||||||||
Db         20 GCTCAGTCATCAAAGCAGAA 1


RESULT 245
US-10-619-253-141/c
; Sequence 141, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 141
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-141

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2052 ATATAGTTGAGGCCGAGGAT 2071
              ||||||||||||||||||||
Db         20 ATATAGTTGAGGCCGAGGAT 1


RESULT 246
US-10-619-253-142/c
; Sequence 142, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
```

```
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 142
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-142

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2136 TTTTTCTTTAATAACAAGGA 2155
              ||||||||||||||||||||
Db         20 TTTTTCTTTAATAACAAGGA 1


RESULT 247
US-10-619-253-143/c
; Sequence 143, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 143
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-143

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2146 ATAACAAGGAGATTTCTTAG 2165
              ||||||||||||||||||||
Db         20 ATAACAAGGAGATTTCTTAG 1


RESULT 248
US-10-619-253-144/c
; Sequence 144, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 144
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-144

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2162 TTAGTTCATATATCAAGAAG 2181
              ||||||||||||||||||||
Db         20 TTAGTTCATATATCAAGAAG 1


RESULT 249
US-10-619-253-145/c
; Sequence 145, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 145
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-145

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 ATATCAAGAAGTCTTGAAGT 2190
              ||||||||||||||||||||
Db         20 ATATCAAGAAGTCTTGAAGT 1


RESULT 250
US-10-619-253-146/c
; Sequence 146, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 146
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-146

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2214 AACAGCAGCTCATGGAATTT 2233
              ||||||||||||||||||||
Db         20 AACAGCAGCTCATGGAATTT 1


RESULT 251
US-10-619-253-147/c
; Sequence 147, Application US/10619253
; Publication No. US20050043256A1
```

; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-147

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2245 TGAGCTGCTCATTACAGTTC 2264
||||||||||||||||||||
Db 20 TGAGCTGCTCATTACAGTTC 1

RESULT 252
US-10-619-253-148/c
; Sequence 148, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 148
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-148

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2272 TTTCTGCTCTGCCATCTTCA 2291
||||||||||||||||||||
Db 20 TTTCTGCTCTGCCATCTTCA 1

RESULT 253
US-10-619-253-149/c
; Sequence 149, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 149
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-149

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2321 AGATGGCTGTGGCATTTCCA 2340
||||||||||||||||||||
Db 20 AGATGGCTGTGGCATTTCCA 1

RESULT 254
US-10-619-253-150/c
; Sequence 150, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-150

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2361 GATTTAAGGAGGTGAAGTCG 2380
||||||||||||||||||||
Db 20 GATTTAAGGAGGTGAAGTCG 1

RESULT 255
US-10-619-253-151/c
; Sequence 151, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 151
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-151

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2397 TATATACATATATACATTGC 2416
              ||||||||||||||||||||
Db         20 TATATACATATATACATTGC 1


RESULT 256
US-10-619-253-152/c
; Sequence 152, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 152
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-152

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2506 AATTTCCTCTCCACTGCTGG 2525
              ||||||||||||||||||||
Db         20 AATTTCCTCTCCACTGCTGG 1


RESULT 257
US-10-619-253-153/c
; Sequence 153, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 153
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-153

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2525 GACATGAGATGGAGAGGCTG 2544
              ||||||||||||||||||||
Db         20 GACATGAGATGGAGAGGCTG 1


RESULT 258
US-10-619-253-154/c
; Sequence 154, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 154
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-154

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2570 TAAGAGCGAACTTCACATAG 2589
              ||||||||||||||||||||
Db         20 TAAGAGCGAACTTCACATAG 1


RESULT 259
US-10-619-253-155/c
; Sequence 155, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 155
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-155

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2589 GGAAGGGATCTGAGAACACG 2608
              ||||||||||||||||||||
Db         20 GGAAGGGATCTGAGAACACG 1


RESULT 260
US-10-619-253-156/c
; Sequence 156, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 156
;   LENGTH: 20
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-156

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2676 GGTCCATTCATTAATTAGTT 2695
              ||||||||||||||||||||
Db         20 GGTCCATTCATTAATTAGTT 1


RESULT 261
US-10-619-253-157/c
; Sequence 157, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 157
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-157

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2700 TTTCTCCTTGAAATGAGTAA 2719
              ||||||||||||||||||||
Db         20 TTTCTCCTTGAAATGAGTAA 1


RESULT 262
US-10-619-253-158/c
; Sequence 158, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 158
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-158

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2715 AGTAAAAACTAGAAGGCTTC 2734
              ||||||||||||||||||||
Db         20 AGTAAAAACTAGAAGGCTTC 1


RESULT 263
US-10-619-253-159/c
; Sequence 159, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 159
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-159

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2726 GAAGGCTTCTCTCCACAGTG 2745
              ||||||||||||||||||||
Db         20 GAAGGCTTCTCTCCACAGTG 1


RESULT 264
US-10-619-253-160/c
; Sequence 160, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 160
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-160

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2732 TTCTCTCCACAGTGTTGTGC 2751
              ||||||||||||||||||||
Db         20 TTCTCTCCACAGTGTTGTGC 1


RESULT 265
US-10-619-253-161/c
; Sequence 161, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
```

```
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 161
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-161

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3679 GGCTTTGCTCTATTAAGATT 3698
             ||||||||||||||||||||
Db         20 GGCTTTGCTCTATTAAGATT 1


RESULT 266
US-10-619-253-162/c
; Sequence 162, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 162
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-162

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3707 ACACTACCAAACACTCAGTC 3726
             ||||||||||||||||||||
Db         20 ACACTACCAAACACTCAGTC 1


RESULT 267
US-10-619-253-163/c
; Sequence 163, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 163
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-163

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3771 GTGTTAATTGCGTAGAGGCT 3790
             ||||||||||||||||||||
Db         20 GTGTTAATTGCGTAGAGGCT 1


RESULT 268
US-10-619-253-164/c
; Sequence 164, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 164
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-164

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3825 TTTTGAGCTATTCACCTCAG 3844
             ||||||||||||||||||||
Db         20 TTTTGAGCTATTCACCTCAG 1


RESULT 269
US-10-619-253-165/c
; Sequence 165, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 165
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-165

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3834 ATTCACCTCAGTAGAAAAGG 3853
             ||||||||||||||||||||
Db         20 ATTCACCTCAGTAGAAAAGG 1
```

```
RESULT 270
US-10-619-253-166/c
; Sequence 166, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 166
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-166

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3911 AATGTCTGCTGGTATTTCTA 3930
             ||||||||||||||||||||
Db         20 AATGTCTGCTGGTATTTCTA 1


RESULT 271
US-10-619-253-167/c
; Sequence 167, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 167
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-167

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3993 TTCCTATTGTAATCGTGTGC 4012
             ||||||||||||||||||||
Db         20 TTCCTATTGTAATCGTGTGC 1


RESULT 272
US-10-619-253-168/c
; Sequence 168, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 168
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-168

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3999 TTGTAATCGTGTGCCATGGA 4018
             ||||||||||||||||||||
Db         20 TTGTAATCGTGTGCCATGGA 1


RESULT 273
US-10-619-253-169/c
; Sequence 169, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 169
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-169

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4004 ATCGTGTGCCATGGATCTGA 4023
             ||||||||||||||||||||
Db         20 ATCGTGTGCCATGGATCTGA 1


RESULT 274
US-10-619-253-170/c
; Sequence 170, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 170
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-170
```

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4041 CATAAGGCTGGATGGCACCT 4060
              ||||||||||||||||||||
Db         20 CATAAGGCTGGATGGCACCT 1
```

RESULT 275
US-10-619-253-171/c
; Sequence 171, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 171
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-171

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4053 TGGCACCTCAGGCTGAGGGC 4072
              ||||||||||||||||||||
Db         20 TGGCACCTCAGGCTGAGGGC 1
```

RESULT 276
US-10-619-253-172/c
; Sequence 172, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 172
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-172

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4132 ATTTTCAAGATTCTAAAGCT 4151
              ||||||||||||||||||||
Db         20 ATTTTCAAGATTCTAAAGCT 1
```

RESULT 277
US-10-619-253-173/c
; Sequence 173, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 173
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-173

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4150 CTCAATTCAAGTGACACATT 4169
              ||||||||||||||||||||
Db         20 CTCAATTCAAGTGACACATT 1
```

RESULT 278
US-10-619-253-174/c
; Sequence 174, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 174
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-174

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4193 AGAGTCCGGATTTCTAACAG 4212
              ||||||||||||||||||||
Db         20 AGAGTCCGGATTTCTAACAG 1
```

RESULT 279
US-10-619-253-175/c
; Sequence 175, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187

```
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 175
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-175

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4205 TCTAACAGTCCCTGCTTTGG 4224
             ||||||||||||||||||||
Db         20 TCTAACAGTCCCTGCTTTGG 1


RESULT 280
US-10-619-253-176/c
; Sequence 176, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 176
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-176

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4261 CTTTTCTAATCACAGTGTTG 4280
             ||||||||||||||||||||
Db         20 CTTTTCTAATCACAGTGTTG 1


RESULT 281
US-10-619-253-177/c
; Sequence 177, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 177
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-177

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4321 CACCTGAGACCCTACTGAAG 4340
             ||||||||||||||||||||
Db         20 CACCTGAGACCCTACTGAAG 1


RESULT 282
US-10-619-253-178/c
; Sequence 178, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 178
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-178

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4331 CCTACTGAAGTGGCTGGTAG 4350
             ||||||||||||||||||||
Db         20 CCTACTGAAGTGGCTGGTAG 1


RESULT 283
US-10-619-253-179/c
; Sequence 179, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 179
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-179

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4347 GTAGAAAAAGGGGCCTGAGT 4366
             ||||||||||||||||||||
Db         20 GTAGAAAAAGGGGCCTGAGT 1


RESULT 284
US-10-619-253-180/c
; Sequence 180, Application US/10619253
```

```
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 180
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-180

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4364 AGTGGAGGATTATCAGTATC 4383
             ||||||||||||||||||||
Db         20 AGTGGAGGATTATCAGTATC 1


RESULT 285
US-10-619-253-181/c
; Sequence 181, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 181
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-181

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4379 GTATCACGATTTGCAGGATT 4398
             ||||||||||||||||||||
Db         20 GTATCACGATTTGCAGGATT 1


RESULT 286
US-10-619-253-182/c
; Sequence 182, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 182
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-182

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4420 AAACTTTTGTTAGGGCTGCT 4439
             ||||||||||||||||||||
Db         20 AAACTTTTGTTAGGGCTGCT 1


RESULT 287
US-10-619-253-183/c
; Sequence 183, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 183
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-183

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4535 GCATTTAAAATGGAAAATTT 4554
             ||||||||||||||||||||
Db         20 GCATTTAAAATGGAAAATTT 1


RESULT 288
US-10-619-253-184/c
; Sequence 184, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 184
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-184

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4578 GGGTGTATTCTCTGTAAGTG 4597
              ||||||||||||||||||||
Db         20 GGGTGTATTCTCTGTAAGTG 1


RESULT 289
US-10-619-253-185/c
; Sequence 185, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 185
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-185

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4584 ATTCTCTGTAAGTGTAGCTC 4603
              ||||||||||||||||||||
Db         20 ATTCTCTGTAAGTGTAGCTC 1


RESULT 290
US-10-619-253-186/c
; Sequence 186, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 186
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-186

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4628 AAAAGCGAGGTGGCCATGTT 4647
              ||||||||||||||||||||
Db         20 AAAAGCGAGGTGGCCATGTT 1


RESULT 291
US-10-619-253-187/c
; Sequence 187, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 187
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-187

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4645 GTTATGCTGGTGGTTAAGGC 4664
              ||||||||||||||||||||
Db         20 GTTATGCTGGTGGTTAAGGC 1


RESULT 292
US-10-619-253-188/c
; Sequence 188, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 188
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-188

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4653 GGTGGTTAAGGCCAGGGCCT 4672
              ||||||||||||||||||||
Db         20 GGTGGTTAAGGCCAGGGCCT 1


RESULT 293
US-10-619-253-189/c
; Sequence 189, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 189
;   LENGTH: 20
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-189

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4658 TTAAGGCCAGGGCCTCTCCA 4677
              ||||||||||||||||||||
Db         20 TTAAGGCCAGGGCCTCTCCA 1


RESULT 294
US-10-619-253-190/c
; Sequence 190, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 190
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-190

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4786 AGGGCAGTTTTGAGGCATGA 4805
              ||||||||||||||||||||
Db         20 AGGGCAGTTTTGAGGCATGA 1


RESULT 295
US-10-619-253-191/c
; Sequence 191, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 191
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-191

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4800 GCATGACTAATGCTTTTTAG 4819
              ||||||||||||||||||||
Db         20 GCATGACTAATGCTTTTTAG 1


RESULT 296
US-10-619-253-192/c
; Sequence 192, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 192
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-192

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4834 TCCTTCAGCACAGGAATTCT 4853
              ||||||||||||||||||||
Db         20 TCCTTCAGCACAGGAATTCT 1


RESULT 297
US-10-619-253-193/c
; Sequence 193, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 193
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-193

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4841 GCACAGGAATTCTCAAGACC 4860
              ||||||||||||||||||||
Db         20 GCACAGGAATTCTCAAGACC 1


RESULT 298
US-10-619-253-194/c
; Sequence 194, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
```

```
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 194
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-194

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4846 GGAATTCTCAAGACCTGAGT 4865
             ||||||||||||||||||||
Db         20 GGAATTCTCAAGACCTGAGT 1


RESULT 299
US-10-619-253-195/c
; Sequence 195, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 195
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-195

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4868 TTTTTATAATAGGAATGTCC 4887
             ||||||||||||||||||||
Db         20 TTTTTATAATAGGAATGTCC 1


RESULT 300
US-10-619-253-196/c
; Sequence 196, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 196
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-196

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4892 TGAACTTGATACGTCCGTGT 4911
             ||||||||||||||||||||
Db         20 TGAACTTGATACGTCCGTGT 1


RESULT 301
US-10-619-253-197/c
; Sequence 197, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 197
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-197

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5024 GCCACGGAAACATACAGAGG 5043
             ||||||||||||||||||||
Db         20 GCCACGGAAACATACAGAGG 1


RESULT 302
US-10-619-253-251/c
; Sequence 251, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 251
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-251

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1158 ACTCTGCCAGTGAGTACCGC 1177
             ||||||||||||||||||||
Db         20 ACTCTGCCAGTGAGTACCGC 1
```

RESULT 303
US-10-619-253-252/c
; Sequence 252, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 252
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-252

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1176 GCTGGCACATCAACTTCACC 1195
||||||||||||||||||||
Db 20 GCTGGCACATCAACTTCACC 1

RESULT 304
US-10-619-253-383/c
; Sequence 383, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 383
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-383

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 902 CTGCTGATGTGCTTCATCCT 921
||||||||||||||||||||
Db 20 CTGCTGATGTGCTTCATCCT 1

RESULT 305
US-10-619-253-384/c
; Sequence 384, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 384
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-384

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 911 TGCTTCATCCTGCCCACGCT 930
||||||||||||||||||||
Db 20 TGCTTCATCCTGCCCACGCT 1

RESULT 306
US-10-619-253-389/c
; Sequence 389, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 389
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-389

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1013 GCCACCTGGCTGGTGAACAG 1032
||||||||||||||||||||
Db 20 GCCACCTGGCTGGTGAACAG 1

RESULT 307
US-10-619-253-392/c
; Sequence 392, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 392
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-619-253-392

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1118 GAGGGCTTCCACAACTACCA 1137
              ||||||||||||||||||||
Db         20 GAGGGCTTCCACAACTACCA 1
```

RESULT 308
US-10-619-253-393/c
; Sequence 393, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 393
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-393

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1154 GACTACTCTGCCAGTGAGTA 1173
              ||||||||||||||||||||
Db         20 GACTACTCTGCCAGTGAGTA 1
```

RESULT 309
US-10-619-253-394/c
; Sequence 394, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-394

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1159 CTCTGCCAGTGAGTACCGCT 1178
              ||||||||||||||||||||
Db         20 CTCTGCCAGTGAGTACCGCT 1
```

RESULT 310
US-10-619-253-395/c
; Sequence 395, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 395
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-395

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1164 CCAGTGAGTACCGCTGGCAC 1183
              ||||||||||||||||||||
Db         20 CCAGTGAGTACCGCTGGCAC 1
```

RESULT 311
US-10-619-253-396/c
; Sequence 396, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 396
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-396

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1169 GAGTACCGCTGGCACATCAA 1188
              ||||||||||||||||||||
Db         20 GAGTACCGCTGGCACATCAA 1
```

RESULT 312
US-10-619-253-397/c
; Sequence 397, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15

```
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 397
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-397

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1178 TGGCACATCAACTTCACCAC 1197
              ||||||||||||||||||||
Db         20 TGGCACATCAACTTCACCAC 1


RESULT 313
US-10-349-143-11421/c
; Sequence 11421, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11421
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..21
;   OTHER INFORMATION: downstream amplification primer 99-5747 for SEQ 3556, in compleme
US-10-349-143-11421

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 75;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4688 CACTGACTTGCTGTGTGACCC 4708
              || ||||||||||||||||||
Db         21 CATTGACTTGCTGTGTGACCC 1


RESULT 314
US-10-619-253-391/c
; Sequence 391, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 391
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-391

  Query Match             0.4%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1080 CCCGGGAGAATATCCTGGT 1098
              |||||||||||||||||||
Db         19 CCCGGGAGAATATCCTGGT 1


RESULT 315
US-10-708-204-928/c
; Sequence 928, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 928
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-708-204-928

  Query Match             0.4%;  Score 18.8;  DB 1;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4698 CTGTGTGACCCTGGGCAAGTCA 4719
              |||||||||||| ||||||| |
Db         22 CTGTGTGACCCTAGGCAAGTGA 1


RESULT 316
US-10-708-204-1661/c
; Sequence 1661, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1661
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-708-204-1661

  Query Match             0.4%;  Score 18.8;  DB 1;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4698 CTGTGTGACCCTGGGCAAGTCA 4719
              |||||||||||| ||||||| |
```

```
Db         22 CTGTGTGACCCTAGGCAAGTGA 1


RESULT 317
US-10-708-204-2379/c
; Sequence 2379, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2379
;   LENGTH: 22
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-708-204-2379

  Query Match             0.4%;  Score 18.8;  DB 1;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4698 CTGTGTGACCCTGGGCAAGTCA 4719
             |||||||||||| ||||||| |
Db         22 CTGTGTGACCCTAGGCAAGTGA 1


RESULT 318
US-10-619-253-249/c
; Sequence 249, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 249
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-249

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1116 GTGAGGGCTTCCACAACTAC 1135
              | ||||||||||||||||||
Db         20 GCGAGGGCTTCCACAACTAC 1


RESULT 319
US-10-619-253-390/c
; Sequence 390, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 390
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-390

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TGGCTGGTGAACAGTGCTGC 1038
              |||||||||||||||||| ||
Db         20 TGGCTGGTGAACAGTGCCGC 1


RESULT 320
US-10-619-253-398/c
; Sequence 398, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 398
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-398

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 1.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1184 ATCAACTTCACCACATTCTT 1203
              |||||||||||||| |||||
Db         20 ATCAACTTCACCACGTTCTT 1


RESULT 321
US-10-108-732-42/c
; Sequence 42, Application US/10108732
; Publication No. US20030175721A1
; GENERAL INFORMATION:
;  APPLICANT: Box, Neil F
;  APPLICANT:  Duffy, David L
;  APPLICANT:  Hayward, Nicholas K
;  APPLICANT:  Martin, Nicholas G
;  APPLICANT:  Sturm, Richard A
;  APPLICANT:  Gruis, Nelleke A
;  APPLICANT:  Van Der Velden, Pieter
;  APPLICANT:  Bergman, Wilma
;  APPLICANT:  Frants, Rune R
;  TITLE OF INVENTION: MELANOMA RISK DETECTION
;  FILE REFERENCE: 8795-27U1
;  CURRENT APPLICATION NUMBER: US/10/108,732
;  CURRENT FILING DATE:  2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/279,515
;  PRIOR FILING DATE: 2001-03-28
;  NUMBER OF SEQ ID NOS: 76
```

```
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: hMSHR C-inner
US-10-108-732-42

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4695 TTGCTGTGTGACCCTGGGCA 4714
              || ||||||||||||||||||
Db         20 TTCCTGTGTGACCCTGGGCA 1


RESULT 322
US-10-270-839-75/c
; Sequence 75, Application US/10270839
; Publication No. US20030143586A1
; GENERAL INFORMATION:
;  APPLICANT: Chao, Qimin
;  APPLICANT:  Grasso, Luigi
;  APPLICANT:  Sass, Philip M.
;  APPLICANT:  Nicolaides, Nicholas  C.
;  TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagnosi
;  FILE REFERENCE: AG0002US (MOR-0133)
;  CURRENT APPLICATION NUMBER: US/10/270,839
;  CURRENT FILING DATE:  2002-10-11
;  PRIOR APPLICATION NUMBER: 60/328,750
;  PRIOR FILING DATE: 2001-10-12
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (22)..(22)
;   OTHER INFORMATION: B is C or G or T/U, not A
US-10-270-839-75

  Query Match             0.4%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTCTC 3201
              :|||||||||| ||| |||||||
Db         22 VCTCTCTCTCTCTCTCTCTCTC 1


RESULT 323
US-09-776-479-908
; Sequence 908, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 908
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-908

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTCTC 21


RESULT 324
US-09-776-479-908
; Sequence 908, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 908
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-908

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1.6e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTCTC 21


RESULT 325
US-10-112-653-877
; Sequence 877, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 877
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
```

US-10-112-653-877

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 326
US-10-017-995-908
; Sequence 908, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 908
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-908

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 327
US-10-314-578-908
; Sequence 908, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 908
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-908

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 328
US-10-766-590-4/c
; Sequence 4, Application US/10766590
; Publication No. US20040180370A1
; GENERAL INFORMATION:
; APPLICANT: Tabakoff, Boris
; APPLICANT: Martinez, Larry
; APPLICANT: Hoffman, Paula
; TITLE OF INVENTION: Genetic Diagnosis of Alcoholic Subtypes
; FILE REFERENCE: UTC-08617
; CURRENT APPLICATION NUMBER: US/10/766,590
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 60/443,072
; PRIOR FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-766-590-4

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 21 CTCTCTCTCTCTCTCTCTC 1

RESULT 329
US-10-831-778-908
; Sequence 908, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 908
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-908

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 330
US-10-893-010-239/c

```
; Sequence 239, Application US/10893010
; Publication No. US20050164224A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Thompson, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
;  TITLE OF INVENTION:  Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/170 (MBHB02-1005-C)
;  CURRENT APPLICATION NUMBER: US/10/893,010
;  CURRENT FILING DATE:  2004-07-16
;  PRIOR APPLICATION NUMBER: PCT/US 03/03662
;  PRIOR FILING DATE: 2003-02-06
;  PRIOR APPLICATION NUMBER: US 60/411,275
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-03
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 526
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-893-010-239

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
                ||||||||||||||| ||||
Db         19 TTTTTTTTTTTTTTGGGGT 1


RESULT 331
US-10-893-010-478
; Sequence 478, Application US/10893010
; Publication No. US20050164224A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Thompson, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
;  TITLE OF INVENTION:  Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/170 (MBHB02-1005-C)
;  CURRENT APPLICATION NUMBER: US/10/893,010
;  CURRENT FILING DATE:  2004-07-16
;  PRIOR APPLICATION NUMBER: PCT/US 03/03662
;  PRIOR FILING DATE: 2003-02-06
;  PRIOR APPLICATION NUMBER: US 60/411,275
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-03
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 526
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 478
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-893-010-478

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   15.8%;  Pred. No. 1.7e+02;
  Matches    3;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
                :::::::::::::::: |||:
Db          1 UUUUUUUUUUUUUUGGGGU 19


RESULT 332
US-09-263-959-849/c
; Sequence 849, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  849:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-849
```

```
  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2126 TTCTTTTCTTTTTTTCTTT 2144
              ||||||| ||||||||||
Db         20 TTCTTTTTTTTTTTTCTTT 2


RESULT 333
US-10-006-191-136
; Sequence 136, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIO
;  FILE REFERENCE: RTS-0274
;  CURRENT APPLICATION NUMBER: US/10/006,191
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 136
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-136

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2392 AAATATATATACATATATA 2410
              |||||||||||| |||||||
Db          2 AAATATATATATATATATA 20


RESULT 334
US-10-160-807-80
; Sequence 80, Application US/10160807
; Publication No. US20030224514A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
;  FILE REFERENCE: RTS-0189
;  CURRENT APPLICATION NUMBER: US/10/160,807
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-807-80

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db          2 CAGGCCCCTCTCTCTGGGT 20


RESULT 335
US-10-160-807-225/c
; Sequence 225, Application US/10160807
; Publication No. US20030224514A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
;  FILE REFERENCE: RTS-0189
;  CURRENT APPLICATION NUMBER: US/10/160,807
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 225
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-160-807-225

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db         19 CAGGCCCCTCTCTCTGGGT 1


RESULT 336
US-10-655-847-80
; Sequence 80, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
;  FILE REFERENCE: RTS-0189
;  CURRENT APPLICATION NUMBER: US/10/655,847
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: US/10/160,807
;  PRIOR FILING DATE: 2003-09-05
;  NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-80

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db          2 CAGGCCCCTCTCTCTGGGT 20


RESULT 337
US-10-655-847-225/c
; Sequence 225, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
;  FILE REFERENCE: RTS-0189
;  CURRENT APPLICATION NUMBER: US/10/655,847
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: US/10/160,807
;  PRIOR FILING DATE: 2003-09-05
;  NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 225
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-655-847-225

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db         19 CAGGCCCCTCTCTCTGGGT 1


RESULT 338
US-10-619-253-250/c
; Sequence 250, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 250
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-250

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1128 ACAACTACCACCACTCCTT 1146
              |||||||||||||||| ||||
Db         20 ACAACTACCACCACACCTT 2


RESULT 339
US-10-619-253-340/c
; Sequence 340, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 340
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-340

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5178 TTTGTTCATAATAAAAGTG 5196
              ||||||| ||||||||||| 
Db         19 TTTGTTCCTAATAAAAGTG 1


RESULT 340
US-10-619-253-385/c
; Sequence 385, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 385
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-385

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        924 CCACGCTTGTGCCCTGGTA 942
              ||||||| ||||||||||| 
Db         20 CCACGCTGGTGCCCTGGTA 2


RESULT 341
US-10-946-914-136
; Sequence 136, Application US/10946914
; Publication No. US20050059629A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Andrew T. Watt
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Mausumee Guha
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
;  FILE REFERENCE: 23546-9505US (RTS-0274US.P1)
;  CURRENT APPLICATION NUMBER: US/10/946,914
;  CURRENT FILING DATE:  2004-09-21
;  PRIOR APPLICATION NUMBER: US 10/006,191
;  PRIOR FILING DATE: 2001-12-10
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-946-914-136

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2392 AAATATATATACATATATA 2410
              |||||||||| |||||||
Db          2 AAATATATATATATATATA 20


RESULT 342
US-10-957-432-758/c
; Sequence 758, Application US/10957432
; Publication No. US20050208512A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: SADEE, WOLFGANG
;  APPLICANT:  HUANG, YING
;  TITLE OF INVENTION: DETERMINING THE CHEMOSENSITIVITY OF CELLS TO CYTOTOXIC AGENTS
;  FILE REFERENCE: 22727/04160
;  CURRENT APPLICATION NUMBER: US/10/957,432
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: 60/508,260
;  PRIOR FILING DATE: 2003-10-01
;  NUMBER OF SEQ ID NOS: 758
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 758
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic polynucleotide sequence
US-10-957-432-758

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3027 CTGAACCACTGCTTCTCTT 3045
                ||||||||||||||||| |||
Db         19 CTGAACCACTGCTTCGCTT 1


RESULT 343
US-09-788-362-3
; Sequence 3, Application US/09788362
; Patent No. US20020009731A1
; GENERAL INFORMATION:
;  APPLICANT: Muramatsu, Takamichi
;  APPLICANT:  Fujita, Takeshi
;  APPLICANT:  Kiyama, Masaharu
;  APPLICANT:  Irie, Takashi
;  TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
;  TITLE OF INVENTION:  EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
;  TITLE OF INVENTION:  NUCLEIC ACID SAMPLES THEREBY
;  FILE REFERENCE: NIT-129-03
;  CURRENT APPLICATION NUMBER: US/09/788,362
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: 09/313,637
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: JP 10-153651
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-788-362-3

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
                ||||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 344
US-09-090-672B-106
; Sequence 106, Application US/09090672B
; Patent No. US20020068707A1
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  106:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-106

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
                ||||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 345
US-09-788-338-3
; Sequence 3, Application US/09788338
; Patent No. US20020102561A1
; GENERAL INFORMATION:
;  APPLICANT: MURAMATSU, TAKAMICHI
;  APPLICANT:  FUJITA, TAKESHI
;  APPLICANT:  KIYAMA, MASAHARU
;  APPLICANT:  IRIE, TAKASHI
;  TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
;  TITLE OF INVENTION:  EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
;  TITLE OF INVENTION:  NUCLEIC ACID SAMPLES THEREBY
;  FILE REFERENCE: NIT-129-02
;  CURRENT APPLICATION NUMBER: US/09/788,338
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: 09/313,637
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: JP 10-153651
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-788-338-3

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 346
US-09-730-559B-108
; Sequence 108, Application US/09730559B
; Publication No. US20030207828A1
; GENERAL INFORMATION:
; APPLICANT: ISHIWATA, TETSUYOSHI
; APPLICANT: SAKURADA, MIKIKO
; APPLICANT: KAWABATA, AYAKO
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: NISHI, TATSUNARI
; APPLICANT: KUGA, TETSURO
; APPLICANT: SAWADA, SHIGEMASA
; APPLICANT: TAKEI, MASAMI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: FURUYA, AKIKO
; TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
; FILE REFERENCE: 766.21 CIP
; CURRENT APPLICATION NUMBER: US/09/730,559B
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
US-09-730-559B-108

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 347
US-10-220-373-9
; Sequence 9, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
; APPLICANT: NAGASU, Takeshi
; APPLICANT: OSHIDA, Tadahiro
; APPLICANT: OBAYASHI, Izumi
; APPLICANT: MATSUI, Keiko
; APPLICANT: SAITO, Hirohisa
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-010US
; CURRENT APPLICATION NUMBER: US/10/220,373
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-61832
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
; OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-9

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 348
US-10-339-793-185
; Sequence 185, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-185

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4832 GATCCTTCAGCACAGGA 4848
||||||||||||||||||
Db 1 GATCCTTCAGCACAGGA 17

RESULT 349
US-10-291-808-64
; Sequence 64, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-64

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

RESULT 350
US-10-380-255-8
; Sequence 8, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64935
; CURRENT APPLICATION NUMBER: US/10/380,255
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08247
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-293021
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-255-8

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

RESULT 351
US-10-380-254-5
; Sequence 5, Application US/10380254
; Publication No. US20040038252A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64773
; CURRENT APPLICATION NUMBER: US/10/380,254
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08246
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-291318
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-254-5

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

RESULT 352
US-10-398-885A-4
; Sequence 4, Application US/10398885A
; Publication No. US20040053282A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahasi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907
; CURRENT APPLICATION NUMBER: US/10/398,885A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-4

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

RESULT 353
US-10-398-877-20
; Sequence 20, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-20

Query Match 0.4%; Score 17; DB 1; Length 17;

```
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 354
US-10-239-734-5
; Sequence 5, Application US/10239734
; Publication No. US20040161746A1
; GENERAL INFORMATION:
;  APPLICANT: GENOX RESEARCH, INC.
;  APPLICANT:  JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR
;  APPLICANT:  CHILD HEALTH AND DEVELOPMENT
;  APPLICANT:  Matsumoto, Yoshiko
;  APPLICANT:  Tsujimoto, Gozoh
;  APPLICANT:  Nagasu, Takeshi
;  APPLICANT:  Sugita, Yuji
;  APPLICANT:  Oshida, Tadahiro
;  APPLICANT:  Imai, Yukiho
;  TITLE OF INVENTION: Method of Testing For Allergic Disease
;  FILE REFERENCE: SHIMIZU-07379
;  CURRENT APPLICATION NUMBER: US/10/239,734
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: PCT/JP01/11286
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 2000-389476 JP
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: "GT15G", an artificially synthesized primer sequence
US-10-239-734-5

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 355
US-10-608-863-5
; Sequence 5, Application US/10608863
; Publication No. US20040214192A1
; GENERAL INFORMATION:
;  APPLICANT: Hashida, Ryoichi
;  APPLICANT:  Kagaya, Shinji
;  APPLICANT:  Yayoi, Yoshihiro
;  APPLICANT:  Sugita, Yuji
;  APPLICANT:  Saito, Hirohisa
;  TITLE OF INVENTION: METHODS FOR EXAMINATION FOR ALLERGIC DISEASES, AND DRUGS FOR TREA
;  TITLE OF INVENTION:  ALLERGIC DISEASES
;  FILE REFERENCE: 3462.1003-000
;  CURRENT APPLICATION NUMBER: US/10/608,863
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: JP 2002-188490
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Artificially
;   OTHER INFORMATION: Synthesized Primer Sequence
US-10-608-863-5

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 356
US-09-005-243-32
; Sequence 32, Application US/09005243
; Patent No. US20020018763A1
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,243
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/449,653
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/34465
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  DNA
US-09-005-243-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 357
US-09-224-683-32
; Sequence 32, Application US/09224683
; Patent No. US20020031491A1
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor: Composition Claims
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/224,683
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/005,893
;      FILING DATE:  12-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/449,653
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/35136
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-224-683-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 358
US-10-164-915-1/c
; Sequence 1, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
;  APPLICANT: Salafsky, Joshua S.
;  TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optica
;  TITLE OF INVENTION:  for Detection of Interactions Involving a Conformational Change
;  FILE REFERENCE: 11100-035-999
;  CURRENT APPLICATION NUMBER: US/10/164,915
;  CURRENT FILING DATE:  2002-06-06
;  PRIOR APPLICATION NUMBER: 60/253,862
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/260,249
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/265,775
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: 60/278,941
;  PRIOR FILING DATE: 2001-01-27
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Aritificial Sequence: Oligonucleotide structure fo
;   OTHER INFORMATION: molecular beacon
US-10-164-915-1

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         17 AGTTTTTTTTTTTTTTT 1


RESULT 359
US-10-374-686-2/c
; Sequence 2, Application US/10374686
; Publication No. US20040002089A1
; GENERAL INFORMATION:
;  APPLICANT: Dubertret, Benoit
;  APPLICANT:  Calame, Michel
;  APPLICANT:  Libchaber, Albert
;  TITLE OF INVENTION: Methods Employing Fluorescent Quenching
;  TITLE OF INVENTION:  by Metal Surfaces
;  FILE REFERENCE: 600-1-260PCTUS
;  CURRENT APPLICATION NUMBER: US/10/374,686
;  CURRENT FILING DATE:  2003-02-26
;  PRIOR APPLICATION NUMBER: PCT/US01/41941
;  PRIOR FILING DATE: 2001-08-29
;  PRIOR APPLICATION NUMBER: 60/228728
;  PRIOR FILING DATE: 2000-08-29
;  PRIOR APPLICATION NUMBER: 60/280350
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 6
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```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-374-686-2

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         17 AGTTTTTTTTTTTTTTT 1


RESULT 360
US-10-671-395-558
; Sequence 558, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 558
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-558

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 361
US-10-671-395-616
; Sequence 616, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 616
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-616

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          2 TTTTTTTTTTTTTTTGG 18


RESULT 362
US-10-671-395-654
; Sequence 654, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 654
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-654

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 363
US-10-671-395-990
; Sequence 990, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 990
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-990

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
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```
                    ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTGG 17


RESULT 364
US-10-175-608-32
; Sequence 32, Application US/10175608
; Publication No. US20040181044A1
;   GENERAL INFORMATION:
;        APPLICANT: Zsebo, Krisztina M.
;                   Bosselman, Robert A.
;                   Suggs, Sidney V.
;                   Martin, Francis H.
;        TITLE OF INVENTION: Stem Cell Factor
;        NUMBER OF SEQUENCES: 104
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: United States of America
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/175,608
;             FILING DATE: 16-Oct-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/635,249
;             FILING DATE: 07-AUG-2000
;             APPLICATION NUMBER: 09/486,546
;             FILING DATE: 24-MAY-1995
;             APPLICATION NUMBER: 08/172,329
;             FILING DATE: 21-DEC-1993
;             APPLICATION NUMBER: 07/982,255
;             FILING DATE: 25-NOV-1992
;             APPLICATION NUMBER: 07/684,535
;             FILING DATE: 10-APR-1991
;             APPLICATION NUMBER: 09/589,701
;             FILING DATE: 10-OCT-1991
;             APPLICATION NUMBER: 07/573,616
;             FILING DATE: 24-AUG-1990
;             APPLICATION NUMBER: 07/537,198
;             FILING DATE: 11-JUN-1990
;             APPLICATION NUMBER: 07/422,383
;             FILING DATE: 16-OCT-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Clough, David W.
;             REGISTRATION NUMBER: 36,107
;             REFERENCE/DOCKET NUMBER: 01017/35199
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 32:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-175-608-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
```

```
                    ||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 365
US-10-620-642-32
; Sequence 32, Application US/10620642
; Publication No. US20050080250A1
;   GENERAL INFORMATION:
;        APPLICANT: Zsebo, Krisztina M.
;                   Bosselman, Robert A.
;                   Suggs, Sidney V.
;                   Martin, Francis H.
;        TITLE OF INVENTION: Stem Cell Factor
;        NUMBER OF SEQUENCES: 104
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: United States of America
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/620,642
;             FILING DATE: 16-Jul-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/175,608
;             FILING DATE: 16-Oct-2002
;             APPLICATION NUMBER: 09/635,249
;             FILING DATE: 07-AUG-2000
;             APPLICATION NUMBER: 09/486,546
;             FILING DATE: 24-MAY-1995
;             APPLICATION NUMBER: 08/172,329
;             FILING DATE: 21-DEC-1993
;             APPLICATION NUMBER: 07/982,255
;             FILING DATE: 25-NOV-1992
;             APPLICATION NUMBER: 07/684,535
;             FILING DATE: 10-APR-1991
;             APPLICATION NUMBER: 09/589,701
;             FILING DATE: 10-OCT-1991
;             APPLICATION NUMBER: 07/573,616
;             FILING DATE: 24-AUG-1990
;             APPLICATION NUMBER: 07/537,198
;             FILING DATE: 11-JUN-1990
;             APPLICATION NUMBER: 07/422,383
;             FILING DATE: 16-OCT-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Clough, David W.
;             REGISTRATION NUMBER: 36,107
;             REFERENCE/DOCKET NUMBER: 01017/35199
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 32:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-620-642-32

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 366
US-10-374-686-3/c
; Sequence 3, Application US/10374686
; Publication No. US20040002089A1
; GENERAL INFORMATION:
;  APPLICANT: Dubertret, Benoit
;  APPLICANT:  Calame, Michel
;  APPLICANT:  Libchaber, Albert
;  TITLE OF INVENTION: Methods Employing Fluorescent Quenching
;  TITLE OF INVENTION:  by Metal Surfaces
;  FILE REFERENCE: 600-1-260PCTUS
;  CURRENT APPLICATION NUMBER: US/10/374,686
;  CURRENT FILING DATE:  2003-02-26
;  PRIOR APPLICATION NUMBER: PCT/US01/41941
;  PRIOR FILING DATE: 2001-08-29
;  PRIOR APPLICATION NUMBER: 60/228728
;  PRIOR FILING DATE: 2000-08-29
;  PRIOR APPLICATION NUMBER: 60/280350
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-374-686-3

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         18 AGTTTTTTTTTTTTTTT 2


RESULT 367
US-09-725-265-31/c
; Sequence 31, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-31

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 368
US-09-752-639-40
; Sequence 40, Application US/09752639
; Patent No. US20020091243A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/752,639
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/10793
;      FILING DATE:
;      APPLICATION NUMBER:  09/081,385
;      FILING DATE:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-752-639-40

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20
```

```
RESULT 369
US-09-891-517-31/c
; Sequence 31, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-31

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 370
US-09-891-517-42
; Sequence 42, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-42

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db          1 AAAAAAAAAATATATATATA 20


RESULT 371
US-09-984-198-40
; Sequence 40, Application US/09984198
; Patent No. US20020106679A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gatanaga, T.
;    APPLICANT:  Granger, G.A.
;    TITLE OF INVENTION:  Factors Altering Tumor Necrosis
;    TITLE OF INVENTION:  Factor Receptor Releasing Enzyme Activity, and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  154
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/984,198
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US99/10793
;      FILING DATE:
;      APPLICATION NUMBER:  09/081,385
;      FILING DATE:
;      APPLICATION NUMBER:  08/964,747
;      FILING DATE:  05-NOV-1997
;      APPLICATION NUMBER:  60/030,761
;      FILING DATE:  06-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wu, Frank
;      REGISTRATION NUMBER:  41,386
;      REFERENCE/DOCKET NUMBER:  22000-20577.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-984-198-40

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20
```

```
RESULT 372
US-09-909-595-56/c
; Sequence 56, Application US/09909595
; Publication No. US20030083278A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Scott E. Davis
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
;  FILE REFERENCE: RTS-0223
;  CURRENT APPLICATION NUMBER: US/09/909,595
;  CURRENT FILING DATE:  2001-07-18
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-909-595-56

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4482 AATGTATTTGATTTATAAGT 4501
              |||| |||||||||||  |||
Db         20 AATGCATTTGATTTATCAGT 1


RESULT 373
US-10-077-383-29/c
; Sequence 29, Application US/10077383
; Publication No. US20030050444A1
; GENERAL INFORMATION:
;  APPLICANT: Haydock, Paul V.
;  APPLICANT:  U'Ren, Jack
;  APPLICANT:  Saigene Corporation
;  TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
;  TITLE OF INVENTION:  DNA/RNA Mixed Polymer Intermediate Products
;  FILE REFERENCE: 018048-001710US
;  CURRENT APPLICATION NUMBER: US/10/077,383
;  CURRENT FILING DATE:  2002-02-15
;  PRIOR APPLICATION NUMBER: US 60/296,812
;  PRIOR FILING DATE: 2001-06-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:(XY)-n spacer
;   OTHER INFORMATION: sequence, where X = a and Y = g
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (13)..(20)
;   OTHER INFORMATION: a or g at positions 13-20 may be present or absent
US-10-077-383-29

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 374
US-10-209-608-31/c
; Sequence 31, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-31

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 375
US-10-301-844-26
; Sequence 26, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
```

```
;            REFERENCE/DOCKET NUMBER: 8907-0057-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-301-844-26

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
             ||||||||| ||||||| ||
Db          1 ATATATATATATATATATAT 20


RESULT 376
US-10-301-844-26/c
; Sequence 26, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;       APPLICANT: Ruddy, David A.
;                  Wolff, Roger K.
;       TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                           HEMOCHROMATOSIS GENE
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds, LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/301,844
;            FILING DATE: 20-No. US20030100747A1-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/852,495C
;            FILING DATE: 07-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Poissant, Brian M
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-0057-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-301-844-26

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
             ||||||||| ||||||| ||
Db         20 ATATATATATATATATATAT 1


RESULT 377
US-10-683-386-31/c
; Sequence 31, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-31

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
             ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1


RESULT 378
US-10-671-395-707
; Sequence 707, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 707
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-707

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       3602 TGGAAAAAAACAAAAACAGA 3621
              |||||||||| ||| |||||
Db          1 TGGAAAAAAAAAAATACAGA 20


RESULT 379
US-10-728-399-87
; Sequence 87, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-87

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||| | ||
Db          1 TTTTTTTTTTTTTTTTGTTT 20


RESULT 380
US-10-728-399-141
; Sequence 141, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-141

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTTA 4521
              |||||||||||||| | |||
Db          1 TTTTTTTTTTTTTTTGTTTA 20


RESULT 381
US-10-728-399-199
; Sequence 199, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-199

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGGGTTAA 4522
              |||||||||||||| | ||||
Db          1 TTTTTTTTTTTTTTGTTTAA 20


RESULT 382
US-10-728-399-273
; Sequence 273, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-273

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4504 TTTTTTTTTTTGGGTTAAA 4523
              |||||||||||| | |||||
Db          1 TTTTTTTTTTTTTGTTTAAA 20


RESULT 383
US-10-661-088-17/c
; Sequence 17, Application US/10661088
; Publication No. US20040162253A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING HSV
;  FILE REFERENCE: 029849/0206
;  CURRENT APPLICATION NUMBER: US/10/661,088
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-088-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 384
US-10-661-088-18
; Sequence 18, Application US/10661088
; Publication No. US20040162253A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING HSV
;  FILE REFERENCE: 029849/0206
;  CURRENT APPLICATION NUMBER: US/10/661,088
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-088-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 385
US-10-661-097-17/c
; Sequence 17, Application US/10661097
; Publication No. US20040162254A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING HSV
;  FILE REFERENCE: 029849/0204
;  CURRENT APPLICATION NUMBER: US/10/661,097
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-097-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 386
US-10-661-097-18
; Sequence 18, Application US/10661097
; Publication No. US20040162254A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING HSV
;  FILE REFERENCE: 029849/0204
;  CURRENT APPLICATION NUMBER: US/10/661,097
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-097-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 387
US-10-661-355-17/c
; Sequence 17, Application US/10661355
; Publication No. US20040170959A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES
;  FILE REFERENCE: 029849/0208
;  CURRENT APPLICATION NUMBER: US/10/661,355
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
```

```
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-355-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 388
US-10-661-355-18
; Sequence 18, Application US/10661355
; Publication No. US20040170959A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES
;  FILE REFERENCE: 029849/0208
;  CURRENT APPLICATION NUMBER: US/10/661,355
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-355-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 389
US-10-661-099-17/c
; Sequence 17, Application US/10661099
; Publication No. US20040171568A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING HIV
;  FILE REFERENCE: 029849/0203
;  CURRENT APPLICATION NUMBER: US/10/661,099
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-099-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 390
US-10-661-099-18
; Sequence 18, Application US/10661099
; Publication No. US20040171568A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING HIV
;  FILE REFERENCE: 029849/0203
;  CURRENT APPLICATION NUMBER: US/10/661,099
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-099-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 391
US-10-476-962-56
; Sequence 56, Application US/10476962
; Publication No. US20040191904A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
;  FILE REFERENCE: RTS-0222
;  CURRENT APPLICATION NUMBER: US/10/476,962
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
;  PRIOR FILING DATE: 2001-05-18
;  NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 56
;   LENGTH: 20
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-476-962-56

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3229 TGTTGAGCCAGTGGGCCAGC 3248
              || |||||  ||||||||||||
Db          1 TGCTGAGCGAGTGGGCCAGC 20


RESULT 392
US-10-741-853A-6
; Sequence 6, Application US/10741853A
; Publication No. US20040203030A1
; GENERAL INFORMATION:
;  APPLICANT: Garrett-Engele, Philip, W
;  TITLE OF INVENTION: Alternatively Spliced Isoform of Human COX1
;  FILE REFERENCE: RS0206
;  CURRENT APPLICATION NUMBER: US/10/741,853A
;  CURRENT FILING DATE:  2003-12-18
;  PRIOR APPLICATION NUMBER: US 60/435,478
;  PRIOR FILING DATE: 2002-12-19
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-853A-6

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3401 GTTCTCACTGGGAAGAAGCA 3420
              || |||||  ||||||||||||
Db          1 GTACTCACAGGGAAGAAGCA 20


RESULT 393
US-10-661-415-17/c
; Sequence 17, Application US/10661415
; Publication No. US20040229828A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING RSV
;  FILE REFERENCE: 029849/0205
;  CURRENT APPLICATION NUMBER: US/10/661,415
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-415-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              |||||||||  |||  ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 394
US-10-661-415-18
; Sequence 18, Application US/10661415
; Publication No. US20040229828A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING RSV
;  FILE REFERENCE: 029849/0205
;  CURRENT APPLICATION NUMBER: US/10/661,415
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-415-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              ||||||||  |||  |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 395
US-10-484-007-56/c
; Sequence 56, Application US/10484007
; Publication No. US20040259824A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Scott E. Davis
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
;  FILE REFERENCE: RTSP-0397
;  CURRENT APPLICATION NUMBER: US/10/484,007
;  CURRENT FILING DATE:  2004-01-15
;  PRIOR APPLICATION NUMBER: 09/909,595
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-007-56

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       4482 AATGTATTTGATTTATAAGT 4501
              |||| |||||||||||  |||
Db         20 AATGCATTTGATTTATCAGT 1


RESULT 396
US-10-646-270-2
; Sequence 2, Application US/10646270
; Publication No. US20050042314A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Rong-Tsun
;  TITLE OF INVENTION: Extracts Of Polygonum multiflorum Thunb., And Preparation Process
;  TITLE OF INVENTION:  And Uses Of The Same
;  FILE REFERENCE: PE-22485-AM
;  CURRENT APPLICATION NUMBER: US/10/646,270
;  CURRENT FILING DATE:  2003-08-22
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: reverse primer for f]-actin
US-10-646-270-2

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4452 CCACATTTGATGGAGGGTGG 4471
              |||||| ||||||| |||||
Db          1 CCACATCTGATGGAAGGTGG 20


RESULT 397
US-10-619-253-242/c
; Sequence 242, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 242
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-242

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        898 CTTGCTGCTGATGTGCTTCA 917
              | | ||||||||||||||||
Db         20 CCTCCTGCTGATGTGCTTCA 1


RESULT 398
US-10-619-253-245/c
; Sequence 245, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 245
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-245

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1008 TTAATGCCACCTGGCTGGTG 1027
              | || ||||||||||||||||
Db         20 TCAACGCCACCTGGCTGGTG 1


RESULT 399
US-10-619-253-400/c
; Sequence 400, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 400
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-400

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1271 GCCAGGATTAAAAGAACCGG 1290
              |||||||||| ||||| ||
Db         20 GCCAGGATTAAGAGAACTGG 1


RESULT 400
US-10-643-801-113/c
; Sequence 113, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
;  APPLICANT: Sanjay Bhanot
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
;  FILE REFERENCE: RTS-0678US
;  CURRENT APPLICATION NUMBER: US/10/643,801
;  CURRENT FILING DATE:  2003-08-18
;  NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 113
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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```
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-113

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4008 TGTGCCATGGATCTGATCTG 4027
              || |||||||| ||||||||
Db         20 TGCGCCATGGAGCTGATCTG 1


RESULT 401
US-10-967-092-40
; Sequence 40, Application US/10967092
; Publication No. US20050090647A1
;   GENERAL INFORMATION:
;        APPLICANT: Gatanaga, T.
;                   Granger, G.A.
;        TITLE OF INVENTION: Factors Altering Tumor Necrosis
;                            Factor Receptor Releasing Enzyme Activity, and Methods
;                            of Use Thereof
;        NUMBER OF SEQUENCES: 154
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/967,092
;             FILING DATE: 15-Oct-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/712,813
;             FILING DATE: 13-Nov-2000
;             APPLICATION NUMBER: US/09/081,385
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/964,747
;             FILING DATE: 05-NOV-1997
;             APPLICATION NUMBER: 60/030,761
;             FILING DATE: 06-NOV-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wu, Frank
;             REGISTRATION NUMBER: 41,386
;             REFERENCE/DOCKET NUMBER: 22000-20577.21
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-813-5600
;             TELEFAX: 650-494-0792
;             TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-967-092-40

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20


RESULT 402
US-10-661-402-17/c
; Sequence 17, Application US/10661402
; Publication No. US20050153912A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING VIRAL FAMILIES
;  FILE REFERENCE: 029849/0207
;  CURRENT APPLICATION NUMBER: US/10/661,402
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-402-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCTCT 1


RESULT 403
US-10-661-402-18
; Sequence 18, Application US/10661402
; Publication No. US20050153912A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING VIRAL FAMILIES
;  FILE REFERENCE: 029849/0207
;  CURRENT APPLICATION NUMBER: US/10/661,402
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-402-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20
```

```
RESULT 404
US-10-661-403-17/c
; Sequence 17, Application US/10661403
; Publication No. US20050176661A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES
;  FILE REFERENCE: 029849/0202
;  CURRENT APPLICATION NUMBER: US/10/661,403
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-403-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCT 1


RESULT 405
US-10-661-403-18
; Sequence 18, Application US/10661403
; Publication No. US20050176661A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, ANDREW
;  APPLICANT:  JUTEAU, JEAN-MARC
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES
;  FILE REFERENCE: 029849/0202
;  CURRENT APPLICATION NUMBER: US/10/661,403
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-661-403-18

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTC 20


RESULT 406
US-10-969-812A-16/c
; Sequence 16, Application US/10969812A
; Publication No. US20050196382A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, Andrew
;  APPLICANT:  JUTEAU, Jean-Marc
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING VIRAL FAMILIES
;  FILE REFERENCE: 16051-11us
;  CURRENT APPLICATION NUMBER: US/10/969,812A
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: US10/661,402
;  PRIOR FILING DATE: 2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: US 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-969-812A-16

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              ||||||||| ||| ||||||
Db         20 CTCTCTCTCTCTCTCTCT 1


RESULT 407
US-10-969-812A-17
; Sequence 17, Application US/10969812A
; Publication No. US20050196382A1
; GENERAL INFORMATION:
;  APPLICANT: VAILLANT, Andrew
;  APPLICANT:  JUTEAU, Jean-Marc
;  TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES TARGETING VIRAL FAMILIES
;  FILE REFERENCE: 16051-11us
;  CURRENT APPLICATION NUMBER: US/10/969,812A
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: US10/661,402
;  PRIOR FILING DATE: 2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/IB03/04573
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 60/430,934
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: US 60/410,264
;  PRIOR FILING DATE: 2002-09-13
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-969-812A-17

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 408
US-11-011-500-40
; Sequence 40, Application US/11011500
; Publication No. US20050158826A1
;   GENERAL INFORMATION:
;        APPLICANT: Gatanaga, T.
;                   Granger, G.A.
;        TITLE OF INVENTION: Factors Altering Tumor Necrosis
;                            Factor Receptor Releasing Enzyme Activity, and Methods
;                            of Use Thereof
;        NUMBER OF SEQUENCES: 154
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/011,500
;             FILING DATE: 13-Dec-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/967,092
;             FILING DATE: 15-Oct-2004
;             APPLICATION NUMBER: US/09/712,813
;             FILING DATE: 13-Nov-2000
;             APPLICATION NUMBER: US/09/081,385
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/964,747
;             FILING DATE: 05-NOV-1997
;             APPLICATION NUMBER: 60/030,761
;             FILING DATE: 06-NOV-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wu, Frank
;             REGISTRATION NUMBER: 41,386
;             REFERENCE/DOCKET NUMBER: 22000-20577.21
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-813-5600
;             TELEFAX: 650-494-0792
;             TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-11-011-500-40

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20


RESULT 409
US-11-012-047-40
; Sequence 40, Application US/11012047
; Publication No. US20050191661A1
;   GENERAL INFORMATION:
;        APPLICANT: Gatanaga, T.
;                   Granger, G.A.
;        TITLE OF INVENTION: Factors Altering Tumor Necrosis
;                            Factor Receptor Releasing Enzyme Activity, and Methods
;                            of Use Thereof
;        NUMBER OF SEQUENCES: 154
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/012,047
;             FILING DATE: 13-Dec-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/967,092
;             FILING DATE: 15-Oct-2004
;             APPLICATION NUMBER: US/09/712,813
;             FILING DATE: 13-Nov-2000
;             APPLICATION NUMBER: US/09/081,385
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/964,747
;             FILING DATE: 05-NOV-1997
;             APPLICATION NUMBER: 60/030,761
;             FILING DATE: 06-NOV-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wu, Frank
;             REGISTRATION NUMBER: 41,386
;             REFERENCE/DOCKET NUMBER: 22000-20577.21
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-813-5600
;             TELEFAX: 650-494-0792
;             TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-11-012-047-40

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTC 3199
              |||||||||| ||| |||||
Db          1 CCTCTCTCTCTCTCTCTCTC 20


RESULT 410
US-09-263-959-807
; Sequence 807, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
```

```
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  807:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-807

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
                ||||||||  ||| |||||||
Db             1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 411
US-09-263-959-1158/c
; Sequence 1158, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  1158:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-1158

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3623 TTTGAGAACCTTGGACCACT 3642
                | |||||||||  ||||||||
Db         21 TCTGAGAACCTAGGACCACT 2


RESULT 412
US-10-270-839-76/c
; Sequence 76, Application US/10270839
; Publication No. US20030143586A1
; GENERAL INFORMATION:
;  APPLICANT: Chao, Qimin
;  APPLICANT:  Grasso, Luigi
;  APPLICANT:  Sass, Philip M.
;  APPLICANT:  Nicolaides, Nicholas  C.
;  TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagnosis
;  FILE REFERENCE: AG0002US (MOR-0133)
;  CURRENT APPLICATION NUMBER: US/10/270,839
;  CURRENT FILING DATE:  2002-10-11
;  PRIOR APPLICATION NUMBER: 60/328,750
;  PRIOR FILING DATE: 2001-10-12
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (21)..(21)
;   OTHER INFORMATION: H is A or C or T/U, not G
US-10-270-839-76

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
                ||||||||  ||| |||||||
Db         20 TCTCTCTCTCTCTCTCTCTC 1


RESULT 413
US-10-606-133-127/c
; Sequence 127, Application US/10606133
; Publication No. US20040132047A1
; GENERAL INFORMATION:
;  APPLICANT: Fortina, Paolo
;  APPLICANT:  Maris, John M.
;  APPLICANT:  Gelfand, Craig A.
;  TITLE OF INVENTION: Methods for Detection of Genetic
;  TITLE OF INVENTION:  Alterations Associated with Cancer
;  FILE REFERENCE: CHOP.0182US
;  CURRENT APPLICATION NUMBER: US/10/606,133
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: 60/391,515
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 282
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 127
;   LENGTH: 21
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-606-133-127

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3930 AATTCCACAGGTCATCAGAT 3949
              ||| |||||||||| ||||
Db         20 AATGCCACAGGTCATGAGAT 1


RESULT 414
US-10-751-736-19427
; Sequence 19427, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19427
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi
US-10-751-736-19427

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   35.0%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative   11;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4484 TGTATTTGATTTATAAGTTT 4503
              :| |:::| :::|:|||::: 
Db          2 UGCAUUUGCUUUAUAAGUUU 21


RESULT 415
US-10-751-736-33961/c
; Sequence 33961, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33961
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-751-736-33961

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2475 CTGAAGGAGAGGAGGAATTA 2494
              |||||||||| |||||| ||
Db         20 CTGAAGGAGATGAGGAAATA 1


RESULT 416
US-10-847-918-9238/c
; Sequence 9238, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9238
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-847-918-9238

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3057 GCTAGCTGCCACTTTCACGT 3076
              ||| |||||||| |||||||
Db         21 GCTGGCTGCCACCTTCACGT 2


RESULT 417
US-10-847-918-9239/c
; Sequence 9239, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9239
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi-sense strand
US-10-847-918-9239

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3056 AGCTAGCTGCCACTTTCACG 3075
              |||| |||||||| ||||||
Db         20 AGCTGGCTGCCACCTTCACG 1
```

```
RESULT 418
US-10-847-918-9240
; Sequence 9240, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9240
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi-antisense strand
US-10-847-918-9240

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   65.0%;  Pred. No. 2.4e+02;
  Matches   13;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3057 GCTAGCTGCCACTTTCACGT 3076
              ||: ||:||||| ::||||:
Db          1 GCUGGCUGCCACCUUCACGU 20


RESULT 419
US-09-725-265-16
; Sequence 16, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-16

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 2.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 420
US-09-891-517-16
; Sequence 16, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS O
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA O
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-16

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 2.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 421
US-09-775-479-8/c
; Sequence 8, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
;  APPLICANT: LECLERC, Guy
;  APPLICANT:  MARTEL, R,mi
;  TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
;  TITLE OF INVENTION:  RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
;  TITLE OF INVENTION:  THERAPEUTIC USES THEREOF
;  FILE REFERENCE: 12168-1US-2
;  CURRENT APPLICATION NUMBER: US/09/775,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: 09/318,106
;  PRIOR FILING DATE: 1999-05-24
;  PRIOR APPLICATION NUMBER: 08/756,728
;  PRIOR FILING DATE: 1996-11-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-09-775-479-8

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 2.5e+02;
```

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4498 AAGTTTTTTTTTTTTTTT 4515
              || ||||||||||||||||
Db         18 AAATTTTTTTTTTTTTTT 1
```

RESULT 422
US-10-209-608-16
; Sequence 16, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-16

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||||
Db          1 CAAAAAAAAAATATATAT 18
```

RESULT 423
US-10-683-386-16
; Sequence 16, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-16

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||||
Db          1 CAAAAAAAAAATATATAT 18
```

RESULT 424
US-10-863-973-877/c
; Sequence 877, Application US/10863973
; Publication No. US20050143333A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; APPLICANT: Polisky, Barry
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and
; TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering
; TITLE OF INVENTION: Nucleic Acid (siNA)
; FILE REFERENCE: 400/163 (MBHB03-084-D)
; CURRENT APPLICATION NUMBER: US/10/863,973
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US03/04566
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1832
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 877
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-863-973-877

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4552 TTTTCTCCTTGGTTTGCT 4569
              ||| ||||||||||||||||
Db         18 TTTCCTCCTTGGTTTGCT 1
```

```
RESULT 425
US-10-863-973-1100
; Sequence 1100, Application US/10863973
; Publication No. US20050143333A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  Polisky, Barry
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and
;  TITLE OF INVENTION:  Interleukin Receptor Gene Expression Using Short Interfering
;  TITLE OF INVENTION:  Nucleic Acid (siNA)
;  FILE REFERENCE: 400/163 (MBHB03-084-D)
;  CURRENT APPLICATION NUMBER: US/10/863,973
;  CURRENT FILING DATE:  2004-06-09
;  PRIOR APPLICATION NUMBER: PCT/US03/04566
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1832
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1100
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-863-973-1100

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   38.9%;  Pred. No. 2.6e+02;
  Matches    7;  Conservative   10;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4552 TTTTCTCCTTGGTTTGCT 4569
                 ::: |:||::||:::||:
Db          2 UUUCCUCCUUGGUUUGCU 19


RESULT 426
US-10-922-675-877/c
; Sequence 877, Application US/10922675
; Publication No. US20050182007A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  Polisky, Barry
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and
;  TITLE OF INVENTION:  Interleukin Receptor Gene Expression Using Short Interfering
;  TITLE OF INVENTION:  Nucleic Acid (siNA)
;  FILE REFERENCE: MBHB03-084-F (400/228)
;  CURRENT APPLICATION NUMBER: US/10/922,675
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: US 10/863,973
;  PRIOR FILING DATE: 2004-07-09
;  PRIOR APPLICATION NUMBER: PCT/US03/04566
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1832
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 877
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense re
US-10-922-675-877

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4552 TTTTCTCCTTGGTTTGCT 4569
                 ||| ||||||||||||||
Db         18 TTTCCTCCTTGGTTTGCT 1


RESULT 427
US-10-922-675-1100
; Sequence 1100, Application US/10922675
; Publication No. US20050182007A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  Polisky, Barry
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and
;  TITLE OF INVENTION:  Interleukin Receptor Gene Expression Using Short Interfering
;  TITLE OF INVENTION:  Nucleic Acid (siNA)
;  FILE REFERENCE: MBHB03-084-F (400/228)
;  CURRENT APPLICATION NUMBER: US/10/922,675
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: US 10/863,973
;  PRIOR FILING DATE: 2004-07-09
;  PRIOR APPLICATION NUMBER: PCT/US03/04566
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
;  NUMBER OF SEQ ID NOS: 1832
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1100
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-922-675-1100

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   38.9%;  Pred. No. 2.6e+02;
  Matches    7;  Conservative   10;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4552 TTTTCTCCTTGGTTTGCT 4569
              ::: |:||::||:::||:
Db          2 UUUCCUCCUUGGUUUGCU 19


RESULT 428
US-11-014-373-192/c
; Sequence 192, Application US/11014373
; Publication No. US20050196781A1
; GENERAL INFORMATION:
;  APPLICANT: Robin, Howard
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION
;  TITLE OF INVENTION:  USING SHORT INTERFERING NUCLEIC ACID (siNA)
;  FILE REFERENCE: 400/241 MBHB04-1067
;  CURRENT APPLICATION NUMBER: US/11/014,373
;  CURRENT FILING DATE:  2004-12-15
;  PRIOR APPLICATION NUMBER: PCT/US 04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Target Sequence/siNA sense region
US-11-014-373-192

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||| |
Db         19 TTTTTTTTTTTTTTTGAG 2


RESULT 429
US-11-014-373-469
; Sequence 469, Application US/11014373
; Publication No. US20050196781A1
; GENERAL INFORMATION:
;  APPLICANT: Robin, Howard
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION
;  TITLE OF INVENTION:  USING SHORT INTERFERING NUCLEIC ACID (siNA)
;  FILE REFERENCE: 400/241 MBHB04-1067
;  CURRENT APPLICATION NUMBER: US/11/014,373
;  CURRENT FILING DATE:  2004-12-15
;  PRIOR APPLICATION NUMBER: PCT/US 04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 469
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Target Sequence/siNA sense region
US-11-014-373-469

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   11.1%;  Pred. No. 2.6e+02;
  Matches    2;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ::::::::::::::::| |
Db          1 UUUUUUUUUUUUUUUGAG 18


RESULT 430
US-10-002-491-55/c
; Sequence 55, Application US/10002491
; Publication No. US20030109467A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
;  FILE REFERENCE: RTS-0239
;  CURRENT APPLICATION NUMBER: US/10/002,491
;  CURRENT FILING DATE:  2001-11-15
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-002-491-55

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       5032 AACATACAGAGGATGCCT 5049
              |||| ||||||||||||||
Db         20 AACAAACAGAGGATGCCT 3


RESULT 431
US-10-257-158A-7871/c
; Sequence 7871, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
;  APPLICANT: Barany, Francis
;  APPLICANT:  Zirvi, Monib
;  APPLICANT:  Gerry, Norman P.
;  APPLICANT:  Favis, Reyna
;  APPLICANT:  Kliman, Richard
;  TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC AC
;  TITLE OF INVENTION:  SEQUENCE DIFFERENCES USING LIGASE DETECTION REACTION
;  FILE REFERENCE: 19603/2834
;  CURRENT APPLICATION NUMBER: US/10/257,158A
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: PCT/US01/10958
;  PRIOR FILING DATE: 2001-04-04
;  PRIOR APPLICATION NUMBER: US 60/197,271
;  PRIOR FILING DATE: 2000-04-14
;  NUMBER OF SEQ ID NOS: 9544
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7871
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Hypothetical Probe Sequence
US-10-257-158A-7871

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2527 CATGAGATGGAGAGGCTG 2544
              |||||||||| ||||||
Db         18 CATGAGATGGACAGGCTG 1


RESULT 432
US-09-263-959-544/c
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  544:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-544

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||||||||||||
Db         16 TATATATACATATATA 1


RESULT 433
US-09-090-672B-105
; Sequence 105, Application US/09090672B
; Patent No. US20020068707A1
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-105

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
```

```
Db          1 GTTTTTTTTTTTTTT 16


RESULT 434
US-09-090-672B-107
; Sequence 107, Application US/09090672B
; Patent No. US20020068707A1
;  GENERAL INFORMATION:
;    APPLICANT:  Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
;    APPLICANT:  Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
;    APPLICANT:  Shigemasa; Takei, Masami
;    TITLE OF INVENTION:  IgA Nephropathy-Related Genes
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitzpatrick, Cella, Harper & Scinto
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      ZIP:  10112-3801
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  Compaq PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,672B
;      FILING DATE:  04-JUNE-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/04468
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  JP-8-325763
;      FILING DATE:  05-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perry, Lawrence S.
;      REGISTRATION NUMBER:  31865
;      REFERENCE/DOCKET NUMBER:  766.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 218-2100
;      TELEFAX:  (212) 218-2200
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
US-09-090-672B-107

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 435
US-09-730-559B-107
; Sequence 107, Application US/09730559B
; Publication No. US20030207828A1
; GENERAL INFORMATION:
;  APPLICANT: ISHIWATA, TETSUYOSHI
;  APPLICANT:  SAKURADA, MIKIKO
;  APPLICANT:  KAWABATA, AYAKO
;  APPLICANT:  NAKAGAWA, SATOSHI
;  APPLICANT:  NISHI, TATSUNARI
;  APPLICANT:  KUGA, TETSURO
;  APPLICANT:  SAWADA, SHIGEMASA
;  APPLICANT:  TAKEI, MASAMI
;  APPLICANT:  SHIBATA, KENJI
;  APPLICANT:  FURUYA, AKIKO
;  TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
;  FILE REFERENCE: 766.21 CIP
;  CURRENT APPLICATION NUMBER: US/09/730,559B
;  CURRENT FILING DATE:  2000-12-07
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
US-09-730-559B-107

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 436
US-09-730-559B-109
; Sequence 109, Application US/09730559B
; Publication No. US20030207828A1
; GENERAL INFORMATION:
;  APPLICANT: ISHIWATA, TETSUYOSHI
;  APPLICANT:  SAKURADA, MIKIKO
;  APPLICANT:  KAWABATA, AYAKO
;  APPLICANT:  NAKAGAWA, SATOSHI
;  APPLICANT:  NISHI, TATSUNARI
;  APPLICANT:  KUGA, TETSURO
;  APPLICANT:  SAWADA, SHIGEMASA
;  APPLICANT:  TAKEI, MASAMI
;  APPLICANT:  SHIBATA, KENJI
;  APPLICANT:  FURUYA, AKIKO
;  TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
;  FILE REFERENCE: 766.21 CIP
;  CURRENT APPLICATION NUMBER: US/09/730,559B
;  CURRENT FILING DATE:  2000-12-07
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
US-09-730-559B-109

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 437
US-10-309-152A-3
; Sequence 3, Application US/10309152A
; Publication No. US20030175759A1
; GENERAL INFORMATION:
;  APPLICANT: Hitachi LTD.
;  TITLE OF INVENTION: A method for prediction of genes and a method for providing a lis
;  FILE REFERENCE: H02001031A
;  CURRENT APPLICATION NUMBER: US/10/309,152A
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: JP 2002-047297
;  PRIOR FILING DATE: 2002-02-25
```

```
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo-d(T) primer by Nippon Flour Mills
US-10-309-152A-3

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 438
US-10-220-373-7
; Sequence 7, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
;  APPLICANT: NAGASU, Takeshi
;  APPLICANT:  OSHIDA, Tadahiro
;  APPLICANT:  OBAYASHI, Izumi
;  APPLICANT:  MATSUI, Keiko
;  APPLICANT:  SAITO, Hirohisa
;  TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
;  FILE REFERENCE: SHZ-010US
;  CURRENT APPLICATION NUMBER: US/10/220,373
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: JP 2000-61832
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Artificially
;   OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-7

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 439
US-10-220-373-8
; Sequence 8, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
;  APPLICANT: NAGASU, Takeshi
;  APPLICANT:  OSHIDA, Tadahiro
;  APPLICANT:  OBAYASHI, Izumi
;  APPLICANT:  MATSUI, Keiko
;  APPLICANT:  SAITO, Hirohisa
;  TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
;  FILE REFERENCE: SHZ-010US
;  CURRENT APPLICATION NUMBER: US/10/220,373
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: JP 2000-61832
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Artificially
;   OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-8

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 440
US-10-408-025-5
; Sequence 5, Application US/10408025
; Publication No. US20030224423A1
; GENERAL INFORMATION:
;  APPLICANT: Matsumoto, Yoshiko
;  APPLICANT:  Imai, Yukiho
;  APPLICANT:  Yoshida, Nei
;  APPLICANT:  Oshida, Tadahiro
;  APPLICANT:  Sugita, Yuji
;  APPLICANT:  Saito, Hirohisa
;  TITLE OF INVENTION: Method of Testing for Allergic Diseases
;  FILE REFERENCE: SHIMIZU-07914
;  CURRENT APPLICATION NUMBER: US/10/408,025
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 2002-100908
;  PRIOR FILING DATE: 2002-04-03
;  PRIOR APPLICATION NUMBER: PCT/JP03/02047
;  PRIOR FILING DATE: 2003-02-25
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-408-025-5

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 441
US-10-380-255-6
; Sequence 6, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
;  APPLICANT: Sugita et al.
;  TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
;  FILE REFERENCE: 6235-64935
;  CURRENT APPLICATION NUMBER: US/10/380,255
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: PCT/JP01/08247
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: JP 2000-293021
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 17
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:an artificially
;   OTHER INFORMATION: synthesized primer sequence
US-10-380-255-6

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 442
US-10-380-255-7
; Sequence 7, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
;  APPLICANT: Sugita et al.
;  TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
;  FILE REFERENCE: 6235-64935
;  CURRENT APPLICATION NUMBER: US/10/380,255
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: PCT/JP01/08247
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: JP 2000-293021
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:an artificially
;   OTHER INFORMATION: synthesized primer sequence
US-10-380-255-7

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 443
US-10-380-254-3
; Sequence 3, Application US/10380254
; Publication No. US20040038252A1
; GENERAL INFORMATION:
;  APPLICANT: Sugita et al.
;  TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
;  FILE REFERENCE: 6235-64773
;  CURRENT APPLICATION NUMBER: US/10/380,254
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: PCT/JP01/08246
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: JP 2000-291318
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:an artificially
;   OTHER INFORMATION: synthesized primer sequence
US-10-380-254-3

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 444
US-10-380-254-4
; Sequence 4, Application US/10380254
; Publication No. US20040038252A1
; GENERAL INFORMATION:
;  APPLICANT: Sugita et al.
;  TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
;  FILE REFERENCE: 6235-64773
;  CURRENT APPLICATION NUMBER: US/10/380,254
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: PCT/JP01/08246
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: JP 2000-291318
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:an artificially
;   OTHER INFORMATION: synthesized primer sequence
US-10-380-254-4

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 445
US-10-398-885A-2
; Sequence 2, Application US/10398885A
; Publication No. US20040053282A1
; GENERAL INFORMATION:
;  APPLICANT: Sugita, Yuji
;  APPLICANT:  Hashida, Ryoichi
;  APPLICANT:  Ogawa, Kaoru
;  APPLICANT:  Nagasu, Takeshi
;  APPLICANT:  Obayashi, Masaya
;  APPLICANT:  Saito, Hirohisa
;  APPLICANT:  Takahasi, Eiki
;  TITLE OF INVENTION: Method of Testing For Allergic Diseases
;  FILE REFERENCE: SHIMIZU-07907
;  CURRENT APPLICATION NUMBER: US/10/398,885A
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/JP01/08937
;  PRIOR FILING DATE: 2001-10-11
;  PRIOR APPLICATION NUMBER: JP 2000-314093
;  PRIOR FILING DATE: 2000-10-13
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
```

US-10-398-885A-2

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 446
US-10-398-885A-3
; Sequence 3, Application US/10398885A
; Publication No. US20040053282A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahasi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907
; CURRENT APPLICATION NUMBER: US/10/398,885A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-3

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 447
US-10-398-877-18
; Sequence 18, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-18

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 448
US-10-398-877-19
; Sequence 19, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-19

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 449
US-10-239-734-3
; Sequence 3, Application US/10239734
; Publication No. US20040161746A1
; GENERAL INFORMATION:
; APPLICANT: GENOX RESEARCH, INC.
; APPLICANT: JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR
; APPLICANT: CHILD HEALTH AND DEVELOPMENT
; APPLICANT: Matsumoto, Yoshiko
; APPLICANT: Tsujimoto, Gozoh
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Sugita, Yuji
; APPLICANT: Oshida, Tadahiro
; APPLICANT: Imai, Yukiho
; TITLE OF INVENTION: Method of Testing For Allergic Disease
; FILE REFERENCE: SHIMIZU-07379
; CURRENT APPLICATION NUMBER: US/10/239,734
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/JP01/11286
; PRIOR FILING DATE: 2001-12-21

```
;  PRIOR APPLICATION NUMBER: 2000-389476 JP
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: "GT15A", an artificially synthesized primer sequence
US-10-239-734-3

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 450
US-10-239-734-4
; Sequence 4, Application US/10239734
; Publication No. US20040161746A1
; GENERAL INFORMATION:
;  APPLICANT: GENOX RESEARCH, INC.
;  APPLICANT:  JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR
;  APPLICANT:  CHILD HEALTH AND DEVELOPMENT
;  APPLICANT:  Matsumoto, Yoshiko
;  APPLICANT:  Tsujimoto, Gozoh
;  APPLICANT:  Nagasu, Takeshi
;  APPLICANT:  Sugita, Yuji
;  APPLICANT:  Oshida, Tadahiro
;  APPLICANT:  Imai, Yukiho
;  TITLE OF INVENTION: Method of Testing For Allergic Disease
;  FILE REFERENCE: SHIMIZU-07379
;  CURRENT APPLICATION NUMBER: US/10/239,734
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: PCT/JP01/11286
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 2000-389476 JP
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: "GT15C", an artificially synthesized primer sequence
US-10-239-734-4

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 451
US-10-735-592-12
; Sequence 12, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-12

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 452
US-10-608-863-3
; Sequence 3, Application US/10608863
; Publication No. US20040214192A1
; GENERAL INFORMATION:
;  APPLICANT: Hashida, Ryoichi
;  APPLICANT:  Kagaya, Shinji
;  APPLICANT:  Yayoi, Yoshihiro
;  APPLICANT:  Sugita, Yuji
;  APPLICANT:  Saito, Hirohisa
;  TITLE OF INVENTION: METHODS FOR EXAMINATION FOR ALLERGIC DISEASES, AND DRUGS FOR TREA
;  TITLE OF INVENTION:  ALLERGIC DISEASES
;  FILE REFERENCE: 3462.1003-000
;  CURRENT APPLICATION NUMBER: US/10/608,863
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: JP 2002-188490
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Artificially
;   OTHER INFORMATION: Synthesized Primer Sequence
US-10-608-863-3

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 453
US-10-608-863-4
; Sequence 4, Application US/10608863
; Publication No. US20040214192A1
; GENERAL INFORMATION:
;  APPLICANT: Hashida, Ryoichi
;  APPLICANT:  Kagaya, Shinji
;  APPLICANT:  Yayoi, Yoshihiro
;  APPLICANT:  Sugita, Yuji
;  APPLICANT:  Saito, Hirohisa
;  TITLE OF INVENTION: METHODS FOR EXAMINATION FOR ALLERGIC DISEASES, AND DRUGS FOR TREA
;  TITLE OF INVENTION:  ALLERGIC DISEASES
;  FILE REFERENCE: 3462.1003-000
;  CURRENT APPLICATION NUMBER: US/10/608,863
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: JP 2002-188490
;  PRIOR FILING DATE: 2002-06-27
```

```
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Artificially
;   OTHER INFORMATION: Synthesized Primer Sequence
US-10-608-863-4

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 454
US-09-904-744-2
; Sequence 2, Application US/09904744
; Patent No. US20020150905A1
; GENERAL INFORMATION:
;  APPLICANT: Barbera-Guillem, Emilio
;  APPLICANT:  Nelson, M. Bud
;  APPLICANT:  Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  TITLE OF INVENTION:  dendrimers in a signal amplification system
;  FILE REFERENCE: B-73
;  CURRENT APPLICATION NUMBER: US/09/904,744
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/437076
;  PRIOR FILING DATE: 1999-11-09
;  PRIOR APPLICATION NUMBER: 60/107828
;  PRIOR FILING DATE: 1998-11-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthesized
US-09-904-744-2

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          3 GTTTTTTTTTTTTTTT 18


RESULT 455
US-09-994-311-5
; Sequence 5, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-5

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 456
US-09-994-311-6
; Sequence 6, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-6

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 457
US-10-872-984-5
; Sequence 5, Application US/10872984
; Publication No. US20040265888A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/10/872,984
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: US/09/994,311
;  PRIOR FILING DATE: 2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-872-984-5

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.9e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 2 TTTTTTTTTTTTTTTG 17

RESULT 458
US-10-872-984-6
; Sequence 6, Application US/10872984
; Publication No. US20040265888A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/10/872,984
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/994,311
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-872-984-6

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.9e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 2 TTTTTTTTTTTTTTTG 17

RESULT 459
US-10-669-962-29
; Sequence 29, Application US/10669962
; Publication No. US20050081264A1
; GENERAL INFORMATION:
; APPLICANT: Brugliera, Filippa
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/10/669,962
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/142,108C
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: PN8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-669-962-29

  Query Match 0.4%; Score 16; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.9e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 3 TTTTTTTTTTTTTTTG 18

RESULT 460
US-10-205-309-325/c
; Sequence 325, Application US/10205309
; Publication No. US20030190635A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
; TITLE OF INVENTION: Interfering RNA
; FILE REFERENCE: 900/033
; CURRENT APPLICATION NUMBER: US/10/205,309
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 325
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-205-309-325

  Query Match 0.4%; Score 16; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 3.1e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
         ||||||||||||||||
Db 16 TTTTTTTTTTTTTTTG 1

RESULT 461
US-10-205-309-650
; Sequence 650, Application US/10205309
; Publication No. US20030190635A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
; TITLE OF INVENTION: Interfering RNA
; FILE REFERENCE: 900/033
; CURRENT APPLICATION NUMBER: US/10/205,309
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 650
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-205-309-650

  Query Match 0.4%; Score 16; DB 1; Length 19;
  Best Local Similarity 6.2%; Pred. No. 3.1e+02;
  Matches 1; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTG 4516
              ::::::::::::::|
Db          4 UUUUUUUUUUUUUUG 19


RESULT 462
US-10-670-011-18/c
; Sequence 18, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/132 (MBHB02-742-G)
;  CURRENT APPLICATION NUMBER: US/10/670,011
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 427
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-670-011-18

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGC 2278
              ||||||||||||||||
Db         16 TCTTTCCTCTTTCTGC 1


RESULT 463
US-10-670-011-114
; Sequence 114, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/132 (MBHB02-742-G)
;  CURRENT APPLICATION NUMBER: US/10/670,011
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 427
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-670-011-114

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   43.8%;  Pred. No. 3.1e+02;
  Matches    7;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGC 2278
              :|:::||:|:::|:||
Db          4 UCUUUCCUCUUUCUGC 19


RESULT 464
US-10-764-957-18/c
; Sequence 18, Application US/10764957
; Publication No. US20050054596A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/144 (MBHB02-742-O)
;  CURRENT APPLICATION NUMBER: US/10/764,957
;  CURRENT FILING DATE:  2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US60/399,348
```

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;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 473
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-764-957-18

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGC 2278
              ||||||||||||||||
Db         16 TCTTTCCTCTTTCTGC 1


RESULT 465
US-10-764-957-114
; Sequence 114, Application US/10764957
; Publication No. US20050054596A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/144 (MBHB02-742-O)
;  CURRENT APPLICATION NUMBER: US/10/764,957
;  CURRENT FILING DATE:  2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 473
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-764-957-114

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   43.8%;  Pred. No. 3.1e+02;
  Matches    7;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGC 2278
              :|:::||:|:::|:||
Db          4 UCUUUCCUCUUUCUGC 19


RESULT 466
US-10-871-222-404/c
; Sequence 404, Application US/10871222
; Publication No. US20050119212A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Haeberli, Peter
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Mediated Inhibition Fatty Acid Synthase (FAS) and Fatty Acids
;  TITLE OF INVENTION:  Synthase Ligand (FASL) Gene Expression Using Short Interfering
;  TITLE OF INVENTION:  Nucleic Acid (SINA)
;  FILE REFERENCE: 400/164  (MBHB04-487)
;  CURRENT APPLICATION NUMBER: US/10/871,222
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US10/826966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US10/757803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US10/720448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US10/693059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US10/444853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 706
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 404
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-871-222-404

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         19 TTTTTTTTTTTTTTTG 4


RESULT 467
US-10-871-222-508
; Sequence 508, Application US/10871222
; Publication No. US20050119212A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Haeberli, Peter
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Mediated Inhibition Fatty Acid Synthase (FAS) and Fatty Acids
;  TITLE OF INVENTION:  Synthase Ligand (FASL) Gene Expression Using Short Interfering
;  TITLE OF INVENTION:  Nucleic Acid (SINA)
;  FILE REFERENCE: 400/164  (MBHB04-487)
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;  CURRENT APPLICATION NUMBER: US/10/871,222
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US10/826966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US10/757803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US10/720448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US10/693059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US10/444853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 706
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 508
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-871-222-508

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   6.2%;  Pred. No. 3.1e+02;
  Matches    1;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ::::::::::::::|
Db          1 UUUUUUUUUUUUUUG 16


RESULT 468
US-10-962-898-2014/c
; Sequence 2014, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor And Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/236 (MBHB02-742-U)
;  CURRENT APPLICATION NUMBER: US/10/962,898
;  CURRENT FILING DATE:  2004-10-12
;  PRIOR APPLICATION NUMBER: US 10/944,644
;  PRIOR FILING DATE: 2004-09-16
;  PRIOR APPLICATION NUMBER: US 10/844,076
;  PRIOR FILING DATE: 2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: US 10/664,767
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2014
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense re
US-10-962-898-2014

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGC 2278
              ||||||||||||||||
Db         16 TCTTTCCTCTTTCTGC 1


RESULT 469
US-10-962-898-2110
; Sequence 2110, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor And Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/236 (MBHB02-742-U)
;  CURRENT APPLICATION NUMBER: US/10/962,898
;  CURRENT FILING DATE:  2004-10-12
;  PRIOR APPLICATION NUMBER: US 10/944,644
;  PRIOR FILING DATE: 2004-09-16
;  PRIOR APPLICATION NUMBER: US 10/844,076
;  PRIOR FILING DATE: 2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: US 10/664,767
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2110
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-962-898-2110

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   43.8%;  Pred. No. 3.1e+02;
  Matches    7;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGC 2278
```

```
              :|:::||:|:::|:||
Db          4 UCUUUCCUCUUUCUGC 19


RESULT 470
US-09-953-047-91/c
; Sequence 91, Application US/09953047
; Publication No. US20030087854A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
;  FILE REFERENCE: RTS-0157
;  CURRENT APPLICATION NUMBER: US/09/953,047
;  CURRENT FILING DATE:  2001-09-10
;  NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 91
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-047-91

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||||||||||||
Db         17 TATATATACATATATA 2


RESULT 471
US-10-181-177-55
; Sequence 55, Application US/10181177
; Publication No. US20030083296A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
;  FILE REFERENCE: RTSP-0334
;  CURRENT APPLICATION NUMBER: US/10/181,177
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/00955
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: 09/487,445
;  PRIOR FILING DATE: 2000-01-19
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-177-55

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1772 GTTGATTATCTTCAGC 1787
              ||||||||||||||||
Db          3 GTTGATTATCTTCAGC 18


RESULT 472
US-10-630-401-91/c
; Sequence 91, Application US/10630401
; Publication No. US20040048824A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
;  FILE REFERENCE: RTS-0157
;  CURRENT APPLICATION NUMBER: US/10/630,401
;  CURRENT FILING DATE:  2003-07-30
;  PRIOR APPLICATION NUMBER: US/09/953,047
;  PRIOR FILING DATE: 2001-09-10
;  NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 91
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-630-401-91

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||||||||||||
Db         17 TATATATACATATATA 2


RESULT 473
US-10-275-080A-5
; Sequence 5, Application US/10275080A
; Publication No. US20040053214A1
; GENERAL INFORMATION:
;  APPLICANT: Schroder, Klaus Hobe
;  APPLICANT:  Schubler, Andrea
;  APPLICANT:  Koike, Katsuro
;  TITLE OF INVENTION: Method of Diagnosing HBV Infection Stages
;  FILE REFERENCE: 012627-033
;  CURRENT APPLICATION NUMBER: US/10/275,080A
;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: PCT/EP01/04918
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: EP 00 109 436.6
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-275-080A-5

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 474
US-10-275-080A-6
; Sequence 6, Application US/10275080A
; Publication No. US20040053214A1
; GENERAL INFORMATION:
;  APPLICANT: Schroder, Klaus Hobe
;  APPLICANT:  Schubler, Andrea
;  APPLICANT:  Koike, Katsuro
;  TITLE OF INVENTION: Method of Diagnosing HBV Infection Stages
;  FILE REFERENCE: 012627-033
;  CURRENT APPLICATION NUMBER: US/10/275,080A
;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: PCT/EP01/04918
;  PRIOR FILING DATE: 2001-05-02
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;  PRIOR APPLICATION NUMBER: EP 00 109 436.6
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-275-080A-6

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 475
US-10-671-395-433
; Sequence 433, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 433
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-433

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          5 TTTTTTTTTTTTTTTG 20


RESULT 476
US-10-671-395-938
; Sequence 938, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 938
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-938

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTGG 16


RESULT 477
US-10-728-078-14/c
; Sequence 14, Application US/10728078
; Publication No. US20050038229A1
; GENERAL INFORMATION:
;  APPLICANT: Lipovsek, Dasa
;  APPLICANT:  Wagner, Richard W
;  APPLICANT:  Kuimelis, Robert G
;  TITLE OF INVENTION: PROTEIN SCAFFOLDS FOR ANTIBODY MIMICS
;  TITLE OF INVENTION:  AND OTHER BINDING PROTEINS
;  FILE REFERENCE: 50036/021004
;  CURRENT APPLICATION NUMBER: US/10/728,078
;  CURRENT FILING DATE:  2003-12-03
;  PRIOR APPLICATION NUMBER: US/09/688,566
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: US 60/111,737
;  PRIOR FILING DATE: 1998-12-10
;  PRIOR APPLICATION NUMBER: US 09/456,693
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: US 09/515,260
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 202
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Puromycin linker oligonucleotide
US-10-728-078-14

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db         19 GTTTTTTTTTTTTTTT 4


RESULT 478
US-10-644-052A-376
; Sequence 376, Application US/10644052A
; Publication No. US20050059619A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M
;  APPLICANT:  Samulowitz, Ulrike
;  APPLICANT:  Vollmer, Joerg
;  APPLICANT:  Uhlmann, Eugen
;  APPLICANT:  Jurk, Marion
;  APPLICANT:  Lipford, Grayson
;  APPLICANT:  Rankin, Robert
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS
;  FILE REFERENCE: C1037.70048US00
;  CURRENT APPLICATION NUMBER: US/10/644,052A
;  CURRENT FILING DATE:  2003-08-19
;  PRIOR APPLICATION NUMBER: US 60/404,479
;  PRIOR FILING DATE: 2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/404,820
```

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;  PRIOR FILING DATE: 2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/429,701
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: US 60/447,377
;  PRIOR FILING DATE: 2003-02-14
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 376
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Oligodeoxynucleotide
US-10-644-052A-376

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          5 GTTTTTTTTTTTTTTT 20


RESULT 479
US-10-644-052A-377
; Sequence 377, Application US/10644052A
; Publication No. US20050059619A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M
;  APPLICANT:  Samulowitz, Ulrike
;  APPLICANT:  Vollmer, Joerg
;  APPLICANT:  Uhlmann, Eugen
;  APPLICANT:  Jurk, Marion
;  APPLICANT:  Lipford, Grayson
;  APPLICANT:  Rankin, Robert
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS
;  FILE REFERENCE: C1037.70048US00
;  CURRENT APPLICATION NUMBER: US/10/644,052A
;  CURRENT FILING DATE:  2003-08-19
;  PRIOR APPLICATION NUMBER: US 60/404,479
;  PRIOR FILING DATE: 2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/404,820
;  PRIOR FILING DATE: 2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/429,701
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: US 60/447,377
;  PRIOR FILING DATE: 2003-02-14
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 377
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Oligodeoxynucleotide
US-10-644-052A-377

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          5 GTTTTTTTTTTTTTTT 20


RESULT 480
US-10-831-901A-29727
; Sequence 29727, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29727
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense compound
US-10-831-901A-29727

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 481
US-10-831-901A-29728
; Sequence 29728, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
```

```
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29728
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-29728

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 482
US-10-831-901A-29729
; Sequence 29729, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29729
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-29729

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 483
US-10-831-901A-29730
; Sequence 29730, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29730
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-29730

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          4 TTTTTTTTTTTTTTTG 19


RESULT 484
US-10-831-901A-29731
; Sequence 29731, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
```

```
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29731
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-29731

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          5 TTTTTTTTTTTTTTTG 20


RESULT 485
US-09-969-373-4453
; Sequence 4453, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4453
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-4453

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCT 3200
              || ||||| ||||||||||
Db          1 TCCCTCTCTCTCCCTCTCT 19


RESULT 486
US-09-263-959-643
; Sequence 643, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  643:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-643

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCT 2142
              ||||||||||||||| || |
Db          1 TTTTCTTTTCTTTTCTTTT 19


RESULT 487
US-09-263-959-761/c
; Sequence 761, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
```

```
;  INFORMATION FOR SEQ ID NO:  761:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-761

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCT 2142
              ||||||||||||||| || |
Db         19 TTTTCTTTTCTTTTCTTTT 1


RESULT 488
US-09-263-959-836
; Sequence 836, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  836:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-836

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATACAT 2413
              |||||||| ||||||| ||
Db          1 TATATATAAATATATATAT 19


RESULT 489
US-10-272-552-2/c
; Sequence 2, Application US/10272552
; Publication No. US20030143740A1
; GENERAL INFORMATION:
;  APPLICANT: Mirus Corporation
;  APPLICANT:  Wooddell, Christine I
;  APPLICANT:  Herweijer, Hans
;  APPLICANT:  Wolff, Jon
;  TITLE OF INVENTION: Processes for Integrating Nucleic Acid in Mammalian Cells
;  FILE REFERENCE: Mirus.031.02
;  CURRENT APPLICATION NUMBER: US/10/272,552
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: US 60/329474
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;    LENGTH: 19
;    TYPE: DNA
;    ORGANISM: Transposon Tn5
US-10-272-552-2

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 490
US-10-291-342-2/c
; Sequence 2, Application US/10291342
; Publication No. US20040126887A1
; GENERAL INFORMATION:
;  APPLICANT: Mirus Corporation
;  APPLICANT:  Wooddell, Christine
;  APPLICANT:  Herweijer, Hans
;  APPLICANT:  Wolff, Jon
;  TITLE OF INVENTION: ENHANCING INTERMOLECULAR INTEGRATION OF NUCLEIC ACIDS USING INTEGR
;  TITLE OF INVENTION:  COMPLEXES
;  FILE REFERENCE: Mirus.031.03
;  CURRENT APPLICATION NUMBER: US/10/291,342
;  CURRENT FILING DATE:  2002-11-08
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;    LENGTH: 19
;    TYPE: DNA
;    ORGANISM: Transposon Tn5
US-10-291-342-2

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 491
US-10-665-951-390
; Sequence 390, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/131 (MBHB02-742-F)
;  CURRENT APPLICATION NUMBER: US/10/665,951
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
```

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;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2455
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 390
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-665-951-390

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 3.4e+02;
  Matches   10;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              :|:|:|  :|:|||:|:||
Db          1 UGUGUGUGUGUGGGUGUGG 19


RESULT 492
US-10-665-951-817/c
; Sequence 817, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/131 (MBHB02-742-F)
;  CURRENT APPLICATION NUMBER: US/10/665,951
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2455
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 817
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-665-951-817

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              ||||||  ||||||||||||
Db         19 TGTGTGTGTGTGGGTGTGG 1


RESULT 493
US-10-683-990-97
; Sequence 97, Application US/10683990
; Publication No. US20040198682A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Usman, Nassim
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
;  TITLE OF INVENTION:  Gene Expression Using SHort Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/134 (02-742-H)
;  CURRENT APPLICATION NUMBER: US/10/683,990
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US 60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US 60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 256
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-683-990-97

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3599 GTCTGGAAAAAAACAAAAA 3617
              |: :|||||||| |||||
Db          1 GUGUGGAAAAAAAAAAAAA 19
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RESULT 494
US-10-683-990-194/c
; Sequence 194, Application US/10683990
; Publication No. US20040198682A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Usman, Nassim
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
;  TITLE OF INVENTION:  Gene Expression Using SHort Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/134 (02-742-H)
;  CURRENT APPLICATION NUMBER: US/10/683,990
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US 60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US 60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 256
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-683-990-194

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3599 GTCTGGAAAAAAACAAAAA 3617
              || |||||||||| |||||
Db         19 GTGTGGAAAAAAAAAAAAA 1


RESULT 495
US-10-826-573-4/c
; Sequence 4, Application US/10826573
; Publication No. US20040235103A1
; GENERAL INFORMATION:
;  APPLICANT: Reznikoff, William S.
;  APPLICANT:  Steiniger-White, Mindy M.
;  APPLICANT:  Metzler, Jeremy
;  TITLE OF INVENTION: Tn5 Transposase Mutants And The Use Thereof
;  FILE REFERENCE: 960296.99195
;  CURRENT APPLICATION NUMBER: US/10/826,573
;  CURRENT FILING DATE:  2004-04-16
;  PRIOR APPLICATION NUMBER: 60/463,470
;  PRIOR FILING DATE: 2003-04-17
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Transposon Tn5
US-10-826-573-4

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 496
US-10-758-155-390
; Sequence 390, Application US/10758155
; Publication No. US20050075304A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/141 (MBHB02742-N)
;  CURRENT APPLICATION NUMBER: US/10/758,155
;  CURRENT FILING DATE:  2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 390
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense re
US-10-758-155-390

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 3.4e+02;
  Matches   10;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              :|:|:|  :|:|||:|:||
Db          1 UGUGUGUGUGUGGGUGUGG 19


RESULT 497
US-10-758-155-817/c
; Sequence 817, Application US/10758155
; Publication No. US20050075304A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/141 (MBHB02742-N)
;  CURRENT APPLICATION NUMBER: US/10/758,155
;  CURRENT FILING DATE:  2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 817
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-758-155-817

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
                ||||||  ||||||||||
Db         19 TGTGTGTGTGTGGGTGTGG 1


RESULT 498
US-10-831-620-390
; Sequence 390, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/152 (MBHB02-742-Q)
;  CURRENT APPLICATION NUMBER: US/10/831,620
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 390
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-831-620-390

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 3.4e+02;
  Matches   10;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
                :|:|:|  :|:|||:|:||
Db          1 UGUGUGUGUGGGUGUGG 19


RESULT 499
US-10-831-620-817/c
; Sequence 817, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/152 (MBHB02-742-Q)
;  CURRENT APPLICATION NUMBER: US/10/831,620
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 817
;   LENGTH: 19
```

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;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-831-620-817

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              ||||||  ||||||||||
Db         19 TGTGTGTGTGTGGGTGTGG 1


RESULT 500
US-10-844-076-390
; Sequence 390, Application US/10844076
; Publication No. US20050171039A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/159 (MBHB02-742-R)
;  CURRENT APPLICATION NUMBER: US/10/844,076
;  CURRENT FILING DATE:  2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2755
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 390
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-844-076-390

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 3.4e+02;
  Matches   10;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              :|:|:|  :|:|||:|:||
Db          1 UGUGUGUGUGUGGGUGUGG 19


RESULT 501
US-10-844-076-817/c
; Sequence 817, Application US/10844076
; Publication No. US20050171039A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/159 (MBHB02-742-R)
;  CURRENT APPLICATION NUMBER: US/10/844,076
;  CURRENT FILING DATE:  2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2755
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 817
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-844-076-817

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              ||||||  ||||||||||
Db         19 TGTGTGTGTGTGGGTGTGG 1


RESULT 502
US-10-877-889-723/c
; Sequence 723, Application US/10877889
; Publication No. US20050209179A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/166 (MBHB02-728-I)
;  CURRENT APPLICATION NUMBER: US/10/877,889
;  CURRENT FILING DATE:  2004-06-25
;  PRIOR APPLICATION NUMBER: US 10/607933
;  PRIOR FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: US 09/930423
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: PCT/US03/04710
;  PRIOR FILING DATE: 2003-02-18
;  PRIOR APPLICATION NUMBER: US 10/205309
;  PRIOR FILING DATE: 2002-07-25
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;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444853
;  PRIOR FILING DATE: 2003-05-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1904
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 723
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-877-889-723

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||||  ||
Db         19 TTTTTTTTTTTTTTGACTT 1


RESULT 503
US-10-877-889-1048
; Sequence 1048, Application US/10877889
; Publication No. US20050209179A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/166 (MBHB02-728-I)
;  CURRENT APPLICATION NUMBER: US/10/877,889
;  CURRENT FILING DATE:  2004-06-25
;  PRIOR APPLICATION NUMBER: US 10/607933
;  PRIOR FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: US 09/930423
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: PCT/US03/04710
;  PRIOR FILING DATE: 2003-02-18
;  PRIOR APPLICATION NUMBER: US 10/205309
;  PRIOR FILING DATE: 2002-07-25
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444853
;  PRIOR FILING DATE: 2003-05-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1904
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1048
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-877-889-1048

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   5.3%;  Pred. No. 3.4e+02;
  Matches    1;  Conservative   16;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
                :::::::::::::::|  ::
Db          1 UUUUUUUUUUUUUUGACUU 19


RESULT 504
US-10-962-898-390
; Sequence 390, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor And Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/236 (MBHB02-742-U)
;  CURRENT APPLICATION NUMBER: US/10/962,898
;  CURRENT FILING DATE:  2004-10-12
;  PRIOR APPLICATION NUMBER: US 10/944,644
;  PRIOR FILING DATE: 2004-09-16
;  PRIOR APPLICATION NUMBER: US 10/844,076
;  PRIOR FILING DATE: 2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: US 10/664,767
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 390
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-962-898-390

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 3.4e+02;
  Matches   10;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              :|:|:|  :|:|||:|:||
Db          1 UGUGUGUGUGGGUGUGG 19


RESULT 505
US-10-962-898-817/c
; Sequence 817, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
```

```
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor And Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/236 (MBHB02-742-U)
;  CURRENT APPLICATION NUMBER: US/10/962,898
;  CURRENT FILING DATE:  2004-10-12
;  PRIOR APPLICATION NUMBER: US 10/944,644
;  PRIOR FILING DATE: 2004-09-16
;  PRIOR APPLICATION NUMBER: US 10/844,076
;  PRIOR FILING DATE: 2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: US 10/664,767
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 817
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-962-898-817

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              ||||||  ||||||||||
Db         19 TGTGTGTGTGTGGGTGTGG 1


RESULT 506
US-10-146-474-17
; Sequence 17, Application US/10146474
; Publication No. US20030023061A1
;   GENERAL INFORMATION:
;        APPLICANT: Umansky, Samuil
;                   Melkonyan, Hovsep
;        TITLE OF INVENTION: A FAMILY OF GENES ENCODING
;                            APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
;                            METHODS OF USE THEREOF
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 Page Mill Road
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/146,474
;             FILING DATE: 14-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/937,067
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lehnhardt, Susan K.
;             REGISTRATION NUMBER: 33,943
;             REFERENCE/DOCKET NUMBER: 23647-20018.00
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 813-5600
;             TELEFAX: (650) 494-0792
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-146-474-17

  Query Match             0.4%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+02;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  :
Db          1 TTTTTTTTTTTTTTTNS 17


RESULT 507
US-10-301-764-17
; Sequence 17, Application US/10301764
; Publication No. US20040039184A1
;   GENERAL INFORMATION:
;        APPLICANT: Umansky, Samuil
;                   Melkonyan, Hovsep
;        TITLE OF INVENTION: A FAMILY OF GENES ENCODING
;                            APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
;                            METHODS OF USE THEREOF
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 Page Mill Road
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,764
;             FILING DATE: 20-No. US20040039184A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/937,067
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lehnhardt, Susan K.
;             REGISTRATION NUMBER: 33,943
;             REFERENCE/DOCKET NUMBER: 23647-20018.00
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 813-5600
;             TELEFAX: (650) 494-0792
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
```

US-10-301-764-17

Query Match 0.4%; Score 15.6; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||  :
Db          1 TTTTTTTTTTTTTTNS 17
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RESULT 508
US-10-238-700-1260
; Sequence 1260, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1260
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-1260

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 3.6e+02;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1475 ACAACTCTGCCTTTATG 1491
              ||||  :|:|||:::|:|
Db          1 ACAAAUCUGCCUUUAUG 17
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RESULT 509
US-10-138-674-1073
; Sequence 1073, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1073

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 5.9%; Pred. No. 3.6e+02;
Matches 1; Conservative 15; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | :::::::::::::::
Db          1 ACUUUUUUUUUUUUUUU 17
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RESULT 510
US-10-138-674-7622/c
; Sequence 7622, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7622
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7622

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3653 TAGCTCAGTCATCAAAG 3669
              |||||||||||||| ||
Db         17 TAGCTCAGTCATCAGAG 1
```

RESULT 511
US-10-287-949A-1073
; Sequence 1073, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1073

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 5.9%; Pred. No. 3.6e+02;
Matches 1; Conservative 15; Mismatches 1; Indels 0; Gaps 0;

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Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | :::::::::::::::
Db          1 ACUUUUUUUUUUUUUUU 17
```

RESULT 512
US-10-287-949A-7622/c
; Sequence 7622, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

```
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7622
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-7622

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 3.6e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3653 TAGCTCAGTCATCAAAG 3669
              ||||||||||||||| ||
Db         17 TAGCTCAGTCATCAGAG 1


RESULT 513
US-10-735-592-11
; Sequence 11, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-11

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 3.6e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTTCG 17


RESULT 514
US-10-735-592-14
; Sequence 14, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-14

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 3.6e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              | ||||||||||||||||
Db          1 ACGTTTTTTTTTTTTTT 17


RESULT 515
US-10-712-633-664/c
; Sequence 664, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Sandberg, Jennifer
;  APPLICANT:  Gordon, Gilad
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Stinchcomb, Dan
;  TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO
;  TITLE OF INVENTION:  RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND O
;  FILE REFERENCE: MBHB02-325PCT (400/047)
;  CURRENT APPLICATION NUMBER: US/10/712,633
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  PRIOR APPLICATION NUMBER: US 09/708,690
;  PRIOR FILING DATE: 2000-11-07
;  PRIOR APPLICATION NUMBER: US 09/870,161
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 60/334,461
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/138,674
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 5989
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 664
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-712-633-664

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 3.6e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3653 TAGCTCAGTCATCAAAG 3669
              ||||||||||||||| ||
Db         17 TAGCTCAGTCATCAGAG 1


RESULT 516
US-10-724-270-1260
; Sequence 1260, Application US/10724270
; Publication No. US20050080031A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
;  TITLE OF INVENTION:  RAS, HER2 and HIV
;  FILE REFERENCE: 400/046-US  (MBHB02-326-A)
;  CURRENT APPLICATION NUMBER: US/10/724,270
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/US02/16840
;  PRIOR FILING DATE: 2002-05-29
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;  PRIOR APPLICATION NUMBER: US 60/318,471
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: US 60/296,249
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/294,140
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 10/238,700
;  PRIOR FILING DATE: 2002-09-10
;  PRIOR APPLICATION NUMBER: US 10/163,552
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 10/157,580
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2002-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 10/417,012
;  PRIOR FILING DATE: 2003-04-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 6810
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1260
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-724-270-1260

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   58.8%;  Pred. No. 3.6e+02;
  Matches   10;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1475 ACAACTCTGCCTTTATG 1491
              |||| :|:|||:::|:|
Db          1 ACAAAUCUGCCUUUAUG 17


RESULT 517
US-10-951-303-1073
; Sequence 1073, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/10/951,303
;  CURRENT FILING DATE:  2004-09-27
;  PRIOR APPLICATION NUMBER: US/09/685,664
;  PRIOR FILING DATE: 2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-951-303-1073

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 3.6e+02;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | :::::::::::::::
Db          1 ACUUUUUUUUUUUUUUU 17


RESULT 518
US-09-725-265-17
; Sequence 17, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 519
US-09-725-265-20
; Sequence 20, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
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;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 520
US-09-891-517-17
; Sequence 17, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 521
US-09-891-517-20
; Sequence 20, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-20

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 522
US-09-888-326-85
; Sequence 85, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 85
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-85

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          1 ATATATATATATATATA 17


RESULT 523
US-09-888-326-85/c
; Sequence 85, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
```

```
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 85
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-85

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         18 ATATATATATATATATA 2


RESULT 524
US-09-823-887C-5
; Sequence 5, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
;  APPLICANT: Kumar, Sanjay
;  APPLICANT:  Lal, Lakhvir
;  APPLICANT:  Ahuja, Paramvir
;  TITLE OF INVENTION: Cloning of No. US20030180723A1el Gene Sequences Expressed and Rep
;  TITLE OF INVENTION:  Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
;  FILE REFERENCE: HO53916.0001US0
;  CURRENT APPLICATION NUMBER: US/09/823,887C
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer_bind
US-09-823-887C-5

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| |||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 525
US-09-823-887C-6
; Sequence 6, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
;  APPLICANT: Kumar, Sanjay
;  APPLICANT:  Lal, Lakhvir
;  APPLICANT:  Ahuja, Paramvir
;  TITLE OF INVENTION: Cloning of No. US20030180723A1el Gene Sequences Expressed and Rep
;  TITLE OF INVENTION:  Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
;  FILE REFERENCE: HO53916.0001US0
;  CURRENT APPLICATION NUMBER: US/09/823,887C
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer_bind
US-09-823-887C-6

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| |||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 526
US-09-823-887C-7
; Sequence 7, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
;  APPLICANT: Kumar, Sanjay
;  APPLICANT:  Lal, Lakhvir
;  APPLICANT:  Ahuja, Paramvir
;  TITLE OF INVENTION: Cloning of No. US20030180723A1el Gene Sequences Expressed and Rep
;  TITLE OF INVENTION:  Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
;  FILE REFERENCE: HO53916.0001US0
;  CURRENT APPLICATION NUMBER: US/09/823,887C
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer_bind
US-09-823-887C-7

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| |||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 527
US-10-209-608-17
; Sequence 17, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 528
US-10-209-608-20
; Sequence 20, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-20

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 529
US-10-272-970-18/c
; Sequence 18, Application US/10272970
; Publication No. US20030139578A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice K.
;  APPLICANT:  Cocks, Benjamin G.
;  APPLICANT:  Coleman, Roger T.
;  APPLICANT:  Seilhamer, Jeffrey J.
;  APPLICANT:  Fisher, Douglas A.
;  TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING PDE8A and PDE8B
;  FILE REFERENCE: PC-0054 CIP
;  CURRENT APPLICATION NUMBER: US/10/272,970
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 09/454,060
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: 09/255,748
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: 08/974,565
;  PRIOR FILING DATE: 1997-11-19
;  PRIOR APPLICATION NUMBER: 08/624,663
;  PRIOR FILING DATE: 1996-03-25
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PERL Program
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030139578A1 oligomer1
US-10-272-970-18

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              | ||||||||||||||||
Db         17 TTCTGCTGATGTGCTTC 1


RESULT 530
US-10-106-799-1
; Sequence 1, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
;  APPLICANT: Council of Scientific and Industrial Research
;  TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
;  TITLE OF INVENTION:  method thereof
;  FILE REFERENCE: US 673
;  CURRENT APPLICATION NUMBER: US/10/106,799
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: T11A anchored primers for differential display
US-10-106-799-1

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 531
US-10-106-799-2
; Sequence 2, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
;  APPLICANT: Council of Scientific and Industrial Research
;  TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
;  TITLE OF INVENTION:  method thereof
;  FILE REFERENCE: US 673
;  CURRENT APPLICATION NUMBER: US/10/106,799
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
```

```
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: T11C (anchored) primer for differential display
US-10-106-799-2

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 532
US-10-106-799-3
; Sequence 3, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
;  APPLICANT: Council of Scientific and Industrial Research
;  TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
;  TITLE OF INVENTION:  method thereof
;  FILE REFERENCE: US 673
;  CURRENT APPLICATION NUMBER: US/10/106,799
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: T11G (anchored) primer for differential display
US-10-106-799-3

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 533
US-10-333-461-18
; Sequence 18, Application US/10333461
; Publication No. US20030165952A1
; GENERAL INFORMATION:
;  APPLICANT: Global Genomics AB
;  APPLICANT:  Linnarsson, Sten
;  APPLICANT:  Ernfors, Patrik
;  APPLICANT:  Bauren, Goran
;  TITLE OF INVENTION: Methods for analysis and identification of transcribed
;  TITLE OF INVENTION:  genes, and fingerprinting
;  FILE REFERENCE: smwfp5941752
;  CURRENT APPLICATION NUMBER: US/10/333,461
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: GB 0018016.6
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/219,925
;  PRIOR FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Double-stranded product DNA
US-10-333-461-18

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 534
US-10-352-253A-18
; Sequence 18, Application US/10352253A
; Publication No. US20030175908A1
; GENERAL INFORMATION:
;  APPLICANT: Linnarsson, Sten
;  APPLICANT:  Ernfors, Patrik
;  APPLICANT:  Bauren, Goran
;  APPLICANT:  Metsis, Ats
;  APPLICANT:  Pihlak, Arno
;  APPLICANT:  Montelius, Andreas
;  TITLE OF INVENTION: Methods And Means For Manipulating Nucleic Acid
;  FILE REFERENCE: 620-234
;  CURRENT APPLICATION NUMBER: US/10/352,253A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: US 60/352,215
;  PRIOR FILING DATE: 2002-01-29
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Double-stranded product DNA
US-10-352-253A-18

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 535
US-10-109-363-16
; Sequence 16, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
;  APPLICANT: SHARMA, PRITI
;  APPLICANT:  KUMAR, SANJAY
;  APPLICANT:  AHUJA, PARAMVIR SINGH
;  TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
;  TITLE OF INVENTION:  METHOD OF INTRODUCING WATER-STRESS TOLERANCE
;  FILE REFERENCE: 3097-4009
;  CURRENT APPLICATION NUMBER: US/10/109,363
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Camellia sinensis
US-10-109-363-16

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 536
US-10-109-363-17
; Sequence 17, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
;  APPLICANT: SHARMA, PRITI
;  APPLICANT:  KUMAR, SANJAY
;  APPLICANT:  AHUJA, PARAMVIR SINGH
;  TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
;  TITLE OF INVENTION:  METHOD OF INTRODUCING WATER-STRESS TOLERANCE
;  FILE REFERENCE: 3097-4009
;  CURRENT APPLICATION NUMBER: US/10/109,363
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Camellia sinensis
US-10-109-363-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 537
US-10-109-363-18
; Sequence 18, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
;  APPLICANT: SHARMA, PRITI
;  APPLICANT:  KUMAR, SANJAY
;  APPLICANT:  AHUJA, PARAMVIR SINGH
;  TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
;  TITLE OF INVENTION:  METHOD OF INTRODUCING WATER-STRESS TOLERANCE
;  FILE REFERENCE: 3097-4009
;  CURRENT APPLICATION NUMBER: US/10/109,363
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Camellia sinensis
US-10-109-363-18

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 17


RESULT 538
US-10-352-255A-18
; Sequence 18, Application US/10352255A
; Publication No. US20030215839A1
; GENERAL INFORMATION:
;  APPLICANT: LONNERBERG, Peter
;  APPLICANT:  OLDIN, Mats
;  APPLICANT:  LINNARSSON, Sten
;  APPLICANT:  ERNFORS, Patrik
;  TITLE OF INVENTION: Methods and Means for Identification of Gene Features
;  FILE REFERENCE: 620-235
;  CURRENT APPLICATION NUMBER: US/10/352,255A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: US 60/352,245
;  PRIOR FILING DATE: 2002-01-29
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Double-stranded product DNA
US-10-352-255A-18

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 539
US-10-297-068-878/c
; Sequence 878, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 878
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-878

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4390 TGCAGGATTCCCTTCTG 4406
              | ||||||||||||||||
Db         17 TCCAGGATTCCCTTCTG 1


RESULT 540
US-10-108-260A-5080/c
; Sequence 5080, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
```

```
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5080
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-10-108-260A-5080

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3812 AGGCATCCTTGTCTTTT 3828
              ||||||| |||||||||
Db         17 AGGCATCGTTGTCTTTT 1


RESULT 541
US-10-627-929-10/c
; Sequence 10, Application US/10627929
; Publication No. US20040018605A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice; Cocks, Benjamin G.
;  APPLICANT:  Coleman, Roger; Seilhamer, Jeffrey J.
;  APPLICANT:  Fisher, Douglas A.
;  TITLE OF INVENTION: CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
;  FILE REFERENCE: PF-0057-4 CON
;  CURRENT APPLICATION NUMBER: US/10/627,929
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: US 09/454,060
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: US 08/974,565
;  PRIOR FILING DATE: 1997-11-19
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 10
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-627-929-10

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              | |||||||||||||||
Db         17 TTCTGCTGATGTGCTTC 1


RESULT 542
US-10-683-386-17
; Sequence 17, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-17

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 543
US-10-683-386-20
; Sequence 20, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-20

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 544
US-09-917-138-2/c
; Sequence 2, Application US/09917138
; Patent No. US20020031776A1
; GENERAL INFORMATION:
;  APPLICANT: TULLIS, Richard
;  APPLICANT:  STEIFFEL, Jerome
;  TITLE OF INVENTION: ENZYMATIC LABELIING AND DETECTION OF DNA
;  TITLE OF INVENTION:  HYBRIDIZATION PROBES
;  FILE REFERENCE: 24730-2207B
;  CURRENT APPLICATION NUMBER: US/09/917,138
;  CURRENT FILING DATE:  2001-07-26
```

```
;  PRIOR APPLICATION NUMBER: 09/580,358
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/136,545
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Combined DNA/RNA
US-09-917-138-2

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ||||||||||||||||
Db         19 ATTTTTTTTTTTTTTTT 3


RESULT 545
US-09-750-373-40/c
; Sequence 40, Application US/09750373
; Patent No. US20020062013A1
; GENERAL INFORMATION:
;  APPLICANT: Lind, Peter
;  APPLICANT:  Wood, Linda S.
;  APPLICANT:  Hiebsch, Ronald
;  APPLICANT:  Ruff, Valerie
;  APPLICANT:  Lindberg, Eleni
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Vogeli, Gabriel
;  TITLE OF INVENTION: No. US20020062013A1el G Protein Coupled Receptors
;  FILE REFERENCE: PHRM-0300
;  CURRENT APPLICATION NUMBER: US/09/750,373
;  CURRENT FILING DATE:  2000-12-28
;  PRIOR APPLICATION NUMBER: 60/184,305
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/188,880
;  PRIOR FILING DATE: 2000-03-13
;  PRIOR APPLICATION NUMBER: 60/219,492
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/173,339
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/224,321
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: 60/200,534
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/239,062
;  PRIOR FILING DATE: 2000-10-09
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: No. US20020062013A1el Sequence
US-09-750-373-40

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3422 GGGCAAGAACCCAAGTG 3438
              |||||||||| ||||||
Db         19 GGGCAAGAACACAAGTG 3


RESULT 546
US-09-923-327-224/c
; Sequence 224, Application US/09923327
; Publication No. US20030096236A1
; GENERAL INFORMATION:
;  APPLICANT: MURPHY, Patricia D.
;  TITLE OF INVENTION: Determining Common Functional Alleles in a Population and Uses The
;  FILE REFERENCE: 044921-5054-02
;  CURRENT APPLICATION NUMBER: US/09/923,327
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: US 08/598,591
;  PRIOR FILING DATE: 1996-02-12
;  PRIOR APPLICATION NUMBER: US 08/798,691
;  PRIOR FILING DATE: 1997-02-12
;  PRIOR APPLICATION NUMBER: US 08/905,772
;  PRIOR FILING DATE: 1997-08-04
;  PRIOR APPLICATION NUMBER: US 09/084,471
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: US 09/129,134
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: US 09/524,794
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 260
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 224
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-923-327-224

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4353 AAAGGGGCCTGAGTGGA 4369
              ||||||||||||  ||||
Db         19 AAAGGGGCCTGATTGGA 3


RESULT 547
US-10-665-951-939/c
; Sequence 939, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/131 (MBHB02-742-F)
;  CURRENT APPLICATION NUMBER: US/10/665,951
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
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;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2455
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 939
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-665-951-939

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              ||||||||| |||||||
Db         18 CTGCTTCTCCTTTGAAA 2


RESULT 548
US-10-665-951-1263
; Sequence 1263, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/131 (MBHB02-742-F)
;  CURRENT APPLICATION NUMBER: US/10/665,951
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2455
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1263
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-665-951-1263

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   52.9%;  Pred. No. 4e+02;
  Matches    9;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              |:||::|:| :::||||
Db          2 CUGCUUCUCCUUUGAAA 18


RESULT 549
US-10-800-487-162
; Sequence 162, Application US/10800487
; Publication No. US20050048529A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Intercellular Adhesion
;  TITLE OF INVENTION:  Molecule (ICAM) Gene Expression Using Short Interfering Nucleic
;  TITLE OF INVENTION:  Acid (siNA)
;  FILE REFERENCE: 400/148 (MBHB04-218)
;  CURRENT APPLICATION NUMBER: US/10/800,487
;  CURRENT FILING DATE:  2004-03-15
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-15
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 10/427,160
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 438
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-800-487-162

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   5.9%;  Pred. No. 4e+02;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ::::::::::::::::
Db          2 AUUUUUUUUUUUUUUUU 18


RESULT 550
US-10-800-487-328/c
; Sequence 328, Application US/10800487
; Publication No. US20050048529A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Intercellular Adhesion
;  TITLE OF INVENTION:  Molecule (ICAM) Gene Expression Using Short Interfering Nucleic
;  TITLE OF INVENTION:  Acid (siNA)
;  FILE REFERENCE: 400/148 (MBHB04-218)
;  CURRENT APPLICATION NUMBER: US/10/800,487
;  CURRENT FILING DATE:  2004-03-15
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-15
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;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 10/427,160
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 438
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 328
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-800-487-328

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ||||||||||||||||
Db         18 ATTTTTTTTTTTTTTTT 2


RESULT 551
US-10-758-155-939/c
; Sequence 939, Application US/10758155
; Publication No. US20050075304A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/141 (MBHB02742-N)
;  CURRENT APPLICATION NUMBER: US/10/758,155
;  CURRENT FILING DATE:  2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 939
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense re
US-10-758-155-939

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              ||||||||| |||||||
Db         18 CTGCTTCTCCTTTGAAA 2


RESULT 552
US-10-758-155-1263
; Sequence 1263, Application US/10758155
; Publication No. US20050075304A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/141 (MBHB02742-N)
;  CURRENT APPLICATION NUMBER: US/10/758,155
;  CURRENT FILING DATE:  2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/287,949
;  PRIOR FILING DATE: 2002-11-04
;  PRIOR APPLICATION NUMBER: US 10/306,747
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: PCT/US 02/17674
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1263
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-758-155-1263

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   52.9%;  Pred. No. 4e+02;
  Matches    9;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              |:||::|:| :::||||
Db          2 CUGCUUCUCCUUUGAAA 18
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RESULT 553
US-10-831-620-939/c
; Sequence 939, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/152 (MBHB02-742-Q)
;  CURRENT APPLICATION NUMBER: US/10/831,620
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 939
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-831-620-939

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              ||||||||| |||||||
Db         18 CTGCTTCTCCTTTGAAA 2


RESULT 554
US-10-831-620-1263
; Sequence 1263, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/152 (MBHB02-742-Q)
;  CURRENT APPLICATION NUMBER: US/10/831,620
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2751
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1263
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-831-620-1263

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   52.9%;  Pred. No. 4e+02;
  Matches    9;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              |:||::|:| :::||||
Db          2 CUGCUUCUCCUUUGAAA 18


RESULT 555
US-10-844-076-939/c
; Sequence 939, Application US/10844076
; Publication No. US20050171039A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/159 (MBHB02-742-R)
;  CURRENT APPLICATION NUMBER: US/10/844,076
;  CURRENT FILING DATE:  2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
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;  PRIOR FILING DATE: 2003-09-18
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2755
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 939
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-844-076-939

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              ||||||||| |||||||
Db         18 CTGCTTCTCCTTTGAAA 2


RESULT 556
US-10-844-076-1263
; Sequence 1263, Application US/10844076
; Publication No. US20050171039A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/159 (MBHB02-742-R)
;  CURRENT APPLICATION NUMBER: US/10/844,076
;  CURRENT FILING DATE:  2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/758,155
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/712,633
;  PRIOR FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,951
;  PRIOR FILING DATE: 2003-09-18
;  PRIOR APPLICATION NUMBER: US 10/664,668
;  PRIOR FILING DATE: 2003-09-18
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2755
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1263
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-844-076-1263

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   52.9%;  Pred. No. 4e+02;
  Matches    9;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              |:||::|:| :::||||
Db          2 CUGCUUCUCCUUUGAAA 18


RESULT 557
US-10-923-181-162
; Sequence 162, Application US/10923181
; Publication No. US20050187174A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Intercellular Adhesion
;  TITLE OF INVENTION:  Molecule (ICAM) Gene Expression Using Short Interfering Nucleic
;  TITLE OF INVENTION:  Acid (siNA)
;  FILE REFERENCE: 400/221 (MBHB04-218-A)
;  CURRENT APPLICATION NUMBER: US/10/923,181
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: US 10/800,487
;  PRIOR FILING DATE: 2004-03-15
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: PCT/US04/13456
;  PRIOR FILING DATE: 2004-04-30
;  PRIOR APPLICATION NUMBER: US 10/780,447
;  PRIOR FILING DATE: 2004-02-13
;  PRIOR APPLICATION NUMBER: US 60/292,217
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/362,016
;  PRIOR FILING DATE: 2002-03-06
;  PRIOR APPLICATION NUMBER: US 60/306,883
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/311,865
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: US 10/727,780
;  PRIOR FILING DATE: 2003-12-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense re
US-10-923-181-162

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   5.9%;  Pred. No. 4e+02;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              | ::::::::::::::::
Db          2 AUUUUUUUUUUUUUUUU 18


RESULT 558
US-10-923-181-328/c
; Sequence 328, Application US/10923181
; Publication No. US20050187174A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Intercellular Adhesion
;  TITLE OF INVENTION:  Molecule (ICAM) Gene Expression Using Short Interfering Nucleic
;  TITLE OF INVENTION:  Acid (siNA)
;  FILE REFERENCE: 400/221 (MBHB04-218-A)
;  CURRENT APPLICATION NUMBER: US/10/923,181
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: US 10/800,487
;  PRIOR FILING DATE: 2004-03-15
```

```
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: PCT/US04/13456
;  PRIOR FILING DATE: 2004-04-30
;  PRIOR APPLICATION NUMBER: US 10/780,447
;  PRIOR FILING DATE: 2004-02-13
;  PRIOR APPLICATION NUMBER: US 60/292,217
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/362,016
;  PRIOR FILING DATE: 2002-03-06
;  PRIOR APPLICATION NUMBER: US 60/306,883
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/311,865
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: US 10/727,780
;  PRIOR FILING DATE: 2003-12-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 328
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-923-181-328

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4515
              | ||||||||||||||||
Db         18 ATTTTTTTTTTTTTTT 2


RESULT 559
US-10-708-204-3039
; Sequence 3039, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
;  APPLICANT: ROSETTA GENOMICS LTD
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 55033
;  CURRENT APPLICATION NUMBER: US/10/708,204
;  CURRENT FILING DATE:  2004-02-16
;  NUMBER OF SEQ ID NOS: 7351
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3039
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Homo Sapiens
US-10-708-204-3039

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 4e+02;
  Matches   12;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2982 TGCTGTCCAGGCAGCTC 2998
              :| :|:|||||||||:|
Db          1 UGUUGUCCAGGCAGCUC 17


RESULT 560
US-10-962-898-939/c
; Sequence 939, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor And Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/236 (MBHB02-742-U)
;  CURRENT APPLICATION NUMBER: US/10/962,898
;  CURRENT FILING DATE:  2004-10-12
;  PRIOR APPLICATION NUMBER: US 10/944,644
;  PRIOR FILING DATE: 2004-09-16
;  PRIOR APPLICATION NUMBER: US 10/844,076
;  PRIOR FILING DATE: 2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: US 10/664,767
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 939
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-962-898-939

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              ||||||||| |||||||
Db         18 CTGCTTCTCCTTTGAAA 2


RESULT 561
US-10-962-898-1263
; Sequence 1263, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor And Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/236 (MBHB02-742-U)
;  CURRENT APPLICATION NUMBER: US/10/962,898
;  CURRENT FILING DATE:  2004-10-12
;  PRIOR APPLICATION NUMBER: US 10/944,644
;  PRIOR FILING DATE: 2004-09-16
;  PRIOR APPLICATION NUMBER: US 10/844,076
;  PRIOR FILING DATE: 2004-05-11
;  PRIOR APPLICATION NUMBER: US 10/831,620
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 10/764,957
;  PRIOR FILING DATE: 2004-01-26
;  PRIOR APPLICATION NUMBER: US 10/670,011
;  PRIOR FILING DATE: 2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/665,255
```

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;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: US 10/664,767
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1263
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-962-898-1263

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   52.9%;  Pred. No. 4e+02;
  Matches    9;  Conservative    7;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3035 CTGCTTCTCTTTTGAAA 3051
              |:||::|:| :::||||
Db          2 CUGCUUCUCCUUUGAAA 18


RESULT 562
US-10-015-593-2
; Sequence 2, Application US/10015593
; Publication No. US20020090636A1
; GENERAL INFORMATION:
;  APPLICANT: Kozian, Detlef
;  APPLICANT:  Reuner, Birgit
;  TITLE OF INVENTION: Two-color differential display as a method for
;  TITLE OF INVENTION:  detecting regulated genes
;  FILE REFERENCE: 2481-1635
;  CURRENT APPLICATION NUMBER: US/10/015,593
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/390,324
;  PRIOR FILING DATE: 2001-05-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-10-015-593-2

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.9e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTTV 16


RESULT 563
US-10-380-596A-5
; Sequence 5, Application US/10380596A
; Publication No. US20040053275A1
; GENERAL INFORMATION:
;  APPLICANT: Shafer, David A.
;  TITLE OF INVENTION: Systems and Methods to Quantify and Amplify
;  TITLE OF INVENTION:  Both Signaling and Probes for cDNA Chips and
;  TITLE OF INVENTION:  Gene Expression Microarrays
;  FILE REFERENCE: D6430
;  CURRENT APPLICATION NUMBER: US/10/380,596A
;  CURRENT FILING DATE:  2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/US01/07508
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: random_base
;   LOCATION: 16...17
;   OTHER INFORMATION: Modified poly-T primer; v=a, c, or g at position 16;
;   OTHER INFORMATION: n=a, c, g, or t at position 17
US-10-380-596A-5

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.9e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTTV 16


RESULT 564
US-10-872-645-29
; Sequence 29, Application US/10872645
; Publication No. US20050100887A1
; GENERAL INFORMATION:
;  APPLICANT: AXXIMA Pharmaceuticals AG
;  APPLICANT:  Salassidis, Konstadinos
;  APPLICANT:  Schubart, Daniel
;  APPLICANT:  Gutbrod, Heidrun
;  APPLICANT:  Mueller, Stefan
;  APPLICANT:  Kraetzer, Friedrich
;  APPLICANT:  Obert, Sabine
;  TITLE OF INVENTION: Targets for Hepatitis C Virus Infections
;  FILE REFERENCE: AXM-014.1 US
;  CURRENT APPLICATION NUMBER: US/10/872,645
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: PCT/EP02/14578
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/341,757
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: v = a or g or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (18)..(18)
;   OTHER INFORMATION: n=a or g or t or c
US-10-872-645-29

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 3.9e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTTV 16
```

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RESULT 565
US-09-981-397A-1
; Sequence 1, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
;  APPLICANT: Axxima Pharmaceuticals AG
;  APPLICANT:  Schubart, Daniel
;  APPLICANT:  Habenberger, Peter
;  APPLICANT:  Stein-Gerlach, Matthias
;  APPLICANT:  Bevec, Dorian
;  TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
;  TITLE OF INVENTION:  Inhibition
;  FILE REFERENCE: AXM-004.1 US
;  CURRENT APPLICATION NUMBER: US/09/981,397A
;  CURRENT FILING DATE:  2002-06-28
;  PRIOR APPLICATION NUMBER: 60/240,750
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polyT primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (18)..(18)
;   OTHER INFORMATION: n = a,c,g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: v = a,g or c
US-09-981-397A-1

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          2 TTTTTTTTTTTTTTV 17


RESULT 566
US-09-371-307-85
; Sequence 85, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Sherri M.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: Piller, Kenneth J.
;  APPLICANT: Kishore, Ganesh M.
;  APPLICANT: Elich, Tedd D.
;  APPLICANT: Logusch, Eugene W.
;  APPLICANT: Rao, Sudabathula
;  APPLICANT: Ream, Joel E.
;  APPLICANT: Logusch, Sherry J.
;  TITLE OF INVENTION: Methods for controlling gibberellin levels
;  FILE REFERENCE: MOBT:216
;  CURRENT APPLICATION NUMBER: US/09/371,307A
;  CURRENT FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-371-307-85

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 567
US-10-103-614A-4/c
; Sequence 4, Application US/10103614A
; Publication No. US20030059796A1
; GENERAL INFORMATION:
;  APPLICANT: SALMAN AL-MAHMOOD
;  TITLE OF INVENTION: METHOD FOR IDENTIFYING NOVEL GENES INVOLVED IN THE
;  TITLE OF INVENTION:  REGULATION OF ANGIOGENESIS, STUDY OF SAID GENES AND USE
;  TITLE OF INVENTION:  THEREOF FOR THERAPEUTIC PURPOSES
;  FILE REFERENCE: 1071-02
;  CURRENT APPLICATION NUMBER: US/10/103,614A
;  CURRENT FILING DATE:  2002-08-22
;  PRIOR APPLICATION NUMBER: PCT/FR00/02607
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: FR 99/11790
;  PRIOR FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   NAME/KEY: modified_base
;   LOCATION: (1)
;   OTHER INFORMATION: a, t, c or g
;   NAME/KEY: modified_base
;   LOCATION: (19)
;   OTHER INFORMATION: a, t, c or g
US-10-103-614A-4

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db         17 TTTTTTTTTTTTTTB 2


RESULT 568
US-10-176-884-44
; Sequence 44, Application US/10176884
; Publication No. US20030126642A1
; GENERAL INFORMATION:
;  APPLICANT: Fischer, Robert
;  APPLICANT:  Kinoshita, Tetsu
;  APPLICANT:  Yadegari, Ramin
;  APPLICANT:  Gehring, Mary
;  APPLICANT:  Okamuro, Jack
;  APPLICANT:  Dang, Van-Dinh
;  APPLICANT:  The Regents of the University of California
;  APPLICANT:  Ceres, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Modulating Plant
;  TITLE OF INVENTION:  Development
;  FILE REFERENCE: 02307O-116710US
;  CURRENT APPLICATION NUMBER: US/10/176,884
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/300,506
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
```

```
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo(dT)-18
;   OTHER INFORMATION: primer, oligo dTV
US-10-176-884-44

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 569
US-10-177-478-1
; Sequence 1, Application US/10177478
; Publication No. US20030165903A1
; GENERAL INFORMATION:
;  APPLICANT: Dang, Van-Dinh
;  APPLICANT:  Okamuro, Jack
;  TITLE OF INVENTION: Chimeric Histone Acetyltransferase
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 11696-037001
;  CURRENT APPLICATION NUMBER: US/10/177,478
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: U.S. 60/300,135
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-177-478-1

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 570
US-10-182-230-196
; Sequence 196, Application US/10182230
; Publication No. US20030215817A1
; GENERAL INFORMATION:
;  APPLICANT: Leonardi, Amedeo
;  APPLICANT:  Sartani, Abraham
;  APPLICANT:  Glass, James R.
;  APPLICANT:  Sutcliffe, J. Gregor
;  APPLICANT:  Hasel, Karl W.
;  TITLE OF INVENTION: Modulation of Gene Expression in Formation of Fatty Atherosclerot
;  TITLE OF INVENTION:  Lesions
;  FILE REFERENCE: 216019-143
;  CURRENT APPLICATION NUMBER: US/10/182,230
;  CURRENT FILING DATE:  2003-02-03
;  PRIOR APPLICATION NUMBER: 60/177,963
;  PRIOR FILING DATE: 2000-01-25
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 3' sequencing primer for dire
;   OTHER INFORMATION: ct sequencing
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (19)..(19)
;   OTHER INFORMATION: v stands for a, c, or g
US-10-182-230-196

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 571
US-10-401-321-85
; Sequence 85, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Sherri M.
;  APPLICANT:  Heck, Gregory R.
;  APPLICANT:  Piller, Kenneth J.
;  APPLICANT:  Kilshore, Ganesh M.
;  APPLICANT:  Elich, Tedd D.
;  APPLICANT:  Logusch, Eugene W.
;  APPLICANT:  Rao, Sudabathula
;  APPLICANT:  Ream, Joel E.
;  APPLICANT:  Logusch, Sherry J.
;  APPLICANT:  Baerson, Scott R.
;  TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
;  FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
;  CURRENT APPLICATION NUMBER: US/10/401,321
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-401-321-85

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 572
US-10-965-470-1
; Sequence 1, Application US/10965470
; Publication No. US20050204429A1
; GENERAL INFORMATION:
;  APPLICANT: PENNELL, Roger
;  APPLICANT:  APUYA, Nestor
;  APPLICANT:  MEDRANO, Leonard
;  APPLICANT:  FELDMANN, Kenneth
;  TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2750-1580PUS2
;  CURRENT APPLICATION NUMBER: US/10/965,470
;  CURRENT FILING DATE:  2004-10-13
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
```

```
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-965-470-1

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 573
US-10-950-095-73
; Sequence 73, Application US/10950095
; Publication No. US20050223434A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai, et. al.
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
;  TITLE OF INVENTION:  MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1578PUS2
;  CURRENT APPLICATION NUMBER: US/10/950,095
;  CURRENT FILING DATE:  2004-09-23
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligo(dT)18 primer
US-10-950-095-73

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 574
US-10-950-321-1
; Sequence 1, Application US/10950321
; Publication No. US20050223422A1
; GENERAL INFORMATION:
;  APPLICANT: COOK, Zhihong et al.
;  TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2750-1577PUS2
;  CURRENT APPLICATION NUMBER: US/10/950,321
;  CURRENT FILING DATE:  2004-09-23
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligo(dT)18 primer
US-10-950-321-1

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 575
US-11-051-456-44
; Sequence 44, Application US/11051456
; Publication No. US20050229270A1
; GENERAL INFORMATION:
;  APPLICANT: Fischer, Robert
;  APPLICANT:  Kinoshita, Tetsu
;  APPLICANT:  Yadegari, Ramin
;  APPLICANT:  Gehring, Mary
;  APPLICANT:  Okamuro, Jack
;  APPLICANT:  Dang, Van-Dinh
;  APPLICANT:  The Regents of the University of California
;  APPLICANT:  Ceres, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Modulating Plant
;  TITLE OF INVENTION:  Development
;  FILE REFERENCE: 02307O-116710US
;  CURRENT APPLICATION NUMBER: US/11/051,456
;  CURRENT FILING DATE:  2005-02-04
;  PRIOR APPLICATION NUMBER: US/10/176,884
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/300,506
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo(dT)-18
;   OTHER INFORMATION: primer, oligo dTV
US-11-051-456-44

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 4.3e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 576
US-09-504-231A-22
; Sequence 22, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 15
;   TYPE: RNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-22

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 3.8e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 577
US-09-930-218-5
; Sequence 5, Application US/09930218
; Patent No. US20020034810A1
; GENERAL INFORMATION:
;  APPLICANT: goldshmidt, orit
;  APPLICANT:  pecker, iris
;  APPLICANT:  vlodavsky, israel
;  APPLICANT:  israel, michal
;  TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H
;  TITLE OF INVENTION:  HEPARANASE ACTIVITY
;  FILE REFERENCE: 01/22335
;  CURRENT APPLICATION NUMBER: US/09/930,218
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/666,390
;  PRIOR FILING DATE: 2000-09-20
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide
US-09-930-218-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 578
US-09-274-553D-22
; Sequence 22, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/274,553D
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3148
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-274-553D-22

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 3.8e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 579
US-09-776-874A-5
; Sequence 5, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY A
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 01/22603
;  CURRENT APPLICATION NUMBER: US/09/776,874A
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: US 08/922,170
;  PRIOR FILING DATE: 1997-09-02
;  PRIOR APPLICATION NUMBER: US 09/109,386
;  PRIOR FILING DATE: 1998-07-10
;  PRIOR APPLICATION NUMBER: PCT/US98/17954
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
US-09-776-874A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 580
US-09-955-410-17
; Sequence 17, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
;  FILE REFERENCE: ISIS4800
;  CURRENT APPLICATION NUMBER: US/09/955,410
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: 09/686,114
;  PRIOR FILING DATE: 1996-07-24
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20020146718A1el Sequence
US-09-955-410-17

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 581
US-09-955-410-18/c
; Sequence 18, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
;  FILE REFERENCE: ISIS4800
;  CURRENT APPLICATION NUMBER: US/09/955,410
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: 09/686,114
;  PRIOR FILING DATE: 1996-07-24
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20020146718A1el Sequence
US-09-955-410-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 582
US-09-263-959-543/c
; Sequence 543, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  543:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-543

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATAT 2409
              |||||||||||||||
Db         15 TATATATACATATAT 1


RESULT 583
US-09-263-959-545/c
; Sequence 545, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  545:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-545

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATAT 2409
              ||||||||||||||||
Db         15 TATATATACATATAT 1


RESULT 584
US-09-805-296D-10
; Sequence 10, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
;  FILE REFERENCE: AM102.P.1US
;  CURRENT APPLICATION NUMBER: US/09/805,296D
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: SynthetiConstruct
US-09-805-296D-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 585
US-09-983-210-19
; Sequence 19, Application US/09983210
; Patent No. US20020160383A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;    TITLE OF INVENTION:  DIAGNOSTICS AND ANALYTICAL PROCEDURES
;    NUMBER OF SEQUENCES:  40
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/983,210
;      FILING DATE:  2001-OCT-23
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150156
;      FILING DATE:  1994-APR-05
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0986/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0987/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0510/92
;      FILING DATE:  15-APR-1992
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      DOCUMENT NUMBER:  WO PCT/EP92/01220
;      FILING DATE:  22-MAY-1992
US-09-983-210-19

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 586
US-09-983-210-20/c
; Sequence 20, Application US/09983210
; Patent No. US20020160383A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;    TITLE OF INVENTION:  DIAGNOSTICS AND ANALYTICAL PROCEDURES
;    NUMBER OF SEQUENCES:  40
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/983,210
;      FILING DATE:  2001-OCT-23
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/150156
;      FILING DATE:  1994-APR-05
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0986/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0987/91
;      FILING DATE:  24-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 0510/92
;      FILING DATE:  15-APR-1992
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      DOCUMENT NUMBER:  WO PCT/EP92/01220
;      FILING DATE:  22-MAY-1992
US-09-983-210-20

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
```

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1
```

RESULT 587
US-09-850-982B-4
; Sequence 4, Application US/09850982B
; Patent No. US20020166145A1
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: COFFEE MANNANASE
; FILE REFERENCE: 88265-4025
; CURRENT APPLICATION NUMBER: US/09/850,982B
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotides provided by Eurogentec (Parc Scientifi
; OTHER INFORMATION: que due Sart Tilman [Sart Tilman Scientific Park]-4102 Seraing-Be
; OTHER INFORMATION: lguim).
US-09-850-982B-4

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

RESULT 588
US-09-988-113-5
; Sequence 5, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-5

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

RESULT 589
US-09-793-146-54
; Sequence 54, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-54

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

RESULT 590
US-09-793-146-55
; Sequence 55, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-55

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 591
US-10-208-357-21/c
; Sequence 21, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 50036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,357
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/619,103
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 60/145,834
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-21

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 592
US-10-176-055-9/c
; Sequence 9, Application US/10176055
; Publication No. US20030013109A1
; GENERAL INFORMATION:
;  APPLICANT: Evident Technologies
;  TITLE OF INVENTION: Haiprin Sensors Using Quenchable Fluorescing Agents
;  FILE REFERENCE: 11739/26
;  CURRENT APPLICATION NUMBER: US/10/176,055
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,460
;  PRIOR FILING DATE: 2001-06-21
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Target sequence
;   FEATURE:
;   OTHER INFORMATION: Target sequence that is desired to be detected and
;   OTHER INFORMATION: that has a nucleotide sequence that is
;   OTHER INFORMATION: complementary to the sequence of complementary
;   OTHER INFORMATION: probe of hairpin loop assembly
US-10-176-055-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 593
US-10-202-189-9
; Sequence 9, Application US/10202189
; Publication No. US20030022225A1
; GENERAL INFORMATION:
;  APPLICANT: Monforte, Joseph A.
;  APPLICANT:  Becker, Christopher H.
;  APPLICANT:  Pollart, Daniel J.
;  APPLICANT:  Shaler, Thomas A.
;  TITLE OF INVENTION: Releasable No. US20030022225A1volatile Mass-Label Molecules
;  FILE REFERENCE: 24736-2057D
;  CURRENT APPLICATION NUMBER: US/10/202,189
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER:
;  PRIOR APPLICATION NUMBER: US 08/988,024
;  PRIOR FILING DATE: 1997-12-10
;  PRIOR APPLICATION NUMBER: US 60/033,037
;  PRIOR FILING DATE: 1996-12-10
;  PRIOR APPLICATION NUMBER: US 60/046,719
;  PRIOR FILING DATE: 1997-05-16
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-202-189-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 594
US-10-072-975-10
; Sequence 10, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USI
;  FILE REFERENCE: AM102.P.1.1US
;  CURRENT APPLICATION NUMBER: US/10/072,975
;  CURRENT FILING DATE:  2002-02-09
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: PCT/US01/0811
;  PRIOR FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 15
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthtic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: SynthetiConstruct
US-10-072-975-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 595
US-10-227-001-23
; Sequence 23, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
;  APPLICANT: Dempcy, Robert O.
;  APPLICANT:  Afonina, Irina Aleksandrovna
;  APPLICANT:  Vermeulen, Nicolaas M.J.
;  APPLICANT:  Epoch Biosciences, Inc.
;  TITLE OF INVENTION: Hybridization-Triggered Fluorescent
;  TITLE OF INVENTION:  Detection of Nucleic Acids
;  FILE REFERENCE: 17682A-004210US
;  CURRENT APPLICATION NUMBER: US/10/227,001
;  CURRENT FILING DATE:  2002-08-21
;  PRIOR APPLICATION NUMBER: US 09/428,236
;  PRIOR FILING DATE: 1999-10-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN
;   OTHER INFORMATION: conjugate
US-10-227-001-23

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 596
US-10-341-582-5
; Sequence 5, Application US/10341582
; Publication No. US20030161823A1
; GENERAL INFORMATION:
;  APPLICANT: Neta Ilan
;  APPLICANT:  Israel Vlodavsky
;  APPLICANT:  Oron Yacoby-Zeevi
;  APPLICANT:  Iris Pecker
;  TITLE OF INVENTION: THERAPEUTIC AND COSMETIC USES OF HEPARANASES
;  FILE REFERENCE: 25449
;  CURRENT APPLICATION NUMBER: US/10/341,582
;  CURRENT FILING DATE:  2003-01-14
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-341-582-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 597
US-10-106-749-1
; Sequence 1, Application US/10106749
; Publication No. US20030165879A1
; GENERAL INFORMATION:
;  APPLICANT: Inscent, Inc.
;  APPLICANT:  Woods, Daniel
;  APPLICANT:  Dimitratos, Spiros
;  TITLE OF INVENTION: EFFICIENT METHODS FOR ISOLATING FUNCTIONAL G-PROTEIN COUPLED RECE
;  TITLE OF INVENTION:  AND IDENTIFYING ACTIVE EFFECTORS AND EFFICEINT METHODS TO ISOLAT
;  TITLE OF INVENTION:  INVOVLVED IN OLFACTION AND IDENTIFYING ACTIVE EFFECTORS
;  FILE REFERENCE: INS-00101.P.1.1
;  CURRENT APPLICATION NUMBER: US/10/106,749
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: 60/279,168
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 60/353,392
;  PRIOR FILING DATE: 2002-01-31
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-106-749-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 598
US-10-106-749-5
; Sequence 5, Application US/10106749
; Publication No. US20030165879A1
; GENERAL INFORMATION:
;  APPLICANT: Inscent, Inc.
;  APPLICANT:  Woods, Daniel
;  APPLICANT:  Dimitratos, Spiros
;  TITLE OF INVENTION: EFFICIENT METHODS FOR ISOLATING FUNCTIONAL G-PROTEIN COUPLED RECE
;  TITLE OF INVENTION:  AND IDENTIFYING ACTIVE EFFECTORS AND EFFICEINT METHODS TO ISOLAT
;  TITLE OF INVENTION:  INVOVLVED IN OLFACTION AND IDENTIFYING ACTIVE EFFECTORS
;  FILE REFERENCE: INS-00101.P.1.1
;  CURRENT APPLICATION NUMBER: US/10/106,749
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: 60/279,168
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 60/353,392
;  PRIOR FILING DATE: 2002-01-31
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Synthetic Construct
US-10-106-749-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 599
US-10-384-451-5
; Sequence 5, Application US/10384451
; Publication No. US20030170860A1
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 25718
;  CURRENT APPLICATION NUMBER: US/10/384,451
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-384-451-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 600
US-10-269-031A-54
; Sequence 54, Application US/10269031A
; Publication No. US20030175749A1
; GENERAL INFORMATION:
;  APPLICANT: JONG-YOON, CHUN
;  TITLE OF INVENTION: ANNEALING CONTROL PRIMER AND ITS USES
;  FILE REFERENCE: 64488-012
;  CURRENT APPLICATION NUMBER: US/10/269,031A
;  CURRENT FILING DATE:  2002-10-11
;  PRIOR APPLICATION NUMBER: 10/014,496
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: PCT/KR01/02133
;  PRIOR FILING DATE: 2001-12-08
;  NUMBER OF SEQ ID NOS: 125
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-269-031A-54

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 601
US-10-352-704-10
; Sequence 10, Application US/10352704
; Publication No. US20030176690A1
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..15
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-352-704-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 602
US-10-352-704-16/c
; Sequence 16, Application US/10352704
; Publication No. US20030176690A1
```

```
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..15
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-352-704-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 603
US-10-154-890-17
; Sequence 17, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/10/154,890
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: US/08/108,591
;  PRIOR FILING DATE: 2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20030180734A1el Sequence
US-10-154-890-17

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 604
US-10-154-890-18/c
; Sequence 18, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/10/154,890
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: US/08/108,591
;  PRIOR FILING DATE: 2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20030180734A1el Sequence
US-10-154-890-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 605
US-10-431-438-5
; Sequence 5, Application US/10431438
; Publication No. US20030180788A1
; GENERAL INFORMATION:
;  APPLICANT: goldshmidt, orit
;  APPLICANT:  pecker, iris
;  APPLICANT:  vlodavsky, israel
;  APPLICANT:  israel, michal
;  TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H
;  TITLE OF INVENTION:  HEPARANASE ACTIVITY
;  FILE REFERENCE: 26013
;  CURRENT APPLICATION NUMBER: US/10/431,438
;  CURRENT FILING DATE:  2003-05-08
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
```

```
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide
US-10-431-438-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 606
US-10-091-231-2
; Sequence 2, Application US/10091231
; Publication No. US20030181712A1
; GENERAL INFORMATION:
;  APPLICANT: NELSON, Jeffrey S.
;  TITLE OF INVENTION: REAGENTS FOR OLIGONUCLEOTIDE CLEAVAGE AND DEPROTECTION
;  FILE REFERENCE: 4688US
;  CURRENT APPLICATION NUMBER: US/10/091,231
;  CURRENT FILING DATE:  2002-03-04
;  PRIOR APPLICATION NUMBER: US 60/274,309
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-091-231-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 607
US-10-384-450-5
; Sequence 5, Application US/10384450
; Publication No. US20030190737A1
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 25717
;  CURRENT APPLICATION NUMBER: US/10/384,450
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-384-450-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 608
US-10-440-850-323/c
; Sequence 323, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Revers
;  TITLE OF INVENTION:  Immune Responses
;  FILE REFERENCE: 250/130 (MBHB00-900-A)
;  CURRENT APPLICATION NUMBER: US/10/440,850
;  CURRENT FILING DATE:  2003-05-19
;  PRIOR APPLICATION NUMBER: US/09/650,012
;  PRIOR FILING DATE: 2000-08-28
;  PRIOR APPLICATION NUMBER: US 08/585,684
;  PRIOR FILING DATE: 1996-01-12
;  PRIOR APPLICATION NUMBER: US 60/000,951
;  PRIOR FILING DATE: 1995-07-07
;  PRIOR APPLICATION NUMBER: US 09/038,073
;  PRIOR FILING DATE: 1998-03-11
;  NUMBER OF SEQ ID NOS: 2285
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 323
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-10-440-850-323

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGAT 1418
              |||||||||||||||
Db         15 GATGCTAAAGATGAT 1


RESULT 609
US-10-371-218A-5
; Sequence 5, Application US/10371218A
; Publication No. US20030217375A1
; GENERAL INFORMATION:
;  APPLICANT: Zcharia, Eyal
;  APPLICANT:  Vlodavsky, Israel
;  APPLICANT:  Metzger, Shula
;  APPLICANT:  Pecker, Iris
;  APPLICANT:  Ilan, Neta
;  APPLICANT:  Chajek-Shaul, Tova
;  APPLICANT:  Goldshmidt, Orit
;  TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING HEPARANASE AND USES THEREOF
;  FILE REFERENCE: 25783
;  CURRENT APPLICATION NUMBER: US/10/371,218A
;  CURRENT FILING DATE:  2003-07-01
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-371-218A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 610
US-10-291-808-68
; Sequence 68, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
;  APPLICANT: McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE: P-PH 3457
;  CURRENT APPLICATION NUMBER: US/10/291,808
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US/09/300,958
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/083,331
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/098,070
;  PRIOR FILING DATE: 1998-08-27
;  PRIOR APPLICATION NUMBER: 60/118,624
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-68

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 611
US-10-045-674-622
; Sequence 622, Application US/10045674
; Publication No. US20030232333A1
; GENERAL INFORMATION:
;  APPLICANT: LADNER, ROBERT C.
;  APPLICANT:  COHEN, EDWARD H.
;  APPLICANT:  NASTRI, HORACIO G.
;  APPLICANT:  ROOKEY, KRISTIN L.
;  APPLICANT:  HOET, RENE
;  APPLICANT:  HOOGENBOOM, HENDRICUS R. J. M.
;  TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
;  TITLE OF INVENTION:  DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
;  TITLE OF INVENTION:  OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
;  TITLE OF INVENTION:  LIBRARIES
;  FILE REFERENCE: DYAX/002 CIP2
;  CURRENT APPLICATION NUMBER: US/10/045,674
;  CURRENT FILING DATE:  2001-10-25
;  PRIOR APPLICATION NUMBER: 60/198,069
;  PRIOR FILING DATE: 2000-04-17
;  PRIOR APPLICATION NUMBER: 09/837,306
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 635
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Illustrative
;   OTHER INFORMATION: nucleotide sequence
US-10-045-674-622

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 612
US-10-456-573-5
; Sequence 5, Application US/10456573
; Publication No. US20030236215A1
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 25677
;  CURRENT APPLICATION NUMBER: US/10/456,573
;  CURRENT FILING DATE:  2003-06-09
;  PRIOR APPLICATION NUMBER: US 09/435,739
;  PRIOR FILING DATE: 1999-11-08
;  PRIOR APPLICATION NUMBER: US 09/258,892
;  PRIOR FILING DATE: 1999-03-01
;  PRIOR APPLICATION NUMBER: PCT/US98/17954
;  PRIOR FILING DATE: 1998-08-03
;  PRIOR APPLICATION NUMBER: US 08/922,170
;  PRIOR FILING DATE: 1997-09-02
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-456-573-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 613
US-10-360-275-10
; Sequence 10, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Choob, Mikhail
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: AM102.P.1.1.1US
;  CURRENT APPLICATION NUMBER: US/10/360,275
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/072,975
```

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;  PRIOR FILING DATE: 2002-02-09
;  PRIOR APPLICATION NUMBER: US 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthtic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: SynthetiConstruct
US-10-360-275-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 614
US-10-637-935-9
; Sequence 9, Application US/10637935
; Publication No. US20040033525A1
; GENERAL INFORMATION:
;  APPLICANT: Monforte, Joseph A.
;  APPLICANT:  Becker, Christopher H.
;  APPLICANT:  Pollart, Daniel J.
;  APPLICANT:  Shaler, Thomas A.
;  TITLE OF INVENTION: Releasable No. US20040033525A1volatile Mass-Label Molecules
;  FILE REFERENCE: 24736-2057E
;  CURRENT APPLICATION NUMBER: US/10/637,935
;  CURRENT FILING DATE:  2003-08-07
;  PRIOR APPLICATION NUMBER: US 10/202,189
;  PRIOR FILING DATE: 2002-07-22
;  PRIOR APPLICATION NUMBER: US 08/988,024
;  PRIOR FILING DATE: 1997-12-10
;  PRIOR APPLICATION NUMBER: US 60/033,037
;  PRIOR FILING DATE: 1996-12-10
;  PRIOR APPLICATION NUMBER: US 60/046,719
;  PRIOR FILING DATE: 1997-05-16
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-637-935-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 615
US-10-239-655A-4
; Sequence 4, Application US/10239655A
; Publication No. US20040048816A1
; GENERAL INFORMATION:
;  APPLICANT: ZOHLNHOFER, DIETLIND
;  APPLICANT:  BAUERLE, PATRICK
;  APPLICANT:  KLEIN, CHRISTOPH
;  APPLICANT:  NEUMANN, FRANZ-JOSEF
;  TITLE OF INVENTION: RESTENOSIS TREATMENT
;  FILE REFERENCE: 029976/0103
;  CURRENT APPLICATION NUMBER: US/10/239,655A
;  CURRENT FILING DATE:  2003-02-02
;  PRIOR APPLICATION NUMBER: PCT/EP01/03312
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: EP 00106468.2
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-239-655A-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 616
US-10-433-005-4
; Sequence 4, Application US/10433005
; Publication No. US20040072289A1
; GENERAL INFORMATION:
;  APPLICANT: Hwang, Inhwan
;  APPLICANT:  Piao, Hai Lan
;  TITLE OF INVENTION: Novel Transcriptional Factor Enhancing the Resistance
;  TITLE OF INVENTION:  of Plants to Osmotic Stress
;  FILE REFERENCE: 012679-089
;  CURRENT APPLICATION NUMBER: US/10/433,005
;  CURRENT FILING DATE:  2003-07-22
;  PRIOR APPLICATION NUMBER: PCT/KR01/00364
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: KR 10-2000-72720
;  PRIOR FILING DATE: 2000-02-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 3' primer for construction of substraction library of osmotic
;   OTHER INFORMATION: stress genes
US-10-433-005-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 617
US-10-344-092-2
; Sequence 2, Application US/10344092
; Publication No. US20040087807A1
; GENERAL INFORMATION:
;  APPLICANT: Raddatz, Stefan
;  APPLICANT:  Muller-Ibeler, Jochen
```

```
;  APPLICANT:  Schweitzer, Markus
;  APPLICANT:  Brucher, Christoph
;  APPLICANT:  Windhab, Norbert
;  APPLICANT:  Havens, John R.
;  APPLICANT:  Onofrey, Thomas J.
;  APPLICANT:  Greef, Charles H.
;  APPLICANT:  Wang, Daguang
;  TITLE OF INVENTION: NEW HYDRAZIDE BUILDING BLOCKS AND HYDRAZIDE MODIFIED BIOMOLECULES
;  FILE REFERENCE: 612,406-032
;  CURRENT APPLICATION NUMBER: US/10/344,092
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: PCT/US00/22205
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/41663
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Sample oligo
US-10-344-092-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 618
US-10-785-116-5
; Sequence 5, Application US/10785116
; Publication No. US20040142427A1
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Vlodavsky , Israel
;  APPLICANT:  Feinstein, Elena
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
;  TITLE OF INVENTION:  EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
;  FILE REFERENCE: 27674
;  CURRENT APPLICATION NUMBER: US/10/785,116
;  CURRENT FILING DATE:  2004-02-25
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-785-116-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 619
US-10-737-059-2
; Sequence 2, Application US/10737059
; Publication No. US20040191808A1
; GENERAL INFORMATION:
;  APPLICANT: NELSON, Jeffrey S.
;  TITLE OF INVENTION: REAGENTS FOR OLIGONUCLEOTIDE CLEAVAGE AND DEPROTECTION
;  FILE REFERENCE: 4688US
;  CURRENT APPLICATION NUMBER: US/10/737,059
;  CURRENT FILING DATE:  2003-12-16
;  PRIOR APPLICATION NUMBER: US/10/091,231
;  PRIOR FILING DATE: 2002-03-04
;  PRIOR APPLICATION NUMBER: US 60/274,309
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-737-059-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 620
US-10-830-484-4
; Sequence 4, Application US/10830484
; Publication No. US20040220397A1
; GENERAL INFORMATION:
;  APPLICANT: Leuck, Michael
;  APPLICANT:  Wolter, Andreas
;  TITLE OF INVENTION: Solid Support For The Synthesis Of 3' Amino Oligonucleotides
;  FILE REFERENCE: PRO13
;  CURRENT APPLICATION NUMBER: US/10/830,484
;  CURRENT FILING DATE:  2004-04-21
;  PRIOR APPLICATION NUMBER: 60/464,269
;  PRIOR FILING DATE: 2003-04-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Nucleic Acid Ligand
US-10-830-484-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 621
US-10-755-118-3
; Sequence 3, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
```

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;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: NH2
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Hydrogen
US-10-755-118-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 622
US-10-755-118-4
; Sequence 4, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: NH2
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Acr1
US-10-755-118-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 623
US-10-755-118-31
; Sequence 31, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligodeoxyribonucleotide
US-10-755-118-31

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 624
US-10-755-118-32/c
; Sequence 32, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
```

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;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligodeoxyribonucleotide
US-10-755-118-32

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 625
US-10-755-118-36
; Sequence 36, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: BHA resin
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: tert-butoxycarbonyl
US-10-755-118-36

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 626
US-10-755-118-38
; Sequence 38, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: BHA resins
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: tert-butoxycarbonyl
US-10-755-118-38

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 627
US-10-755-118-39
; Sequence 39, Application US/10755118
```

```
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: BHA resin
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Acr1
US-10-755-118-39

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 628
US-10-755-118-40
; Sequence 40, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: BHA resin
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Hydrogen
US-10-755-118-40

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 629
US-10-755-118-43
; Sequence 43, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: NH2
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Hydrogen
US-10-755-118-43

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 630
US-10-755-118-44
; Sequence 44, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Lys-NH2
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Acr1
US-10-755-118-44

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 631
US-10-755-118-45
; Sequence 45, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Lys(ClZ)-BHA resin
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: tert-butoxycarbonyl
US-10-755-118-45

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 632
US-10-755-118-48
; Sequence 48, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
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;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Lys (ClZ)-BHA resin
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Acr1
US-10-755-118-48

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 633
US-10-755-118-49
; Sequence 49, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Lys (ClZ)-BHA resin
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: (2'-aminoethyl)glycine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: Hydrogen
US-10-755-118-49

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 634
US-10-770-989-9
; Sequence 9, Application US/10770989
; Publication No. US20050019789A1
; GENERAL INFORMATION:
;  APPLICANT: Ankenbauer, Waltraud
;  APPLICANT:  Schmitz-Agheguian, Gudrun
;  APPLICANT:  Bonch-Osmolovskaya, Elizaveta
;  APPLICANT:  Svetlichny, Vitaly
;  APPLICANT:  Markau, Ursula
;  APPLICANT:  Angerer, Bernard
;  APPLICANT:  Reiser, Astrid
;  APPLICANT:  Roche Molecular Systems, Inc.
;  TITLE OF INVENTION: Thermostable DNA Polymerase from Anaerocellum
;  TITLE OF INVENTION:  thermophilum
;  FILE REFERENCE: 022101-000610US
;  CURRENT APPLICATION NUMBER: US/10/770,989
;  CURRENT FILING DATE:  2004-02-02
;  PRIOR APPLICATION NUMBER: EP 96115877.1
;  PRIOR FILING DATE: 1996-10-03
;  PRIOR APPLICATION NUMBER: WO PCT/EP97/05390
;  PRIOR FILING DATE: 1997-10-01
;  PRIOR APPLICATION NUMBER: US 09/269,858
;  PRIOR FILING DATE: 1999-06-10
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:(dT)-15,
;   OTHER INFORMATION: oligo dT primer
US-10-770-989-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 635
US-10-833-502-9
; Sequence 9, Application US/10833502
; Publication No. US20050026279A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: TSENG, SCHEFFER C.G.
;  APPLICANT:  ESPANA, EDGAR M.
;  TITLE OF INVENTION: SURGICAL GRAFTS AND METHODS OF PREPARATION
;  FILE REFERENCE: TIS-107
;  CURRENT APPLICATION NUMBER: US/10/833,502
;  CURRENT FILING DATE:  2002-04-28
;  PRIOR APPLICATION NUMBER: 60/465,989
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/473,007
;  PRIOR FILING DATE: 2003-05-22
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-833-502-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 636
US-10-939-214-54
; Sequence 54, Application US/10939214
; Publication No. US20050026817A1
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/10/939,214
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: US/09/793,146
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-10-939-214-54

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 637
US-10-939-214-55
; Sequence 55, Application US/10939214
; Publication No. US20050026817A1
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/10/939,214
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: US/09/793,146
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-10-939-214-55

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 638
US-10-601-140A-5
; Sequence 5, Application US/10601140A
; Publication No. US20050053942A1
; GENERAL INFORMATION:
;  APPLICANT: KAUPPINEN, SAKARI
;  APPLICANT:  JACOBSEN, NANA
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR DETECTION AND ISOLATION OF A
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCE
;  FILE REFERENCE: 57764(71994)
;  CURRENT APPLICATION NUMBER: US/10/601,140A
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US 60/390,928
;  PRIOR FILING DATE: 2002-06-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: LNA monomer
US-10-601-140A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 639
US-10-601-140A-16
; Sequence 16, Application US/10601140A
; Publication No. US20050053942A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: KAUPPINEN, SAKARI
;  APPLICANT:  JACOBSEN, NANA
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR DETECTION AND ISOLATION OF A
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCE
;  FILE REFERENCE: 57764(71994)
;  CURRENT APPLICATION NUMBER: US/10/601,140A
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US 60/390,928
;  PRIOR FILING DATE: 2002-06-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-601-140A-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 640
US-10-601-140A-19
; Sequence 19, Application US/10601140A
; Publication No. US20050053942A1
; GENERAL INFORMATION:
;  APPLICANT: KAUPPINEN, SAKARI
;  APPLICANT:  JACOBSEN, NANA
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR DETECTION AND ISOLATION OF A
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCE
;  FILE REFERENCE: 57764(71994)
;  CURRENT APPLICATION NUMBER: US/10/601,140A
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US 60/390,928
;  PRIOR FILING DATE: 2002-06-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)
;   OTHER INFORMATION: LNA monomer
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (4)
;   OTHER INFORMATION: LNA monomer
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (7)
;   OTHER INFORMATION: LNA monomer
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (10)
;   OTHER INFORMATION: LNA monomer
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (13)
;   OTHER INFORMATION: LNA monomer
US-10-601-140A-19

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 641
US-10-239-919A-4
; Sequence 4, Application US/10239919A
; Publication No. US20050054831A1
; GENERAL INFORMATION:
;  APPLICANT: HWANG, IN-HWAN
;  APPLICANT:  LIM, JEONG-HWA
;  APPLICANT:  PIH, KYOUNG-TAE
;  TITLE OF INVENTION: AN OSMOTIC STRESS-INDUCIBLE PROTEIN FUNCTIONING AS A
;  TITLE OF INVENTION:  NEGATIVE REGULATOR IN OSMOTIC STRESS SIGNALING PATHWAY
;  TITLE OF INVENTION:  OF PLANTS
;  FILE REFERENCE: 7022-0004
;  CURRENT APPLICATION NUMBER: US/10/239,919A
;  CURRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: PCT/KR02/00152
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: KR 2001/5097
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-239-919A-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 642
US-10-938-661A-22
; Sequence 22, Application US/10938661A
; Publication No. US20050070000A1
; GENERAL INFORMATION:
;  APPLICANT: Pecker, Iris
;  APPLICANT:  Michal, Israel
;  APPLICANT:  Itzhaki, Hanan
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY DISTANTLY
;  TITLE OF INVENTION:  HOMOLOGOUS TO HEPARANASE
;  FILE REFERENCE: 28567
;  CURRENT APPLICATION NUMBER: US/10/938,661A
;  CURRENT FILING DATE:  2004-09-13
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-938-661A-22

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 643
US-10-781-758-5
; Sequence 5, Application US/10781758
; Publication No. US20040146497A1
; GENERAL INFORMATION:
;  APPLICANT: Neta Ilan
;  APPLICANT:  Israel Vlodavsky
;  APPLICANT:  Oron Yacoby-Zeevi
;  APPLICANT:  Iris Pecker
;  TITLE OF INVENTION: THERAPEUTIC AND COSMETIC USES OF HEPARANASES
;  FILE REFERENCE: 27525
;  CURRENT APPLICATION NUMBER: US/10/781,758
;  CURRENT FILING DATE:  2004-02-20
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-781-758-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 644
US-10-824-175-3
; Sequence 3, Application US/10824175
; Publication No. US20050170363A1
; GENERAL INFORMATION:
;  APPLICANT: Reddington, Mark
;  APPLICANT:  Lyttle, Matt
;  TITLE OF INVENTION: XANTHENE DYES
;  FILE REFERENCE: 061873-5011-US
;  CURRENT APPLICATION NUMBER: US/10/824,175
;  CURRENT FILING DATE:  2004-04-13
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic DNA fragment
US-10-824-175-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 645
US-10-866-388A-9/c
; Sequence 9, Application US/10866388A
; Publication No. US20050170367A1
; GENERAL INFORMATION:
;  APPLICANT: QUAKE, STEPHEN R.
;  APPLICANT:  BUZBY, PHILIP R.
;  TITLE OF INVENTION: FLORESCENTLY LABLED NUCLEOSIDE TRIPHOSPHATES AND ANALOGS
;  TITLE OF INVENTION:  THEREOF FOR SEQUENCING NUCLEIC ACIDS
;  FILE REFERENCE: HEL-008
;  CURRENT APPLICATION NUMBER: US/10/866,388A
;  CURRENT FILING DATE:  2004-06-10
;  PRIOR APPLICATION NUMBER: 60/477,426
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/477,429
;  PRIOR FILING DATE: 2003-06-10
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hypothetical
;   OTHER INFORMATION: nucleotide sequence
US-10-866-388A-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 646
US-10-601-497B-469
; Sequence 469, Application US/10601497B
; Publication No. US20050175989A1
; GENERAL INFORMATION:
;  APPLICANT: Lin, Ching-Yu
;  APPLICANT:  Lin, Ruey-Wen
;  APPLICANT:  You, Chiou-Mien
;  APPLICANT:  Huang, Hsing-Hsuan
;  APPLICANT:  Lee, Bor-Heng
;  APPLICANT:  Lee, Hsien-Hsiung
;  APPLICANT:  Lin, Yu-Ju
;  APPLICANT:  Pan, Chih-Chun
;  APPLICANT:  Hsu, Han-Chuan
;  APPLICANT:  Shih, Chia-Wen
;  APPLICANT:  Yeh , Chih-Hsing
;  APPLICANT:  Kao, Yi-Feng
;  APPLICANT:  Pan , Chih-Long
;  APPLICANT:  Chan, Peter
;  TITLE OF INVENTION: METHOD AND DETECTOR FOR IDENTIFYING SUBTYPES OF HUMAN PAPILLOMA V
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/601,497B
;  CURRENT FILING DATE:  2003-06-23
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 469
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-601-497B-469

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 647
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US-09-739-928-2
; Sequence 2, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 648
US-09-739-928-3
; Sequence 3, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by 6-aminohexanoic acid
;             (-NH(CH-2)-6COOH)"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-739-928-3

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 649
US-09-739-928-4
; Sequence 4, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
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;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = one
;             4-amino-N-methylpyrrol-2-carboxylic acid residue"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-739-928-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 650
US-09-739-928-5
; Sequence 5, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = two
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-739-928-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 651
US-09-739-928-6
; Sequence 6, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = three
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-739-928-6

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 652
US-09-739-928-7
; Sequence 7, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = four
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-739-928-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 653
US-09-739-928-8
; Sequence 8, Application US/09739928
; Patent No. US20020052482A1
;   GENERAL INFORMATION:
;        APPLICANT: Kutyavin, Igor V.
;                   Lukhtanov, Eugeny A.
;                   Gamper, Howard B.
;                   Meyer Jr., Rich B.
;        TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                            Groove Binder Conjugates
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/739,928
;             FILING DATE: 11-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/415,370
;             FILING DATE: 03-APR-1995
;             APPLICATION NUMBER: US 09/141,764
;             FILING DATE: 27-AUG-1998
;             APPLICATION NUMBER: US 09/507,345
;             FILING DATE: 18-FEB-2000
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kezer, William B.
;             REGISTRATION NUMBER: 37,369
;             REFERENCE/DOCKET NUMBER: 17682A-003510US
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```
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  16
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = thymidine modified by minor groove binder moiety
;             represented by X, where m = five
;             4-amino-N-methylpyrrol-2-carboxylic acid residues"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-739-928-8

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 654
US-09-152-059-70
; Sequence 70, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165 (71994)
;  CURRENT APPLICATION NUMBER: US/09/152,059
;  CURRENT FILING DATE:  1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-152-059-70

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 655
US-09-895-585-9
; Sequence 9, Application US/09895585
; Publication No. US20020081725A1
; GENERAL INFORMATION:
;  APPLICANT: Tsang, Wen-Ghih
;  APPLICANT:  Zheng, Tianli
;  APPLICANT:  Huang, Chang Jiang
;  APPLICANT:  AmCyte, Inc.
;  TITLE OF INVENTION: Culturing Pancreatic Stem Cells Having a Specified,
;  TITLE OF INVENTION:  Intermediate Stage of Development
;  FILE REFERENCE: 021164-000100US
;  CURRENT APPLICATION NUMBER: US/09/895,585
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/215,634
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/246,306
;  PRIOR FILING DATE: 2000-11-06
;  PRIOR APPLICATION NUMBER: US 60/291,787
;  PRIOR FILING DATE: 2001-05-17
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo-(dT)-16
US-09-895-585-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 656
US-09-805-296D-9
; Sequence 9, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USI
;  FILE REFERENCE: AM102.P.1US
;  CURRENT APPLICATION NUMBER: US/09/805,296D
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Construct
US-09-805-296D-9
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  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 657
US-09-843-676-131/c
; Sequence 131, Application US/09843676
; Patent No. US20020164786A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. US20020164786A1el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/843,676
;             FILING DATE: 26-Apr-2001
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002930US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-843-676-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 658
US-09-766-253-131/c
; Sequence 131, Application US/09766253
; Publication No. US20020187471A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. US20020187471A1el Telomerase
;        NUMBER OF SEQUENCES: 171
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,253
;             FILING DATE: 19-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/846,017
;             FILING DATE: 1997-04-25
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002920US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-766-253-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 659
US-09-438-486-131/c
; Sequence 131, Application US/09438486
; Publication No. US20030009019A1
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
```

```
;    TITLE OF INVENTION:  No. US20030009019A1el Telomerase
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/438,486
;      FILING DATE:  12-NOV-1999
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/851,843
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002931US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-438-486-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 660
US-10-208-357-22/c
; Sequence 22, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 50036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,357
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/619,103
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 60/145,834
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-22

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 661
US-10-053-758-131/c
; Sequence 131, Application US/10053758
; Publication No. US20030032075A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. US20030032075A1el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/053,758
;             FILING DATE: 18-Jan-2002
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002930US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
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;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-053-758-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 662
US-10-054-295-131/c
; Sequence 131, Application US/10054295
; Publication No. US20030044953A1
;   GENERAL INFORMATION:
;       APPLICANT: Cech, Thomas R.
;                  Lingner, Joachim
;                  Nakamura, Toru
;                  Chapman, Karen B.
;                  Morin, Gregg B.
;                  Harley, Calvin
;                  Andrews, William H.
;       TITLE OF INVENTION: No. US20030044953A1el Telomerase
;       NUMBER OF SEQUENCES: 225
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, 8th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/054,295
;            FILING DATE: 18-Jan-2002
;            CLASSIFICATION: 536
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/854,050
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/846,017
;            FILING DATE: 25-APR-1997
;            APPLICATION NUMBER: US 08/844,419
;            FILING DATE: 18-APR-1997
;            APPLICATION NUMBER: US 08/724,643
;            FILING DATE: 01-OCT-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Apple,  Randolph T.
;            REGISTRATION NUMBER: 36,429
;            REFERENCE/DOCKET NUMBER: 015389-002930US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-295-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 663
US-10-054-611-131/c
; Sequence 131, Application US/10054611
; Publication No. US20030059787A1
;   GENERAL INFORMATION:
;       APPLICANT: Cech, Thomas R.
;                  Lingner, Joachim
;                  Nakamura, Toru
;                  Chapman, Karen B.
;                  Morin, Gregg B.
;                  Harley, Calvin
;                  Andrews, William H.
;       TITLE OF INVENTION: No. US20030059787A1el Telomerase
;       NUMBER OF SEQUENCES: 225
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, 8th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/054,611
;            FILING DATE: 18-Jan-2002
;            CLASSIFICATION: 536
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/854,050
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/846,017
;            FILING DATE: 25-APR-1997
;            APPLICATION NUMBER: US 08/844,419
;            FILING DATE: 18-APR-1997
;            APPLICATION NUMBER: US 08/724,643
;            FILING DATE: 01-OCT-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Apple,  Randolph T.
;            REGISTRATION NUMBER: 36,429
;            REFERENCE/DOCKET NUMBER: 015389-002930US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 131:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-611-131

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 664
US-10-072-975-9
; Sequence 9, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
```

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;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
;  FILE REFERENCE: AM102.P.1.1US
;  CURRENT APPLICATION NUMBER: US/10/072,975
;  CURRENT FILING DATE:  2002-02-09
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: PCT/US01/0811
;  PRIOR FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Construct
US-10-072-975-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 665
US-10-227-001-20
; Sequence 20, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
;  APPLICANT: Dempcy, Robert O.
;  APPLICANT:  Afonina, Irina Aleksandrovna
;  APPLICANT:  Vermeulen, Nicolaas M.J.
;  APPLICANT:  Epoch Biosciences, Inc.
;  TITLE OF INVENTION: Hybridization-Triggered Fluorescent
;  TITLE OF INVENTION:  Detection of Nucleic Acids
;  FILE REFERENCE: 17682A-004210US
;  CURRENT APPLICATION NUMBER: US/10/227,001
;  CURRENT FILING DATE:  2002-08-21
;  PRIOR APPLICATION NUMBER: US 09/428,236
;  PRIOR FILING DATE: 1999-10-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: polydT-MGB-
;   OTHER INFORMATION: (2-dimethylaminonaphthalene-6-sulfonamide)
;   OTHER INFORMATION: conjugate
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)
;   OTHER INFORMATION: n = thymine modified by MGB-
;   OTHER INFORMATION: (2-dimethylaminonaphthalene-6-sulfonamide)
US-10-227-001-20

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 666
US-10-227-001-21
; Sequence 21, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
;  APPLICANT: Dempcy, Robert O.
;  APPLICANT:  Afonina, Irina Aleksandrovna
;  APPLICANT:  Vermeulen, Nicolaas M.J.
;  APPLICANT:  Epoch Biosciences, Inc.
;  TITLE OF INVENTION: Hybridization-Triggered Fluorescent
;  TITLE OF INVENTION:  Detection of Nucleic Acids
;  FILE REFERENCE: 17682A-004210US
;  CURRENT APPLICATION NUMBER: US/10/227,001
;  CURRENT FILING DATE:  2002-08-21
;  PRIOR APPLICATION NUMBER: US 09/428,236
;  PRIOR FILING DATE: 1999-10-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN
;   OTHER INFORMATION: conjugate
US-10-227-001-21

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 667
US-10-008-029-70
; Sequence 70, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165-C2(71994)
;  CURRENT APPLICATION NUMBER: US/10/008,029
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: 09/152,059
;  PRIOR FILING DATE: 1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
```

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;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-008-029-70

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 668
US-10-208-650-70
; Sequence 70, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
;  APPLICANT: WENGEL, JESPER
;  APPLICANT:  NIELSEN, POUL
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
;  FILE REFERENCE: 49165-C2(71994)
;  CURRENT APPLICATION NUMBER: US/10/208,650
;  CURRENT FILING DATE:  2002-07-29
;  PRIOR APPLICATION NUMBER: US/10/008,029
;  PRIOR FILING DATE: 2001-11-05
;  PRIOR APPLICATION NUMBER: 09/152,059
;  PRIOR FILING DATE: 1998-09-11
;  PRIOR APPLICATION NUMBER: 60/058,541
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/068,293
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/071,682
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: 60/076,591
;  PRIOR FILING DATE: 1998-03-03
;  PRIOR APPLICATION NUMBER: 60/083,507
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/088,309
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/094,355
;  PRIOR FILING DATE: 1998-07-28
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-208-650-70

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 669
US-10-164-915-2/c
; Sequence 2, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
;  APPLICANT: Salafsky, Joshua S.
;  TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optical
;  TITLE OF INVENTION:  for Detection of Interactions Involving a Conformational Change
;  FILE REFERENCE: 11100-035-999
;  CURRENT APPLICATION NUMBER: US/10/164,915
;  CURRENT FILING DATE:  2002-06-06
;  PRIOR APPLICATION NUMBER: 60/253,862
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/260,249
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/265,775
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: 60/278,941
;  PRIOR FILING DATE: 2001-01-27
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Aritificial Sequence: Oligonucleotide structure for
;   OTHER INFORMATION: molecular beacon
US-10-164-915-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 670
US-10-203-780-9
; Sequence 9, Application US/10203780
; Publication No. US20030165914A1
; GENERAL INFORMATION:
;  APPLICANT: CUZIN, MARC
;  APPLICANT:  PELTIE, PHILIPPE
;  APPLICANT:  FONTECAVE, MARC
;  APPLICANT:  DECOUT, JEAN-LUC
;  APPLICANT:  DUEYMES, CECILE
;  TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUORE
;  TITLE OF INVENTION:  MARKER
;  FILE REFERENCE: 226286US0XPCT
;  CURRENT APPLICATION NUMBER: US/10/203,780
;  CURRENT FILING DATE:  2002-11-25
;  PRIOR APPLICATION NUMBER: PCT/FR01/00516
;  PRIOR FILING DATE: 2001-02-22
;  PRIOR APPLICATION NUMBER: FR 00 02236
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: t is modified with a covalent linkage to flavin
US-10-203-780-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
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```
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 671
US-10-360-275-9
; Sequence 9, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Choob, Mikhail
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: AM102.P.1.1.1US
;  CURRENT APPLICATION NUMBER: US/10/360,275
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/072,975
;  PRIOR FILING DATE: 2002-02-09
;  PRIOR APPLICATION NUMBER: US 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Construct
US-10-360-275-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 672
US-10-432-803-4
; Sequence 4, Application US/10432803
; Publication No. US20040029199A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jin Woo
;  TITLE OF INVENTION: HUMAN CERVICAL CANCER 2 PROTOONCOGENE AND PROTEIN ENCODED THEREIN
;  FILE REFERENCE: KJW-0613
;  CURRENT APPLICATION NUMBER: US/10/432,803
;  CURRENT FILING DATE:  2003-05-23
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: KOPATIN 1.5
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: H-T11G anchored oligo-dT primer
US-10-432-803-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
                ||||||||||||||||
Db          1 AAGTTTTTTTTTTTT 15


RESULT 673
US-10-776-099-9
; Sequence 9, Application US/10776099
; Publication No. US20040141957A1
; GENERAL INFORMATION:
;  APPLICANT: Tsang, Wen-Ghih
;  APPLICANT:  Zheng, Tianli
;  APPLICANT:  Huang, Chang Jiang
;  APPLICANT:  AmCyte, Inc.
;  TITLE OF INVENTION: Culturing Pancreatic Stem Cells Having a Specified,
;  TITLE OF INVENTION:  Intermediate Stage of Development
;  FILE REFERENCE: 021164-000100US
;  CURRENT APPLICATION NUMBER: US/10/776,099
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: US/09/895,585
;  PRIOR FILING DATE: 2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/215,634
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/246,306
;  PRIOR FILING DATE: 2000-11-06
;  PRIOR APPLICATION NUMBER: US 60/291,787
;  PRIOR FILING DATE: 2001-05-17
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo-(dT)-16
US-10-776-099-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 674
US-10-398-483-10/c
; Sequence 10, Application US/10398483
; Publication No. US20040166499A1
; GENERAL INFORMATION:
;  APPLICANT: Hayashizaki, Yoshihide
;  TITLE OF INVENTION: Oligonucleotide linkers comprising a variable cohesive portion an
;  TITLE OF INVENTION:  for the preparation of polynucleotide libraries by using said li
;  FILE REFERENCE: 2870-0247P
;  CURRENT APPLICATION NUMBER: US/10/398,483
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence used in the preparation of a full-length cDNA library
US-10-398-483-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2
```

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RESULT 675
US-10-755-118-94
; Sequence 94, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
;  FILE REFERENCE: ISIS-5427
;  CURRENT APPLICATION NUMBER: US/10/755,118
;  CURRENT FILING DATE:  2004-01-09
;  PRIOR APPLICATION NUMBER: US 08/462,977
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  PRIOR APPLICATION NUMBER: PCT/EP92/01219
;  PRIOR FILING DATE: 1992-05-22
;  PRIOR APPLICATION NUMBER: DN 510/92
;  PRIOR FILING DATE: 1992-04-15
;  PRIOR APPLICATION NUMBER: DN 987/91
;  PRIOR FILING DATE: 1991-05-24
;  PRIOR APPLICATION NUMBER: DN 986/91
;  PRIOR FILING DATE: 1991-05-24
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-755-118-94

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 676
US-10-121-641D-1/c
; Sequence 1, Application US/10121641D
; Publication No. US20050175993A1
; GENERAL INFORMATION:
;  APPLICANT: LARGE SCALE BIOLOGY CORPORATION
;  APPLICANT:  WEI, CHIA-LIN
;  TITLE OF INVENTION: METHOD FOR MAKING FULL-LENGTH CODING SEQUENCE CDNA LIBRARIES
;  FILE REFERENCE: LSB.206.NPUS00
;  CURRENT APPLICATION NUMBER: US/10/121,641D
;  CURRENT FILING DATE:  2002-04-12
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Tail Sequence
US-10-121-641D-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          16 TTTTTTTTTTTTTTT 2


RESULT 677
US-09-726-096A-5
; Sequence 5, Application US/09726096A
; Publication No. US20010016652A1
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT:  Maier, Martin A.
;  TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Backb
;  TITLE OF INVENTION:  Oligomeric Compounds
;  FILE REFERENCE: ISIS4528
;  CURRENT APPLICATION NUMBER: US/09/726,096A
;  CURRENT FILING DATE:  2000-11-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(19)
;   OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
;   OTHER INFORMATION: internucleoside linkage
US-09-726-096A-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 678
US-09-843-676-132
; Sequence 132, Application US/09843676
; Patent No. US20020164786A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. US20020164786A1el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/843,676
;             FILING DATE: 26-Apr-2001
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
```

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;              FILING DATE: 25-APR-1997
;              APPLICATION NUMBER: US 08/844,419
;              FILING DATE: 18-APR-1997
;              APPLICATION NUMBER: US 08/724,643
;              FILING DATE: 01-OCT-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Apple,  Randolph T.
;              REGISTRATION NUMBER: 36,429
;              REFERENCE/DOCKET NUMBER: 015389-002930US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 132:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 17 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-843-676-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 679
US-09-766-253-132
; Sequence 132, Application US/09766253
; Publication No. US20020187471A1
;   GENERAL INFORMATION:
;         APPLICANT: Cech, Thomas R.
;                    Lingner, Joachim
;                    Nakamura, Toru
;                    Chapman, Karen B.
;                    Morin, Gregg B.
;                    Harley, Calvin
;                    Andrews, William H.
;         TITLE OF INVENTION: No. US20020187471A1el Telomerase
;         NUMBER OF SEQUENCES: 171
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Townsend and Townsend and Crew LLP
;              STREET: Two Embarcadero Center, 8th Floor
;              CITY: San Francisco
;              STATE: California
;              COUNTRY: United States of America
;              ZIP: 94111
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/766,253
;              FILING DATE: 19-Jan-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/846,017
;              FILING DATE: 1997-04-25
;              APPLICATION NUMBER: US 08/724,643
;              FILING DATE: 01-OCT-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Apple,  Randolph T.
;              REGISTRATION NUMBER: 36,429
;              REFERENCE/DOCKET NUMBER: 015389-002920US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 132:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 17 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-766-253-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 680
US-09-438-486-132
; Sequence 132, Application US/09438486
; Publication No. US20030009019A1
;  GENERAL INFORMATION:
;    APPLICANT:  Cech, Thomas R.
;    APPLICANT:  Lingner, Joachim
;    APPLICANT:  Nakamura, Toru
;    APPLICANT:  Chapman, Karen B.
;    APPLICANT:  Morin, Gregg B.
;    APPLICANT:  Harley, Calvin
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  No. US20030009019A1el Telomerase
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/438,486
;      FILING DATE:  12-NOV-1999
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/851,843
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/846,017
;      FILING DATE:  25-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/844,419
;      FILING DATE:  18-APR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/724,643
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple,  Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  015389-002931US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-438-486-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 681
US-10-208-357-23/c
; Sequence 23, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 50036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,357
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/619,103
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 60/145,834
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-23

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         17 TTTTTTTTTTTTTTT 3


RESULT 682
US-10-053-758-132
; Sequence 132, Application US/10053758
; Publication No. US20030032075A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. US20030032075A1el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/053,758
;             FILING DATE: 18-Jan-2002
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/854,050
;             FILING DATE: 09-MAY-1997
;             APPLICATION NUMBER: US 08/851,843
;             FILING DATE: 06-MAY-1997
;             APPLICATION NUMBER: US 08/846,017
;             FILING DATE: 25-APR-1997
;             APPLICATION NUMBER: US 08/844,419
;             FILING DATE: 18-APR-1997
;             APPLICATION NUMBER: US 08/724,643
;             FILING DATE: 01-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Apple,  Randolph T.
;             REGISTRATION NUMBER: 36,429
;             REFERENCE/DOCKET NUMBER: 015389-002930US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 132:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-053-758-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 683
US-10-054-295-132
; Sequence 132, Application US/10054295
; Publication No. US20030044953A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin
;                   Andrews, William H.
;        TITLE OF INVENTION: No. US20030044953A1el Telomerase
;        NUMBER OF SEQUENCES: 225
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, 8th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94111
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/054,295
;             FILING DATE: 18-Jan-2002
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
```

```
;              APPLICATION NUMBER: 08/854,050
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: US 08/846,017
;              FILING DATE: 25-APR-1997
;              APPLICATION NUMBER: US 08/844,419
;              FILING DATE: 18-APR-1997
;              APPLICATION NUMBER: US 08/724,643
;              FILING DATE: 01-OCT-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Apple,  Randolph T.
;              REGISTRATION NUMBER: 36,429
;              REFERENCE/DOCKET NUMBER: 015389-002930US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 132:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 17 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-054-295-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 684
US-10-117-267-5
; Sequence 5, Application US/10117267
; Publication No. US20030045698A1
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT:  Maier, Ph.D., Martin A.
;  TITLE OF INVENTION: Compounds,Processes And Intermediates For Synthesis Of Mixed Back
;  TITLE OF INVENTION:  Oligomeric Compounds
;  FILE REFERENCE: ISIS-5039
;  CURRENT APPLICATION NUMBER: US/10/117,267
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/726,096
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 09/250,075
;  PRIOR FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(19)
;   OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
;   OTHER INFORMATION: internucleoside linkage
US-10-117-267-5

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 685
US-10-054-611-132
; Sequence 132, Application US/10054611
; Publication No. US20030059787A1
;  GENERAL INFORMATION:
;       APPLICANT: Cech, Thomas R.
;                  Lingner, Joachim
;                  Nakamura, Toru
;                  Chapman, Karen B.
;                  Morin, Gregg B.
;                  Harley, Calvin
;                  Andrews, William H.
;       TITLE OF INVENTION: No. US20030059787A1el Telomerase
;       NUMBER OF SEQUENCES: 225
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, 8th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/054,611
;            FILING DATE: 18-Jan-2002
;            CLASSIFICATION: 536
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/854,050
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/846,017
;            FILING DATE: 25-APR-1997
;            APPLICATION NUMBER: US 08/844,419
;            FILING DATE: 18-APR-1997
;            APPLICATION NUMBER: US 08/724,643
;            FILING DATE: 01-OCT-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Apple,  Randolph T.
;            REGISTRATION NUMBER: 36,429
;            REFERENCE/DOCKET NUMBER: 015389-002930US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 132:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 17 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-054-611-132

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 686
US-10-333-461-24
; Sequence 24, Application US/10333461
; Publication No. US20030165952A1
; GENERAL INFORMATION:
;  APPLICANT: Global Genomics AB
;  APPLICANT:  Linnarsson, Sten
;  APPLICANT:  Ernfors, Patrik
;  APPLICANT:  Bauren, Goran
```

```
;  TITLE OF INVENTION: Methods for analysis and identification of transcribed
;  TITLE OF INVENTION:  genes, and fingerprinting
;  FILE REFERENCE: smwfp5941752
;  CURRENT APPLICATION NUMBER: US/10/333,461
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: GB 0018016.6
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/219,925
;  PRIOR FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Double-stranded product DNA
US-10-333-461-24

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 687
US-10-352-253A-24
; Sequence 24, Application US/10352253A
; Publication No. US20030175908A1
; GENERAL INFORMATION:
;  APPLICANT: Linnarsson, Sten
;  APPLICANT:  Ernfors, Patrik
;  APPLICANT:  Bauren, Goran
;  APPLICANT:  Metsis, Ats
;  APPLICANT:  Pihlak, Arno
;  APPLICANT:  Montelius, Andreas
;  TITLE OF INVENTION: Methods And Means For Manipulating Nucleic Acid
;  FILE REFERENCE: 620-234
;  CURRENT APPLICATION NUMBER: US/10/352,253A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: US 60/352,215
;  PRIOR FILING DATE: 2002-01-29
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Double-stranded product DNA
US-10-352-253A-24

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 688
US-10-352-255A-24
; Sequence 24, Application US/10352255A
; Publication No. US20030215839A1
; GENERAL INFORMATION:
;  APPLICANT: LONNERBERG, Peter
;  APPLICANT:  OLDIN, Mats
;  APPLICANT:  LINNARSSON, Sten
;  APPLICANT:  ERNFORS, Patrik
;  TITLE OF INVENTION: Methods and Means for Identification of Gene Features
;  FILE REFERENCE: 620-235
;  CURRENT APPLICATION NUMBER: US/10/352,255A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: US 60/352,245
;  PRIOR FILING DATE: 2002-01-29
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Double-stranded product DNA
US-10-352-255A-24

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 689
US-10-291-808-63
; Sequence 63, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
;  APPLICANT: McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE: P-PH 3457
;  CURRENT APPLICATION NUMBER: US/10/291,808
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US/09/300,958
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/083,331
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/098,070
;  PRIOR FILING DATE: 1998-08-27
;  PRIOR APPLICATION NUMBER: 60/118,624
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-63

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 690
US-10-138-674-1074
; Sequence 1074, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1074

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 691
US-10-138-674-1075
; Sequence 1075, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1075

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 692
US-10-138-674-1076
; Sequence 1076, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1076

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 693
US-10-138-674-2532/c
; Sequence 2532, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2532
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-10-138-674-2532

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 694
US-10-324-409B-16/c
; Sequence 16, Application US/10324409B
; Publication No. US20040086880A1
; GENERAL INFORMATION:
;  APPLICANT: Sampson, et al.
;  TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
;  TITLE OF INVENTION:  Secondary Structure
;  FILE REFERENCE: 2003309-0028
;  CURRENT APPLICATION NUMBER: US/10/324,409B
;  CURRENT FILING DATE:  2002-12-18
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Anneal Primer
US-10-324-409B-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         17 TTTTTTTTTTTTTTT 3


RESULT 695
US-10-287-949A-1074
; Sequence 1074, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1074

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 696
US-10-287-949A-1075
; Sequence 1075, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1075

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 697
US-10-287-949A-1076
; Sequence 1076, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1076

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 698
US-10-287-949A-2532/c
; Sequence 2532, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2532
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-10-287-949A-2532

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 699
US-10-735-592-2
; Sequence 2, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
```

```
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
             ||||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 700
US-10-735-592-8
; Sequence 8, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-8

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 701
US-10-735-592-15
; Sequence 15, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-15

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
             ||||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 702
US-10-735-592-16
; Sequence 16, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-16

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
             ||||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 703
US-10-735-592-17
; Sequence 17, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-17

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
             ||||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 704
US-10-735-592-25
; Sequence 25, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
```

```
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-25

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 705
US-10-735-592-48
; Sequence 48, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-48

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   6.7%;  Pred. No. 4.2e+02;
  Matches    1;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |:::::::::::::
Db          3 GUUUUUUUUUUUUUU 17


RESULT 706
US-10-735-592-49
; Sequence 49, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-49

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 707
US-10-735-592-54
; Sequence 54, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-54

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 708
US-10-735-592-55
; Sequence 55, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-55

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 4.2e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :|||||||||||||||
Db          3 UTTTTTTTTTTTTTT 17


RESULT 709
US-10-735-592-56
; Sequence 56, Application US/10735592
```

; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-56

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTT 4514
||||||||||||||||
Db 3 GTTTTTTTTTTTTTT 17

RESULT 710
US-10-477-173-865
; Sequence 865, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul
; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: US/10/477,173
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 865
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-477-173-865

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4062 AGGCTGAGGGCCCCA 4076
||||||||||||||||
Db 1 AGGCTGAGGGCCCCA 15

RESULT 711
US-10-951-549-3
; Sequence 3, Application US/10951549
; Publication No. US20050202461A1
; GENERAL INFORMATION:
; APPLICANT: Datascope Investment Corp.
; APPLICANT: Getts, Robert C.
; APPLICANT: Kadushin, James
; APPLICANT: Schwalm, Jaime
; APPLICANT: Howerton, Kevin
; TITLE OF INVENTION: Method for Converting Generic Nucleic Acid Priming Sequences
; FILE REFERENCE: 4081.024.400
; CURRENT APPLICATION NUMBER: US/10/951,549
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: PCT/US03/09232
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 10/825,776
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/261,231
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 10/730,823
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/29589
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/234,060
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 09/908,950
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,397
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 60/187,681
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 09/802,162
; PRIOR FILING DATE: 2001-03-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: poly dT primer
; FEATURE:
; NAME/KEY: polydT
; LOCATION: (1)..(17)
; OTHER INFORMATION: Phosphorylated poly dT, which binds to a bridging oligonucleotide
US-10-951-549-3

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 712
US-10-951-303-1074
; Sequence 1074, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974

```
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-951-303-1074

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 713
US-10-951-303-1075
; Sequence 1075, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/10/951,303
;  CURRENT FILING DATE:  2004-09-27
;  PRIOR APPLICATION NUMBER: US/09/685,664
;  PRIOR FILING DATE: 2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-951-303-1075

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 714
US-10-951-303-1076
; Sequence 1076, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/10/951,303
;  CURRENT FILING DATE:  2004-09-27
;  PRIOR APPLICATION NUMBER: US/09/685,664
;  PRIOR FILING DATE: 2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-951-303-1076

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 4.2e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 715
US-10-951-303-2532/c
; Sequence 2532, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relatec
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/10/951,303
;  CURRENT FILING DATE:  2004-09-27
;  PRIOR APPLICATION NUMBER: US/09/685,664
;  PRIOR FILING DATE: 2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2532
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-10-951-303-2532

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 716
US-09-809-545A-84
; Sequence 84, Application US/09809545A
; Patent No. US20020110804A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  White, R. Tyler
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.017A
;  CURRENT APPLICATION NUMBER: US/09/809,545A
;  CURRENT FILING DATE:  2001-03-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-09-809-545A-84

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 717
US-09-904-744-1/c
; Sequence 1, Application US/09904744
; Patent No. US20020150905A1
; GENERAL INFORMATION:
;  APPLICANT: Barbera-Guillem, Emilio
;  APPLICANT:  Nelson, M. Bud
;  APPLICANT:  Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  TITLE OF INVENTION:  dendrimers in a signal amplification system
;  FILE REFERENCE: B-73
;  CURRENT APPLICATION NUMBER: US/09/904,744
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/437076
;  PRIOR FILING DATE: 1999-11-09
;  PRIOR APPLICATION NUMBER: 60/107828
;  PRIOR FILING DATE: 1998-11-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthesized
US-09-904-744-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 718
US-09-888-326-837
; Sequence 837, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 837
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-837

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 719
US-09-994-311-7
; Sequence 7, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 720
US-09-776-479-913
; Sequence 913, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
```

```
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 721
US-09-776-479-913
; Sequence 913, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 722
US-09-776-479-939
; Sequence 939, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 723
US-09-776-479-939
; Sequence 939, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 724
US-09-370-541-14
; Sequence 14, Application US/09370541
; Publication No. US20030088079A1
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT: Prakash, Thazha P
;  APPLICANT: Kawasaki, Andrew M
;  TITLE OF INVENTION: Aminoxxy-Modified Nucleosidic Compounds And Oligomeric
;  TITLE OF INVENTION: Compounds Prepared Therefrom
;  FILE REFERENCE: ISIS3993
;  CURRENT APPLICATION NUMBER: US/09/370,541
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: 09/130,973
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 09/016,520
;  EARLIER FILING DATE: 1998-01-30
;  EARLIER APPLICATION NUMBER: 60/037,143
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 09/344,260
;  EARLIER FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-370-541-14

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 725
US-09-775-479-9
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
;  APPLICANT: LECLERC, Guy
;  APPLICANT:  MARTEL, R,mi
;  TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
;  TITLE OF INVENTION:  RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
;  TITLE OF INVENTION:  THERAPEUTIC USES THEREOF
;  FILE REFERENCE: 12168-1US-2
;  CURRENT APPLICATION NUMBER: US/09/775,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: 09/318,106
;  PRIOR FILING DATE: 1999-05-24
;  PRIOR APPLICATION NUMBER: 08/756,728
;  PRIOR FILING DATE: 1996-11-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-09-775-479-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 726
US-09-979-275A-7
; Sequence 7, Application US/09979275A
; Publication No. US20040110919A1
; GENERAL INFORMATION:
;  APPLICANT: NAGAI, HIROSHI
;  APPLICANT:  KURODA, KYOKO
;  APPLICANT:  NAKAJIMA, TERUMI
;  TITLE OF INVENTION: NOVEL PROTEINS HAVING HEMOLYTIC ACTIVITY AND GENES
;  TITLE OF INVENTION:  ENCODING THE PROTEIN
;  FILE REFERENCE: 037181.50611US
;  CURRENT APPLICATION NUMBER: US/09/979,275A
;  CURRENT FILING DATE:  2003-05-27
;  PRIOR APPLICATION NUMBER: PCT/JP01/02209
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: JP 2000-78967
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-09-979-275A-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 727
US-10-125-295-9
; Sequence 9, Application US/10125295
; Publication No. US20020164572A1
;   GENERAL INFORMATION:
;        APPLICANT: Lin, Ching-I Patsy
;                   Wallace, Robert Bruce
;                   Cossman, Jeffrey
;                   French, Cynthia
;        TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                            to Preserve RNA and DNA
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/125,295
;             FILING DATE: 17-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/545,225
;             FILING DATE: 07-Apr-2000
;             APPLICATION NUMBER: US 08/884,029
;             FILING DATE: 27-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 02558B-059100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "t at positions 13-18 may be
```

```
;            present or absent"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-125-295-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 728
US-10-208-357-24/c
; Sequence 24, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 50036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,357
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/619,103
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 60/145,834
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-24

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4

RESULT 729
US-10-112-653-882
; Sequence 882, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 882
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-882

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 730
US-10-017-995-913
; Sequence 913, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-913

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 731
US-10-017-995-939
; Sequence 939, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-939

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 732
US-10-206-613-4
; Sequence 4, Application US/10206613
```

```
; Publication No. US20030104432A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Zhidong
;  APPLICANT:  Jablons, David
;  APPLICANT:  You, Liang
;  APPLICANT:  He, Biao
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Methods of Amplifying Long Sense Strand RNA
;  FILE REFERENCE: 023070-119510US
;  CURRENT APPLICATION NUMBER: US/10/206,613
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: US 60/308,190
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo dT-18
;   OTHER INFORMATION: linker primer
US-10-206-613-4

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 733
US-10-056-479A-15
; Sequence 15, Application US/10056479A
; Publication No. US20030175678A1
; GENERAL INFORMATION:
;  APPLICANT: Bowen, Banjamin A.
;  APPLICANT:  Deakin, Edward
;  APPLICANT:  Goldsmith, Neil
;  APPLICANT:  Haudenschild, Christian
;  APPLICANT:  Houck, David
;  APPLICANT:  McAlpine, James B.
;  APPLICANT:  Neilsen, Soren
;  APPLICANT:  Pazoles, Christopher
;  APPLICANT:  Spencer, Marget E.
;  APPLICANT:  Stafford, Angela
;  TITLE OF INVENTION: Methods for Identifying Genes Regulating
;  TITLE OF INVENTION:  Desired Cell Phenotypes
;  FILE REFERENCE: 50273/005002
;  CURRENT APPLICATION NUMBER: US/10/056,479A
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 60/263,807
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-056-479A-15

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 734
US-10-352-704-12
; Sequence 12, Application US/10352704
; Publication No. US20030176690A1
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-352-704-12

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 735
US-10-352-704-18/c
; Sequence 18, Application US/10352704
; Publication No. US20030176690A1
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
```

```
;       TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                           a Solid Support and Apparatus Permitting its
;                           Implementation
;       NUMBER OF SEQUENCES: 31
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Jacobson, Price, Holman & Stern
;            STREET: 400 Seventh St. N.W.
;            CITY: Washington D.C
;            STATE: D.C
;            COUNTRY: U.S.A.
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/352,704
;            FILING DATE: 28-Jan-2003
;            CLASSIFICATION: 536
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/358,556A
;            FILING DATE: 14-DEC-1994
;            APPLICATION NUMBER: FR 9315164
;            FILING DATE: 16-DEC-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Player, William E.
;            REGISTRATION NUMBER: 31,409
;            REFERENCE/DOCKET NUMBER: 10577/P58418
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)638-6666
;            TELEFAX: (202) 393-5350
;            TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       FRAGMENT TYPE: N-terminal
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  1..18
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-352-704-18

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTT 4


RESULT 736
US-10-075-335-9
; Sequence 9, Application US/10075335
; Publication No. US20030186237A1
; GENERAL INFORMATION:
;  APPLICANT: Ginsberg, Stephen
;  APPLICANT:  Che, Shaoli
;  TITLE OF INVENTION: Methods and Compositions of Amplifying RNA
;  FILE REFERENCE: HO-P02202US2
;  CURRENT APPLICATION NUMBER: US/10/075,335
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/268,664
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: 60/348,242
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 60/268,645
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: 60/344,557
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 60/306,216
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 60/350,176
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-075-335-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTT 15


RESULT 737
US-10-292-088-144
; Sequence 144, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-292-088-144

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTT 15


RESULT 738
US-10-314-578-913
; Sequence 913, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
```

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;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-913

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 739
US-10-314-578-939
; Sequence 939, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-939

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 740
US-10-328-578-142
; Sequence 142, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-III
;  FILE REFERENCE: 377882002020
;  CURRENT APPLICATION NUMBER: US/10/328,578
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-328-578-142

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
             ||||||||||||||||
Db          4 GTTTTTTTTTTTTTT 18


RESULT 741
US-10-389-155-97
; Sequence 97, Application US/10389155
; Publication No. US20030229208A1
;  GENERAL INFORMATION:
;       APPLICANT: Queen, Cary L.
;                  Co, Man Sung
;                  Schneider, William P.
;                  Landolfi, Nicholas F.
;                  Coelingh, Kathleen L.
;                  Selick, Harold E.
;       TITLE OF INVENTION: Improved Humanized Immunoglobulins
;       NUMBER OF SEQUENCES: 100
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/389,155
;            FILING DATE: 13-Mar-2003
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/325,000
;            FILING DATE: 01-JUN-1999
;            APPLICATION NUMBER: US 07/290,975
;            FILING DATE: 28-DEC-1988
;            APPLICATION NUMBER: US 07/310,252
;            FILING DATE: 13-FEB-1989
;            APPLICATION NUMBER: US 07/590,274
;            FILING DATE: 28-SEP-1990
;            APPLICATION NUMBER: US 07/634,278
;            FILING DATE: 19-DEC-1990
;            APPLICATION NUMBER: US 08/484,537
;            FILING DATE: 07-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
```

```
;            NAME: Smith, William M.
;            REGISTRATION NUMBER: 30,223
;            REFERENCE/DOCKET NUMBER: 011823-002650US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 97:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  13..18
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "T at positions 13-18 may be
;            present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-389-155-97

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 742
US-10-271-602B-84/c
; Sequence 84, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
;  APPLICANT: Alice Xiang Li
;  APPLICANT:  Ghazala Hashmi
;  APPLICANT:  Michael Seul
;  TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
;  TITLE OF INVENTION:  BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION
;  FILE REFERENCE: eMAP-US
;  CURRENT APPLICATION NUMBER: US/10/271,602B
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,427
;  PRIOR FILING DATE: 2001-10-14
;  PRIOR APPLICATION NUMBER: 60/329,620
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/329,428
;  PRIOR FILING DATE: 2001-10-14
;  PRIOR APPLICATION NUMBER: 60/329,619
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/364,416
;  PRIOR FILING DATE: 2002-03-14
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-84

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 743
US-10-334-143-204
; Sequence 204, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
;  APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
;  TITLE OF INVENTION:  KINASES IDENTIFIED WITH THE METHOD
;  FILE REFERENCE: 038602/1543
;  CURRENT APPLICATION NUMBER: US/10/334,143
;  CURRENT FILING DATE:  2002-12-31
;  PRIOR APPLICATION NUMBER: 60/343,169
;  PRIOR FILING DATE: 2001-12-31
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides in length
US-10-334-143-204

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 744
US-10-389-417-97
; Sequence 97, Application US/10389417
; Publication No. US20040049014A1
;   GENERAL INFORMATION:
;       APPLICANT: Queen, Cary L.
;                  Co, Man Sung
;                  Schneider, William P.
;                  Landolfi, Nicholas F.
;                  Coelingh, Kathleen L.
;                  Selick, Harold E.
;       TITLE OF INVENTION: Improved Humanized Immunoglobulins
;       NUMBER OF SEQUENCES: 100
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/389,417
;            FILING DATE: 13-Mar-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/325,000
;            FILING DATE: 01-JUN-1999
;            APPLICATION NUMBER: US 07/290,975
;            FILING DATE: 28-DEC-1988
;            APPLICATION NUMBER: US 07/310,252
;            FILING DATE: 13-FEB-1989
;            APPLICATION NUMBER: US 07/590,274
;
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;             FILING DATE: 28-SEP-1990
;             APPLICATION NUMBER: US 07/634,278
;             FILING DATE: 19-DEC-1990
;             APPLICATION NUMBER: US 08/484,537
;             FILING DATE: 07-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Smith, William M.
;             REGISTRATION NUMBER: 30,223
;             REFERENCE/DOCKET NUMBER: 011823-002650US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 97:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "T at positions 13-18 may be
;             present or absent"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-389-417-97

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 745
US-10-653-416-26
; Sequence 26, Application US/10653416
; Publication No. US20040110201A1
; GENERAL INFORMATION:
;  APPLICANT: RASHTCHIAN, AYOUB
;  APPLICANT:  SCHUSTER, DAVID M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CDNA SYNTHESIS
;  FILE REFERENCE: 38266-0011
;  CURRENT APPLICATION NUMBER: US/10/653,416
;  CURRENT FILING DATE:  2003-09-03
;  PRIOR APPLICATION NUMBER: 60/407,248
;  PRIOR FILING DATE: 2002-09-03
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according
;   OTHER INFORMATION: to the specification as filed
US-10-653-416-26

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 746
US-10-623-371-142
; Sequence 142, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  APPLICANT:  TUCK, Stephen F.
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-IV
;  FILE REFERENCE: 377882002021
;  CURRENT APPLICATION NUMBER: US/10/623,371
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: US 10/328,578
;  PRIOR FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: US 10/176,883
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 10/177,826
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-623-371-142

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          4 GTTTTTTTTTTTTTT 18


RESULT 747
US-10-785-744-15
; Sequence 15, Application US/10785744
; Publication No. US20040133941A1
; GENERAL INFORMATION:
;  APPLICANT: Bowen, Banjamin A.
;  APPLICANT:  Deakin, Edward
;  APPLICANT:  Goldsmith, Neil
;  APPLICANT:  Haudenschild, Christian
;  APPLICANT:  Houck, David
;  APPLICANT:  McAlpine, James B.
;  APPLICANT:  Neilsen, Soren
;  APPLICANT:  Pazoles, Christopher
;  APPLICANT:  Spencer, Marget E.
;  APPLICANT:  Stafford, Angela
;  TITLE OF INVENTION: Methods for Identifying Genes Regulating
;  TITLE OF INVENTION:  Desired Cell Phenotypes
;  FILE REFERENCE: 50273/005002
;  CURRENT APPLICATION NUMBER: US/10/785,744
;  CURRENT FILING DATE:  2004-02-23
;  PRIOR APPLICATION NUMBER: US/10/056,479
;  PRIOR FILING DATE: 2003-02-07
;  PRIOR APPLICATION NUMBER: US 60/263,807
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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```
;   OTHER INFORMATION: Synthetic
US-10-785-744-15

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 748
US-10-735-592-1
; Sequence 1, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 749
US-10-628-525-30/c
; Sequence 30, Application US/10628525
; Publication No. US20040185114A1
;   GENERAL INFORMATION:
;        APPLICANT: Keeling, Peter
;                   Guan, Hanping
;        TITLE OF INVENTION: Starch Encapsulation
;        NUMBER OF SEQUENCES: 37
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
;             STREET: 5370 Manhattan Circle
;             CITY: Boulder
;             STATE: CO
;             COUNTRY: US
;             ZIP: 80303
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/628,525
;             FILING DATE: 28-Jul-2003
;             CLASSIFICATION: 800
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/941,445
;             FILING DATE: 30-SEP-1997
;             APPLICATION NUMBER: US 60/026,855
;             FILING DATE: 30-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Winner, Ellen P
;             REGISTRATION NUMBER: 28,547
;             REFERENCE/DOCKET NUMBER: 89-97
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (303) 499-8080
;             TELEFAX: (303) 499-8089
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: Not Relevant
;        MOLECULE TYPE: cDNA to mRNA
;        HYPOTHETICAL: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-628-525-30

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 750
US-10-849-072-21/c
; Sequence 21, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
;  APPLICANT: Roche Diagnostics GmbH
;  TITLE OF INVENTION: High density labeling of DNA with modified or
;  TITLE OF INVENTION:  "chromophore" carrying nucleotides and DNA polymerases
;  TITLE OF INVENTION:  used
;  FILE REFERENCE: 4780/00/WO
;  CURRENT APPLICATION NUMBER: US/10/849,072
;  CURRENT FILING DATE:  2004-05-19
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: second
;   OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-21

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 751
US-10-849-072-23
; Sequence 23, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
;  APPLICANT: Roche Diagnostics GmbH
;  TITLE OF INVENTION: High density labeling of DNA with modified or
;  TITLE OF INVENTION:  "chromophore" carrying nucleotides and DNA polymerases
;  TITLE OF INVENTION:  used
;  FILE REFERENCE: 4780/00/WO
;  CURRENT APPLICATION NUMBER: US/10/849,072
;  CURRENT FILING DATE:  2004-05-19
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
```

```
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: second
;   OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-23

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 752
US-10-831-778-913
; Sequence 913, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/831,778
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-831-778-913

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 753
US-10-831-778-939
; Sequence 939, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/831,778
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-831-778-939

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 754
US-10-776-933-150
; Sequence 150, Application US/10776933
; Publication No. US20040241717A1
; GENERAL INFORMATION:
;  APPLICANT: HANSEN, BO
;  APPLICANT:  THRUE, CHARLOTTE ALBAEK
;  APPLICANT:  WESTERGAARD, MAJKEN
;  APPLICANT:  PETERSEN, KAMILLE DUMONG
;  APPLICANT:  WISSENBACH, MARGIT
;  TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF THIOREDOXIN
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 58614(71432)
;  CURRENT APPLICATION NUMBER: US/10/776,933
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 60/446,374
;  PRIOR FILING DATE: 2003-02-10
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 150
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: poly-T oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: This sequence may emcompass 12-18 nucleotides
;   OTHER INFORMATION: according to the specification as filed
US-10-776-933-150

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 755
US-10-674-159A-112
; Sequence 112, Application US/10674159A
; Publication No. US20040242518A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jianzhu
;  APPLICANT:  Ge, Qing
;  APPLICANT:  Eisen, Herman
;  TITLE OF INVENTION: Influenza Therapeutic
;  FILE REFERENCE: 0492611-0506
;  CURRENT APPLICATION NUMBER: US/10/674,159A
;  CURRENT FILING DATE:  2003-09-29
;  NUMBER OF SEQ ID NOS: 271
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mRNA
US-10-674-159A-112
```

```
  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 756
US-10-776-917-141
; Sequence 141, Application US/10776917
; Publication No. US20040248840A1
; GENERAL INFORMATION:
;  APPLICANT: HANSEN, BO
;  APPLICANT:  THRUE, CHARLOTTE ALBAEK
;  APPLICANT:  WESTERGAARD, MAJKEN
;  APPLICANT:  PETERSEN, KAMILLE DUMONG
;  APPLICANT:  WISSENBACH, MARGIT
;  TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF RAS EXPRESSION
;  FILE REFERENCE: 58609(71432)
;  CURRENT APPLICATION NUMBER: US/10/776,917
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 60/446,363
;  PRIOR FILING DATE: 2003-02-10
;  PRIOR APPLICATION NUMBER: DK 2003-01539
;  PRIOR FILING DATE: 2003-10-20
;  NUMBER OF SEQ ID NOS: 201
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 141
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: poly-T oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according to the
;   OTHER INFORMATION: specification as filed
US-10-776-917-141

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 757
US-10-766-096-9
; Sequence 9, Application US/10766096
; Publication No. US20040265786A1
;   GENERAL INFORMATION:
;        APPLICANT: Lin, Ching-I Patsy
;                   Wallace, Robert Bruce
;                   Cossman, Jeffrey
;                   French, Cynthia
;        TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                            to Preserve RNA and DNA
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/766,096
;             FILING DATE: 27-Jan-2004
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/884,029
;             FILING DATE: 27-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 02558B-059100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "t at positions 13-18 may be
;             present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-766-096-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 758
US-10-872-984-7
; Sequence 7, Application US/10872984
; Publication No. US20040265888A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/10/872,984
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: US/09/994,311
;  PRIOR FILING DATE: 2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-872-984-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
```

```
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 759
US-10-638-141-10
; Sequence 10, Application US/10638141
; Publication No. US20050003364A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  Kapoun, Ann Marie
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.013A
;  CURRENT APPLICATION NUMBER: US/10/638,141
;  CURRENT FILING DATE:  2003-08-07
;  PRIOR APPLICATION NUMBER: US/09/665,728
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/156,277
;  PRIOR FILING DATE: 1999-09-27
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-638-141-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 760
US-10-776-934-741
; Sequence 741, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
;  APPLICANT: HANSEN, BO
;  APPLICANT:  THRUE, CHARLOTTE ALBAEK
;  APPLICANT:  WESTERGAARD, MAJKEN
;  APPLICANT:  PETERSEN, KAMILLE DUMONG
;  APPLICANT:  WISSENBACH, MARGIT
;  TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
;  FILE REFERENCE: 58610(71432)
;  CURRENT APPLICATION NUMBER: US/10/776,934
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 60/446,372
;  PRIOR FILING DATE: 2003-02-10
;  PRIOR APPLICATION NUMBER: 60/523,591
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 741
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 741
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: poly-T oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according to the
;   OTHER INFORMATION: specification as filed
US-10-776-934-741

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 761
US-10-741-600-73428/c
; Sequence 73428, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73428
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-73428

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCT 3196
                ||||||||||||||||
Db         18 TCTCTCTCCCTCCCT 4


RESULT 762
US-10-601-140A-24
; Sequence 24, Application US/10601140A
; Publication No. US20050053942A1
; GENERAL INFORMATION:
;  APPLICANT: KAUPPINEN, SAKARI
;  APPLICANT:  JACOBSEN, NANA
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR DETECTION AND ISOLATION OF A
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCE
;  FILE REFERENCE: 57764(71994)
;  CURRENT APPLICATION NUMBER: US/10/601,140A
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US 60/390,928
;  PRIOR FILING DATE: 2002-06-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-10-601-140A-24

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 763
US-10-884-617-2
; Sequence 2, Application US/10884617
```

```
; Publication No. US20050054730A1
; GENERAL INFORMATION:
;  APPLICANT: Fu, Jin
;  APPLICANT:  Gaetani, Silvana
;  APPLICANT:  Piomelli, Daniele
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Compounds, Compositions and Treatments of
;  TITLE OF INVENTION:  Oleoylethanolamide-Like Modulators of PPARalpha
;  FILE REFERENCE: 02307E-133310US
;  CURRENT APPLICATION NUMBER: US/10/884,617
;  CURRENT FILING DATE:  2004-07-01
;  PRIOR APPLICATION NUMBER: US 60/279,542
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: US 60/336,289
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: US 10/112,509
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: US 60/485,062
;  PRIOR FILING DATE: 2003-07-02
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Oligo(dT)-12-18
;   OTHER INFORMATION: primer for reverse transcription of total RNA
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (13)..(18)
;   OTHER INFORMATION: t at positions 13-18 may be present or absent
US-10-884-617-2

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 764
US-10-669-962-27
; Sequence 27, Application US/10669962
; Publication No. US20050081264A1
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/10/669,962
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: US/09/142,108C
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-669-962-27

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 765
US-10-669-962-28
; Sequence 28, Application US/10669962
; Publication No. US20050081264A1
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/10/669,962
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: US/09/142,108C
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-669-962-28

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 766
US-10-503-120-1
; Sequence 1, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-503-120-1

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

```
RESULT 767
US-10-503-120-8
; Sequence 8, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are 2'-O-methyl-D-uridi
;   OTHER INFORMATION: ne
US-10-503-120-8

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   46.7%;  Pred. No. 4.4e+02;
  Matches    7;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :|:|:|:|:|:|:|:
Db          1 UTUTUTUTUTUTUTU 15


RESULT 768
US-10-503-120-9
; Sequence 9, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Residues 1-3, 7-9, and 13-15 are 2'-O-methyl-D-uridine
US-10-503-120-9

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   40.0%;  Pred. No. 4.4e+02;
  Matches    6;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::|||:::|||:::
Db          1 UUUTTTUUUTTTUUU 15


RESULT 769
US-10-503-120-10
; Sequence 10, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine
US-10-503-120-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   40.0%;  Pred. No. 4.4e+02;
  Matches    6;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::||||||:::
Db          1 UUUUUUTTTTTTUUU 15


RESULT 770
US-10-503-120-21/c
; Sequence 21, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Target RNA oligonucleotide
US-10-503-120-21

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 771
US-10-775-973-10
; Sequence 10, Application US/10775973
; Publication No. US20050158729A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  Kapoun, Ann Marie
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.014A
```

```
;  CURRENT APPLICATION NUMBER: US/10/775,973
;  CURRENT FILING DATE:  2004-02-09
;  PRIOR APPLICATION NUMBER: US/09/665,976
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/156,280
;  PRIOR FILING DATE: 1999-09-27
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic
US-10-775-973-10

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 772
US-10-959-440-84
; Sequence 84, Application US/10959440
; Publication No. US20050208605A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  White, R. Tyler
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.017A
;  CURRENT APPLICATION NUMBER: US/10/959,440
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: US/09/809,545
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-10-959-440-84

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 773
US-11-024-428-7
; Sequence 7, Application US/11024428
; Publication No. US20050106676A1
; GENERAL INFORMATION:
;  APPLICANT: NAGAI, HIROSHI
;  APPLICANT:  KURODA, KYOKO
;  APPLICANT:  NAKAJIMA, TERUMI
;  TITLE OF INVENTION: NOVEL PROTEINS HAVING HEMOLYTIC ACTIVITY AND GENES
;  TITLE OF INVENTION:  ENCODING THE PROTEIN
;  FILE REFERENCE: 037181.50611US
;  CURRENT APPLICATION NUMBER: US/11/024,428
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US/09/979,275
;  PRIOR FILING DATE: 2003-05-27
;  PRIOR APPLICATION NUMBER: PCT/JP01/02209
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: JP 2000-78967
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
;    FEATURE:
;    OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-11-024-428-7

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 774
US-10-619-253-146
; Sequence 146, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 146
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-146

  Query Match             0.3%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2239 ATTCCATGAGCTGCT 2253
              |||||||||||||||
Db          3 ATTCCATGAGCTGCT 17


RESULT 775
US-09-263-959-515/c
; Sequence 515, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  515:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-515

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              ||||||||| ||| ||||
Db         18 CTCTCTCTCTCTCTCTCT 1


RESULT 776
US-09-263-959-873/c
; Sequence 873, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  873:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-873

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTC 3199
              ||||||| ||| |||||
Db         18 TCTCTCTCTCTCTCTCTC 1


RESULT 777
US-09-789-210-13
; Sequence 13, Application US/09789210
; Publication No. US20040241646A1
;  GENERAL INFORMATION:
;       APPLICANT: COHEN, MAURICE
;                  COLPITTS, TRACEY L.
;                  FRIEDMAN, PAULA N.
;                  GRANADOS, EDWARD N.
;                  KLASS, MICHAEL R.
;                  RUSSELL, JOHN C.
;                  STEWART, KENT D.
;                  STROUPE, STEVEN D.
;       TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
;                           AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
;                           OF THE PROSTATE
;       NUMBER OF SEQUENCES: 76
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Abbott Laboratories
;            STREET: 100 Abbott Park Road
;            CITY: Abbott Park
;            STATE: IL
;            COUNTRY: USA
;            ZIP: 60064-3500
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/789,210
;            FILING DATE: 20-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/944,483
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Becker, Cheryl L.
;            REGISTRATION NUMBER: 35,441
;            REFERENCE/DOCKET NUMBER: 6183.US.01
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 847/935-1729
;            TELEFAX: 847/938-2623
;            TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-789-210-13

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1960 TCAAGCCCCACCACATAG 1977
              ||||||||| | ||||||
Db          1 TCAAGCCCCGCTACATAG 18


RESULT 778
```

```
US-10-011-204-3/c
; Sequence 3, Application US/10011204
; Publication No. US20020182617A1
; GENERAL INFORMATION:
;  APPLICANT: EKINS, Roger P
;  TITLE OF INVENTION: Binding assay using binding agents with tail groups
;  FILE REFERENCE: 0380-P01180US0
;  CURRENT APPLICATION NUMBER: US/10/011,204
;  CURRENT FILING DATE:  2001-11-08
;  PRIOR APPLICATION NUMBER: US/08/700,530
;  PRIOR FILING DATE: 1996-10-23
;  PRIOR APPLICATION NUMBER: PCT/GB95/00521
;  PRIOR FILING DATE: 1995-03-10
;  PRIOR APPLICATION NUMBER: GB 9404709.9
;  PRIOR FILING DATE: 1994-03-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-011-204-3

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTC 3199
              ||||||||| ||| |||||
Db         18 TCTCTCTCTCTCTCTCTC 1


RESULT 779
US-10-011-204-4
; Sequence 4, Application US/10011204
; Publication No. US20020182617A1
; GENERAL INFORMATION:
;  APPLICANT: EKINS, Roger P
;  TITLE OF INVENTION: Binding assay using binding agents with tail groups
;  FILE REFERENCE: 0380-P01180US0
;  CURRENT APPLICATION NUMBER: US/10/011,204
;  CURRENT FILING DATE:  2001-11-08
;  PRIOR APPLICATION NUMBER: US/08/700,530
;  PRIOR FILING DATE: 1996-10-23
;  PRIOR APPLICATION NUMBER: PCT/GB95/00521
;  PRIOR FILING DATE: 1995-03-10
;  PRIOR APPLICATION NUMBER: GB 9404709.9
;  PRIOR FILING DATE: 1994-03-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-011-204-4

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              ||||||||| ||| ||||
Db          1 CTCTCTCTCTCTCTCTCT 18


RESULT 780
US-10-077-383-31/c
; Sequence 31, Application US/10077383
; Publication No. US20030050444A1
; GENERAL INFORMATION:
;  APPLICANT: Haydock, Paul V.
;  APPLICANT:  U'Ren, Jack
;  APPLICANT:  Saigene Corporation
;  TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
;  TITLE OF INVENTION:  DNA/RNA Mixed Polymer Intermediate Products
;  FILE REFERENCE: 018048-001710US
;  CURRENT APPLICATION NUMBER: US/10/077,383
;  CURRENT FILING DATE:  2002-02-15
;  PRIOR APPLICATION NUMBER: US 60/296,812
;  PRIOR FILING DATE: 2001-06-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:(XY)-n spacer
;   OTHER INFORMATION: sequence, where X = a, Y = g and n = 9
US-10-077-383-31

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              ||||||||| ||| ||||
Db          1 CTCTCTCTCTCTCTCTCT 18


RESULT 781
US-10-077-383-32
; Sequence 32, Application US/10077383
; Publication No. US20030050444A1
; GENERAL INFORMATION:
;  APPLICANT: Haydock, Paul V.
;  APPLICANT:  U'Ren, Jack
;  APPLICANT:  Saigene Corporation
;  TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
;  TITLE OF INVENTION:  DNA/RNA Mixed Polymer Intermediate Products
;  FILE REFERENCE: 018048-001710US
;  CURRENT APPLICATION NUMBER: US/10/077,383
;  CURRENT FILING DATE:  2002-02-15
;  PRIOR APPLICATION NUMBER: US 60/296,812
;  PRIOR FILING DATE: 2001-06-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:(XY)-n spacer
;   OTHER INFORMATION: sequence complement, where X = a, Y = g and n = 9
US-10-077-383-32

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCT 3198
              ||||||||| ||| ||||
Db          1 CTCTCTCTCTCTCTCTCT 18


RESULT 782
US-10-746-547-107/c
; Sequence 107, Application US/10746547
; Publication No. US20040219575A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Neuman, Toomas
;  APPLICANT:  Palm, Kaia
;  TITLE OF INVENTION: Methods and Compositions for the Diagnosis, Prognosis, and
;  TITLE OF INVENTION:  Treatment of Cancer
;  FILE REFERENCE: 33763/US (473322-00003)
;  CURRENT APPLICATION NUMBER: US/10/746,547
;  CURRENT FILING DATE:  2003-12-24
;  PRIOR APPLICATION NUMBER: US 60/436,693
;  PRIOR FILING DATE: 2002-12-26
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-746-547-107

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3184 TCTCTCCCTCCCTCTCTC 3201
              |||||||||||| | |||
Db         18 TCTCTCCCTCCCACCCTC 1


RESULT 783
US-10-473-126-650
; Sequence 650, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Methods and nucleic acids for the analysis of  hematopoietic cell
;  TITLE OF INVENTION:  proliferative disorders
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/473,126
;  CURRENT FILING DATE:  2003-09-26
;  NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 650
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Detection oligonucleotide for ELK1
US-10-473-126-650

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTTGTTTTTGGG 18


RESULT 784
US-10-473-126-826
; Sequence 826, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Methods and nucleic acids for the analysis of  hematopoietic cell
;  TITLE OF INVENTION:  proliferative disorders
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/473,126
;  CURRENT FILING DATE:  2003-09-26
;  NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 826
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Detection oligonucleotide for PTEN
US-10-473-126-826

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 785
US-10-473-126-1242
; Sequence 1242, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Methods and nucleic acids for the analysis of  hematopoietic cell
;  TITLE OF INVENTION:  proliferative disorders
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/473,126
;  CURRENT FILING DATE:  2003-09-26
;  NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 1242
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Detection oligonucleotide for ELK1
US-10-473-126-1242

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTTGTTTTTGGG 18


RESULT 786
US-10-006-191-136/c
; Sequence 136, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
;  FILE REFERENCE: RTS-0274
;  CURRENT APPLICATION NUMBER: US/10/006,191
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 136
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-136

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACATT 2414
              |||||| ||||||| |||
Db         20 TATATATATATATATATT 3


RESULT 787
US-10-946-914-136/c
; Sequence 136, Application US/10946914
; Publication No. US20050059629A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Andrew T. Watt
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Mausumee Guha
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIO
;  FILE REFERENCE: 23546-9505US (RTS-0274US.P1)
;  CURRENT APPLICATION NUMBER: US/10/946,914
;  CURRENT FILING DATE:  2004-09-21
;  PRIOR APPLICATION NUMBER: US 10/006,191
;  PRIOR FILING DATE: 2001-12-10
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-946-914-136

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACATT 2414
              |||||| ||||||| |||
Db         20 TATATATATATATATATT 3


RESULT 788
US-09-953-047-91
; Sequence 91, Application US/09953047
; Publication No. US20030087854A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
;  FILE REFERENCE: RTS-0157
;  CURRENT APPLICATION NUMBER: US/09/953,047
;  CURRENT FILING DATE:  2001-09-10
;  NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 91
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-047-91

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATAC 2411
              |||||||| ||||||||
Db          1 ATATATATGTATATATAC 18


RESULT 789
US-10-630-401-91
; Sequence 91, Application US/10630401
; Publication No. US20040048824A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
;  FILE REFERENCE: RTS-0157
;  CURRENT APPLICATION NUMBER: US/10/630,401
;  CURRENT FILING DATE:  2003-07-30
;  PRIOR APPLICATION NUMBER: US/09/953,047
;  PRIOR FILING DATE: 2001-09-10
;  NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 91
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-630-401-91

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 5.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATAC 2411
              |||||||| ||||||||
Db          1 ATATATATGTATATATAC 18


RESULT 790
US-10-719-956-160951
; Sequence 160951, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 160951
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-160951

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3015 TGCTCAGGGTCACTGAAC 3032
              |||||||||||||  |||
Db          8 TGCTCAGGGTCACACAAC 25


RESULT 791
US-09-263-959-836/c
; Sequence 836, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
```

```
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  836:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-836

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 6.3e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2392 AAATATATATACATATATA 2410
              | ||||||||  |||||||
Db         19 ATATATATATTTATATATA 1


RESULT 792
US-09-917-138-2
; Sequence 2, Application US/09917138
; Patent No. US20020031776A1
; GENERAL INFORMATION:
;  APPLICANT: TULLIS, Richard
;  APPLICANT:  STEIFFEL, Jerome
;  TITLE OF INVENTION: ENZYMATIC LABELIING AND DETECTION OF DNA
;  TITLE OF INVENTION:  HYBRIDIZATION PROBES
;  FILE REFERENCE: 24730-2207B
;  CURRENT APPLICATION NUMBER: US/09/917,138
;  CURRENT FILING DATE:  2001-07-26
;  PRIOR APPLICATION NUMBER: 09/580,358
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/136,545
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Combined DNA/RNA
US-09-917-138-2

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAAT 3623
              ||||||| ||||| | ||:
Db          1 AAAAAAAAAAAAAAAAAAU 19


RESULT 793
US-09-725-265-31
; Sequence 31, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/09/725,265
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-31

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 794
US-09-891-517-31
; Sequence 31, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-31

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 795
US-09-891-517-42/c
```

```
; Sequence 42, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-42

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         19 ATATATATATTTTTTTTTT 1


RESULT 796
US-10-209-608-31
; Sequence 31, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-31

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 797
US-10-683-386-31
; Sequence 31, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLI
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-31

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20


RESULT 798
US-10-138-674-1076/c
; Sequence 1076, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
```

US-10-138-674-1076

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1
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RESULT 799
US-10-287-949A-1076/c
; Sequence 1076, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1076

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1
```

RESULT 800
US-10-735-592-55/c
; Sequence 55, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-55

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| |||
Db         17 AAAAAAAAAAAAAAAGA 1
```

RESULT 801
US-10-951-303-1076/c
; Sequence 1076, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1076

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1
```

RESULT 802
US-09-725-265-17/c
; Sequence 17, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17

Query Match 0.3%; Score 13.8; DB 1; Length 18;

```
  Best Local Similarity   88.2%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 803
US-09-891-517-17/c
; Sequence 17, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-17

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 804
US-10-209-608-17/c
; Sequence 17, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-17

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 805
US-10-683-386-17/c
; Sequence 17, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-17

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTTT 1


RESULT 806
US-09-904-744-1
; Sequence 1, Application US/09904744
; Patent No. US20020150905A1
; GENERAL INFORMATION:
;  APPLICANT: Barbera-Guillem, Emilio
;  APPLICANT:  Nelson, M. Bud
;  APPLICANT:  Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  TITLE OF INVENTION:  dendrimers in a signal amplification system
;  FILE REFERENCE: B-73
```

```
;  CURRENT APPLICATION NUMBER: US/09/904,744
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/437076
;  PRIOR FILING DATE: 1999-11-09
;  PRIOR APPLICATION NUMBER: 60/107828
;  PRIOR FILING DATE: 1998-11-10
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthesized
US-09-904-744-1

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db          2 GGAAAAAAAAAAAAAAA 18


RESULT 807
US-09-918-187-27
; Sequence 27, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-27

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2213 AAACAGCAGCTCATGGA 2229
              ||  |||||||||||||
Db          4 AATGAGCAGCTCATGGA 20


RESULT 808
US-10-484-442-27
; Sequence 27, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-27

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2213 AAACAGCAGCTCATGGA 2229
              ||  |||||||||||||
Db          4 AATGAGCAGCTCATGGA 20


RESULT 809
US-10-619-253-27
; Sequence 27, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-27

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2213 AAACAGCAGCTCATGGA 2229
              ||  |||||||||||||
Db          4 AATGAGCAGCTCATGGA 20


RESULT 810
US-10-467-008-110
; Sequence 110, Application US/10467008
; Publication No. US20040116366A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT B
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: ISPH-0746
;  CURRENT APPLICATION NUMBER: US/10/467,008
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: PCT/US02/02805
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: US 09/780,045
;  PRIOR FILING DATE: 2001-02-09
;  NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-467-008-110

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy       2395 TATATATACATATATACATT 2414
              ||||||| ||||||| ||
Db          1 TATATATGTATATATATTTT 20


RESULT 811
US-10-671-395-938/c
; Sequence 938, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 938
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-938

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAACA 3619
              ||||  |||||| ||||| |
Db         20 TCTGCCAAAAAAAAAAAAAA 1


RESULT 812
US-10-735-592-17/c
; Sequence 17, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-17

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 7.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         16 AAAAAAAAAAAAACA 2


RESULT 813
US-10-735-592-56/c
; Sequence 56, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-56

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 7.8e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         16 AAAAAAAAAAAAACA 2


RESULT 814
US-09-371-307-85/c
; Sequence 85, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Sherri M.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: Piller, Kenneth J.
;  APPLICANT: Kishore, Ganesh M.
;  APPLICANT: Elich, Tedd D.
;  APPLICANT: Logusch, Eugene W.
;  APPLICANT: Rao, Sudabathula
;  APPLICANT: Ream, Joel E.
;  APPLICANT: Logusch, Sherry J.
;  TITLE OF INVENTION: Methods for controlling gibberellin levels
;  FILE REFERENCE: MOBT:216
;  CURRENT APPLICATION NUMBER: US/09/371,307A
;  CURRENT FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-371-307-85

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 815
US-10-176-884-44/c
; Sequence 44, Application US/10176884
; Publication No. US20030126642A1
; GENERAL INFORMATION:
;  APPLICANT: Fischer, Robert
;  APPLICANT:  Kinoshita, Tetsu
;  APPLICANT:  Yadegari, Ramin
;  APPLICANT:  Gehring, Mary
;  APPLICANT:  Okamuro, Jack
```

```
;  APPLICANT:  Dang, Van-Dinh
;  APPLICANT:  The Regents of the University of California
;  APPLICANT:  Ceres, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Modulating Plant
;  TITLE OF INVENTION:  Development
;  FILE REFERENCE: 02307O-116710US
;  CURRENT APPLICATION NUMBER: US/10/176,884
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/300,506
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo(dT)-18
;   OTHER INFORMATION: primer, oligo dTV
US-10-176-884-44

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 816
US-10-177-478-1/c
; Sequence 1, Application US/10177478
; Publication No. US20030165903A1
; GENERAL INFORMATION:
;  APPLICANT: Dang, Van-Dinh
;  APPLICANT:  Okamuro, Jack
;  TITLE OF INVENTION: Chimeric Histone Acetyltransferase
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 11696-037001
;  CURRENT APPLICATION NUMBER: US/10/177,478
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: U.S. 60/300,135
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-177-478-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 817
US-10-182-230-196/c
; Sequence 196, Application US/10182230
; Publication No. US20030215817A1
; GENERAL INFORMATION:
;  APPLICANT: Leonardi, Amedeo
;  APPLICANT:  Sartani, Abraham
;  APPLICANT:  Glass, James R.
;  APPLICANT:  Sutcliffe, J. Gregor
;  APPLICANT:  Hasel, Karl W.
;  TITLE OF INVENTION: Modulation of Gene Expression in Formation of Fatty Atherosclerot
;  TITLE OF INVENTION:  Lesions
;  FILE REFERENCE: 216019-143
;  CURRENT APPLICATION NUMBER: US/10/182,230
;  CURRENT FILING DATE:  2003-02-03
;  PRIOR APPLICATION NUMBER: 60/177,963
;  PRIOR FILING DATE: 2000-01-25
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 3' sequencing primer for dire
;   OTHER INFORMATION: ct sequencing
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (19)..(19)
;   OTHER INFORMATION: v stands for a, c, or g
US-10-182-230-196

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 818
US-10-401-321-85/c
; Sequence 85, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Sherri M.
;  APPLICANT:  Heck, Gregory R.
;  APPLICANT:  Piller, Kenneth J.
;  APPLICANT:  Kilshore, Ganesh M.
;  APPLICANT:  Elich, Tedd D.
;  APPLICANT:  Logusch, Eugene W.
;  APPLICANT:  Rao, Sudabathula
;  APPLICANT:  Ream, Joel E.
;  APPLICANT:  Logusch, Sherry J.
;  APPLICANT:  Baerson, Scott R.
;  TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
;  FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
;  CURRENT APPLICATION NUMBER: US/10/401,321
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-401-321-85

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 819
US-10-965-470-1/c
; Sequence 1, Application US/10965470
; Publication No. US20050204429A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: PENNELL, Roger
;  APPLICANT:  APUYA, Nestor
;  APPLICANT:  MEDRANO, Leonard
;  APPLICANT:  FELDMANN, Kenneth
;  TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2750-1580PUS2
;  CURRENT APPLICATION NUMBER: US/10/965,470
;  CURRENT FILING DATE:  2004-10-13
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-965-470-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 820
US-10-950-095-73/c
; Sequence 73, Application US/10950095
; Publication No. US20050223434A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai, et. al.
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
;  TITLE OF INVENTION:  MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1578PUS2
;  CURRENT APPLICATION NUMBER: US/10/950,095
;  CURRENT FILING DATE:  2004-09-23
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligo(dT)18 primer
US-10-950-095-73

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 821
US-10-950-321-1/c
; Sequence 1, Application US/10950321
; Publication No. US20050223422A1
; GENERAL INFORMATION:
;  APPLICANT: COOK, Zhihong et al.
;  TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2750-1577PUS2
;  CURRENT APPLICATION NUMBER: US/10/950,321
;  CURRENT FILING DATE:  2004-09-23
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligo(dT)18 primer
US-10-950-321-1

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 822
US-11-051-456-44/c
; Sequence 44, Application US/11051456
; Publication No. US20050229270A1
; GENERAL INFORMATION:
;  APPLICANT: Fischer, Robert
;  APPLICANT:  Kinoshita, Tetsu
;  APPLICANT:  Yadegari, Ramin
;  APPLICANT:  Gehring, Mary
;  APPLICANT:  Okamuro, Jack
;  APPLICANT:  Dang, Van-Dinh
;  APPLICANT:  The Regents of the University of California
;  APPLICANT:  Ceres, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Modulating Plant
;  TITLE OF INVENTION:  Development
;  FILE REFERENCE: 02307O-116710US
;  CURRENT APPLICATION NUMBER: US/11/051,456
;  CURRENT FILING DATE:  2005-02-04
;  PRIOR APPLICATION NUMBER: US/10/176,884
;  PRIOR FILING DATE: 2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/300,506
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligo(dT)-18
;   OTHER INFORMATION: primer, oligo dTV
US-11-051-456-44

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 823
US-09-775-479-8
; Sequence 8, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
;  APPLICANT: LECLERC, Guy
;  APPLICANT:  MARTEL, R,mi
;  TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
;  TITLE OF INVENTION:  RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
;  TITLE OF INVENTION:  THERAPEUTIC USES THEREOF
;  FILE REFERENCE: 12168-1US-2
;  CURRENT APPLICATION NUMBER: US/09/775,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: 09/318,106
;  PRIOR FILING DATE: 1999-05-24
```

```
;  PRIOR APPLICATION NUMBER: 08/756,728
;  PRIOR FILING DATE: 1996-11-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-09-775-479-8

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3608 AAAACAAAAACAGAATTT 3625
              |||| ||||| | |||||
Db          1 AAAAAAAAAAAAAAATTT 18


RESULT 824
US-09-809-545A-84/c
; Sequence 84, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  White, R. Tyler
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.017A
;  CURRENT APPLICATION NUMBER: US/09/809,545A
;  CURRENT FILING DATE:  2001-03-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-09-809-545A-84

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 825
US-09-888-326-837/c
; Sequence 837, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 837
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-837

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 826
US-09-994-311-7/c
; Sequence 7, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/09/994,311
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
              || ||||||| ||||| |
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 827
US-09-776-479-913/c
; Sequence 913, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913
```

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 828
US-09-776-479-913/c
; Sequence 913, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 829
US-09-776-479-939/c
; Sequence 939, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 830
US-09-776-479-939/c
; Sequence 939, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 831
US-09-370-541-14/c
; Sequence 14, Application US/09370541
; Publication No. US20030088079A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxxy-Modified Nucleosidic Compounds And Oligomeric
; TITLE OF INVENTION: Compounds Prepared Therefrom
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/130,973
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-370-541-14

Query Match 0.3%; Score 13.2; DB 1; Length 18;

```
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 832
US-09-979-275A-7/c
; Sequence 7, Application US/09979275A
; Publication No. US20040110919A1
; GENERAL INFORMATION:
;  APPLICANT: NAGAI, HIROSHI
;  APPLICANT:  KURODA, KYOKO
;  APPLICANT:  NAKAJIMA, TERUMI
;  TITLE OF INVENTION: NOVEL PROTEINS HAVING HEMOLYTIC ACTIVITY AND GENES
;  TITLE OF INVENTION:  ENCODING THE PROTEIN
;  FILE REFERENCE: 037181.50611US
;  CURRENT APPLICATION NUMBER: US/09/979,275A
;  CURRENT FILING DATE:  2003-05-27
;  PRIOR APPLICATION NUMBER: PCT/JP01/02209
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: JP 2000-78967
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-09-979-275A-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 833
US-10-125-295-9/c
; Sequence 9, Application US/10125295
; Publication No. US20020164572A1
;   GENERAL INFORMATION:
;        APPLICANT: Lin, Ching-I Patsy
;                   Wallace, Robert Bruce
;                   Cossman, Jeffrey
;                   French, Cynthia
;        TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                            to Preserve RNA and DNA
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/125,295
;             FILING DATE: 17-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/545,225
;             FILING DATE: 07-Apr-2000
;             APPLICATION NUMBER: US 08/884,029
;             FILING DATE: 27-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 02558B-059100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "t at positions 13-18 may be
;             present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-125-295-9

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 834
US-10-208-357-24
; Sequence 24, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lohse, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 50036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,357
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/619,103
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 60/145,834
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-24

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18
```

```
RESULT 835
US-10-112-653-882/c
; Sequence 882, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 882
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-882

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 836
US-10-017-995-913/c
; Sequence 913, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Sequence
US-10-017-995-913

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 837
US-10-017-995-939/c
; Sequence 939, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Sequence
US-10-017-995-939

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 838
US-10-206-613-4/c
; Sequence 4, Application US/10206613
; Publication No. US20030104432A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Zhidong
;  APPLICANT:  Jablons, David
;  APPLICANT:  You, Liang
;  APPLICANT:  He, Biao
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Methods of Amplifying Long Sense Strand RNA
;  FILE REFERENCE: 02307O-119510US
;  CURRENT APPLICATION NUMBER: US/10/206,613
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: US 60/308,190
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:oligo dT-18
;    OTHER INFORMATION: linker primer
US-10-206-613-4

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 839
US-10-056-479A-15/c
; Sequence 15, Application US/10056479A
; Publication No. US20030175678A1
; GENERAL INFORMATION:
;  APPLICANT: Bowen, Banjamin A.
;  APPLICANT:  Deakin, Edward
;  APPLICANT:  Goldsmith, Neil
;  APPLICANT:  Haudenschild, Christian
;  APPLICANT:  Houck, David
;  APPLICANT:  McAlpine, James B.
;  APPLICANT:  Neilsen, Soren
;  APPLICANT:  Pazoles, Christopher
;  APPLICANT:  Spencer, Marget E.
```

```
;  APPLICANT:  Stafford, Angela
;  TITLE OF INVENTION: Methods for Identifying Genes Regulating
;  TITLE OF INVENTION:  Desired Cell Phenotypes
;  FILE REFERENCE: 50273/005002
;  CURRENT APPLICATION NUMBER: US/10/056,479A
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 60/263,807
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-056-479A-15

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 840
US-10-352-704-12/c
; Sequence 12, Application US/10352704
; Publication No. US20030176690A1
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-352-704-12

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 841
US-10-352-704-18
; Sequence 18, Application US/10352704
; Publication No. US20030176690A1
;   GENERAL INFORMATION:
;        APPLICANT: Chatelain, Francois
;                   Kumarev, Viktor
;        TITLE OF INVENTION: Process for Preparing Polynucleotides on
;                            a Solid Support and Apparatus Permitting its
;                            Implementation
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jacobson, Price, Holman & Stern
;             STREET: 400 Seventh St. N.W.
;             CITY: Washington D.C
;             STATE: D.C
;             COUNTRY: U.S.A.
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,704
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 536
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/358,556A
;             FILING DATE: 14-DEC-1994
;             APPLICATION NUMBER: FR 9315164
;             FILING DATE: 16-DEC-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Player, William E.
;             REGISTRATION NUMBER: 31,409
;             REFERENCE/DOCKET NUMBER: 10577/P58418
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)638-6666
;             TELEFAX: (202) 393-5350
;             TELEX: RCA 248593 IDEA UR
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: N-terminal
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..18
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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US-10-352-704-18

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 842
US-10-075-335-9/c
; Sequence 9, Application US/10075335
; Publication No. US20030186237A1
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Stephen
; APPLICANT: Che, Shaoli
; TITLE OF INVENTION: Methods and Compositions of Amplifying RNA
; FILE REFERENCE: HO-P02202US2
; CURRENT APPLICATION NUMBER: US/10/075,335
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/268,664
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/348,242
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/268,645
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/344,557
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/306,216
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/350,176
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-075-335-9

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 843
US-10-292-088-144/c
; Sequence 144, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-292-088-144

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 844
US-10-314-578-913/c
; Sequence 913, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-913

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 845
US-10-314-578-939/c
; Sequence 939, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 939
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-939

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 846
US-10-389-155-97/c
; Sequence 97, Application US/10389155
; Publication No. US20030229208A1
;   GENERAL INFORMATION:
;        APPLICANT: Queen, Cary L.
;                   Co, Man Sung
;                   Schneider, William P.
;                   Landolfi, Nicholas F.
;                   Coelingh, Kathleen L.
;                   Selick, Harold E.
;        TITLE OF INVENTION: Improved Humanized Immunoglobulins
;        NUMBER OF SEQUENCES: 100
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/389,155
;             FILING DATE: 13-Mar-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/325,000
;             FILING DATE: 01-JUN-1999
;             APPLICATION NUMBER: US 07/290,975
;             FILING DATE: 28-DEC-1988
;             APPLICATION NUMBER: US 07/310,252
;             FILING DATE: 13-FEB-1989
;             APPLICATION NUMBER: US 07/590,274
;             FILING DATE: 28-SEP-1990
;             APPLICATION NUMBER: US 07/634,278
;             FILING DATE: 19-DEC-1990
;             APPLICATION NUMBER: US 08/484,537
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith, William M.
;             REGISTRATION NUMBER: 30,223
;             REFERENCE/DOCKET NUMBER: 011823-002650US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 97:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "T at positions 13-18 may be
;             present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-389-155-97

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 847
US-10-271-602B-84
; Sequence 84, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
;  APPLICANT: Alice Xiang Li
;  APPLICANT:  Ghazala Hashmi
;  APPLICANT:  Michael Seul
;  TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
;  TITLE OF INVENTION:  BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION
;  FILE REFERENCE: eMAP-US
;  CURRENT APPLICATION NUMBER: US/10/271,602B
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,427
;  PRIOR FILING DATE: 2001-10-14
;  PRIOR APPLICATION NUMBER: 60/329,620
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/329,428
;  PRIOR FILING DATE: 2001-10-14
;  PRIOR APPLICATION NUMBER: 60/329,619
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/364,416
;  PRIOR FILING DATE: 2002-03-14
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-84

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 848
US-10-334-143-204/c
; Sequence 204, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
;  APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
;  TITLE OF INVENTION:  KINASES IDENTIFIED WITH THE METHOD
;  FILE REFERENCE: 038602/1543
;  CURRENT APPLICATION NUMBER: US/10/334,143
;  CURRENT FILING DATE:  2002-12-31
;  PRIOR APPLICATION NUMBER: 60/343,169
;  PRIOR FILING DATE: 2001-12-31
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;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
;    FEATURE:
;    OTHER INFORMATION: this sequence may encompass 12-18 nucleotides in length
US-10-334-143-204

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 849
US-10-389-417-97/c
; Sequence 97, Application US/10389417
; Publication No. US20040049014A1
;   GENERAL INFORMATION:
;        APPLICANT: Queen, Cary L.
;                   Co, Man Sung
;                   Schneider, William P.
;                   Landolfi, Nicholas F.
;                   Coelingh, Kathleen L.
;                   Selick, Harold E.
;        TITLE OF INVENTION: Improved Humanized Immunoglobulins
;        NUMBER OF SEQUENCES: 100
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/389,417
;             FILING DATE: 13-Mar-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/325,000
;             FILING DATE: 01-JUN-1999
;             APPLICATION NUMBER: US 07/290,975
;             FILING DATE: 28-DEC-1988
;             APPLICATION NUMBER: US 07/310,252
;             FILING DATE: 13-FEB-1989
;             APPLICATION NUMBER: US 07/590,274
;             FILING DATE: 28-SEP-1990
;             APPLICATION NUMBER: US 07/634,278
;             FILING DATE: 19-DEC-1990
;             APPLICATION NUMBER: US 08/484,537
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith, William M.
;             REGISTRATION NUMBER: 30,223
;             REFERENCE/DOCKET NUMBER: 011823-002650US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 97:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "T at positions 13-18 may be
;             present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-389-417-97

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 850
US-10-653-416-26/c
; Sequence 26, Application US/10653416
; Publication No. US20040110201A1
; GENERAL INFORMATION:
;  APPLICANT: RASHTCHIAN, AYOUB
;  APPLICANT:  SCHUSTER, DAVID M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CDNA SYNTHESIS
;  FILE REFERENCE: 38266-0011
;  CURRENT APPLICATION NUMBER: US/10/653,416
;  CURRENT FILING DATE:  2003-09-03
;  PRIOR APPLICATION NUMBER: 60/407,248
;  PRIOR FILING DATE: 2002-09-03
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: oligonucleotide
;    FEATURE:
;    OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according
;    OTHER INFORMATION: to the specification as filed
US-10-653-416-26

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 851
US-10-785-744-15/c
; Sequence 15, Application US/10785744
; Publication No. US20040133941A1
; GENERAL INFORMATION:
;  APPLICANT: Bowen, Banjamin A.
;  APPLICANT:  Deakin, Edward
;  APPLICANT:  Goldsmith, Neil
;  APPLICANT:  Haudenschild, Christian
;  APPLICANT:  Houck, David
;  APPLICANT:  McAlpine, James B.
;  APPLICANT:  Neilsen, Soren
;  APPLICANT:  Pazoles, Christopher
;  APPLICANT:  Spencer, Marget E.
```

```
;  APPLICANT:  Stafford, Angela
;  TITLE OF INVENTION: Methods for Identifying Genes Regulating
;  TITLE OF INVENTION:  Desired Cell Phenotypes
;  FILE REFERENCE: 50273/005002
;  CURRENT APPLICATION NUMBER: US/10/785,744
;  CURRENT FILING DATE:  2004-02-23
;  PRIOR APPLICATION NUMBER: US/10/056,479
;  PRIOR FILING DATE: 2003-02-07
;  PRIOR APPLICATION NUMBER: US 60/263,807
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-785-744-15

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 852
US-10-735-592-1/c
; Sequence 1, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
;  APPLICANT: Art, Krieg
;  APPLICANT:  Joerg, Vollmer
;  TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
;  FILE REFERENCE: C1037.70038US01
;  CURRENT APPLICATION NUMBER: US/10/735,592
;  CURRENT FILING DATE:  2003-12-11
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-1

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 853
US-10-628-525-30
; Sequence 30, Application US/10628525
; Publication No. US20040185114A1
;   GENERAL INFORMATION:
;        APPLICANT: Keeling, Peter
;                   Guan, Hanping
;        TITLE OF INVENTION: Starch Encapsulation
;        NUMBER OF SEQUENCES: 37
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
;             STREET: 5370 Manhattan Circle
;             CITY: Boulder
;             STATE: CO
;             COUNTRY: US
;             ZIP: 80303
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/628,525
;             FILING DATE: 28-Jul-2003
;             CLASSIFICATION: 800
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/941,445
;             FILING DATE: 30-SEP-1997
;             APPLICATION NUMBER: US 60/026,855
;             FILING DATE: 30-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Winner, Ellen P
;             REGISTRATION NUMBER: 28,547
;             REFERENCE/DOCKET NUMBER: 89-97
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (303) 499-8080
;             TELEFAX: (303) 499-8089
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: Not Relevant
;        MOLECULE TYPE: cDNA to mRNA
;        HYPOTHETICAL: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-628-525-30

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 854
US-10-849-072-21
; Sequence 21, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
;  APPLICANT: Roche Diagnostics GmbH
;  TITLE OF INVENTION: High density labeling of DNA with modified or
;  TITLE OF INVENTION:  "chromophore" carrying nucleotides and DNA polymerases
;  TITLE OF INVENTION:  used
;  FILE REFERENCE: 4780/00/WO
;  CURRENT APPLICATION NUMBER: US/10/849,072
;  CURRENT FILING DATE:  2004-05-19
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: second
;   OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-21

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18
```

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RESULT 855
US-10-849-072-23/c
; Sequence 23, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
;  APPLICANT: Roche Diagnostics GmbH
;  TITLE OF INVENTION: High density labeling of DNA with modified or
;  TITLE OF INVENTION:  "chromophore" carrying nucleotides and DNA polymerases
;  TITLE OF INVENTION:  used
;  FILE REFERENCE: 4780/00/WO
;  CURRENT APPLICATION NUMBER: US/10/849,072
;  CURRENT FILING DATE:  2004-05-19
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: second
;   OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-23

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 856
US-10-831-778-913/c
; Sequence 913, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/831,778
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 913
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-831-778-913

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 857
US-10-831-778-939/c
; Sequence 939, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/831,778
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 939
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-831-778-939

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 858
US-10-776-933-150/c
; Sequence 150, Application US/10776933
; Publication No. US20040241717A1
; GENERAL INFORMATION:
;  APPLICANT: HANSEN, BO
;  APPLICANT:  THRUE, CHARLOTTE ALBAEK
;  APPLICANT:  WESTERGAARD, MAJKEN
;  APPLICANT:  PETERSEN, KAMILLE DUMONG
;  APPLICANT:  WISSENBACH, MARGIT
;  TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF THIOREDOXIN
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 58614(71432)
;  CURRENT APPLICATION NUMBER: US/10/776,933
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 60/446,374
;  PRIOR FILING DATE: 2003-02-10
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 150
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: poly-T oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: This sequence may emcompass 12-18 nucleotides
;   OTHER INFORMATION: according to the specification as filed
US-10-776-933-150

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 859
US-10-674-159A-112/c
; Sequence 112, Application US/10674159A
; Publication No. US20040242518A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jianzhu
;  APPLICANT:  Ge, Qing
;  APPLICANT:  Eisen, Herman
;  TITLE OF INVENTION: Influenza Therapeutic
;  FILE REFERENCE: 0492611-0506
;  CURRENT APPLICATION NUMBER: US/10/674,159A
;  CURRENT FILING DATE:  2003-09-29
;  NUMBER OF SEQ ID NOS: 271
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mRNA
US-10-674-159A-112

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 860
US-10-776-917-141/c
; Sequence 141, Application US/10776917
; Publication No. US20040248840A1
; GENERAL INFORMATION:
;  APPLICANT: HANSEN, BO
;  APPLICANT:  THRUE, CHARLOTTE ALBAEK
;  APPLICANT:  WESTERGAARD, MAJKEN
;  APPLICANT:  PETERSEN, KAMILLE DUMONG
;  APPLICANT:  WISSENBACH, MARGIT
;  TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF RAS EXPRESSION
;  FILE REFERENCE: 58609(71432)
;  CURRENT APPLICATION NUMBER: US/10/776,917
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 60/446,363
;  PRIOR FILING DATE: 2003-02-10
;  PRIOR APPLICATION NUMBER: DK 2003-01539
;  PRIOR FILING DATE: 2003-10-20
;  NUMBER OF SEQ ID NOS: 201
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 141
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: poly-T oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according to the
;   OTHER INFORMATION: specification as filed
US-10-776-917-141

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 861
US-10-766-096-9/c
; Sequence 9, Application US/10766096
; Publication No. US20040265786A1
;   GENERAL INFORMATION:
;        APPLICANT: Lin, Ching-I Patsy
;                   Wallace, Robert Bruce
;                   Cossman, Jeffrey
;                   French, Cynthia
;        TITLE OF INVENTION: Lyophilization of Cultured Human Cells
;                            to Preserve RNA and DNA
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/766,096
;             FILING DATE: 27-Jan-2004
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/884,029
;             FILING DATE: 27-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 02558B-059100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  13..18
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "t at positions 13-18 may be
;             present or absent"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-766-096-9

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 862
US-10-872-984-7/c
; Sequence 7, Application US/10872984
; Publication No. US20040265888A1
; GENERAL INFORMATION:
;  APPLICANT: Kaufman, Joseph C.
;  APPLICANT:  Roth, Matthew E.
;  APPLICANT:  Lizardi, Paul M.
;  APPLICANT:  Feng, Li
;  APPLICANT:  Latimer, Darin R.
;  TITLE OF INVENTION: Binary Encoded Sequence Tags
;  FILE REFERENCE: AGL 100
;  CURRENT APPLICATION NUMBER: US/10/872,984
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: US/09/994,311
;  PRIOR FILING DATE: 2001-11-26
```

```
;  PRIOR APPLICATION NUMBER: US/09/637,751
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-872-984-7

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACA 3619
              || ||||||| ||||| |
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 863
US-10-638-141-10/c
; Sequence 10, Application US/10638141
; Publication No. US20050003364A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  Kapoun, Ann Marie
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.013A
;  CURRENT APPLICATION NUMBER: US/10/638,141
;  CURRENT FILING DATE:  2003-08-07
;  PRIOR APPLICATION NUMBER: US/09/665,728
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/156,277
;  PRIOR FILING DATE: 1999-09-27
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic
US-10-638-141-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 864
US-10-776-934-741/c
; Sequence 741, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
;  APPLICANT: HANSEN, BO
;  APPLICANT:  THRUE, CHARLOTTE ALBAEK
;  APPLICANT:  WESTERGAARD, MAJKEN
;  APPLICANT:  PETERSEN, KAMILLE DUMONG
;  APPLICANT:  WISSENBACH, MARGIT
;  TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
;  FILE REFERENCE: 58610(71432)
;  CURRENT APPLICATION NUMBER: US/10/776,934
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 60/446,372
;  PRIOR FILING DATE: 2003-02-10
;  PRIOR APPLICATION NUMBER: 60/523,591
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 741
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 741
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: poly-T oligonucleotide
;    FEATURE:
;    OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according to the
;    OTHER INFORMATION: specification as filed
US-10-776-934-741

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 865
US-10-601-140A-24/c
; Sequence 24, Application US/10601140A
; Publication No. US20050053942A1
; GENERAL INFORMATION:
;  APPLICANT: KAUPPINEN, SAKARI
;  APPLICANT:  JACOBSEN, NANA
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR DETECTION AND ISOLATION OF A
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCE
;  FILE REFERENCE: 57764(71994)
;  CURRENT APPLICATION NUMBER: US/10/601,140A
;  CURRENT FILING DATE:  2003-06-20
;  PRIOR APPLICATION NUMBER: US 60/390,928
;  PRIOR FILING DATE: 2002-06-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
;    LENGTH: 18
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)..(18)
;    OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-10-601-140A-24

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 866
US-10-884-617-2/c
; Sequence 2, Application US/10884617
; Publication No. US20050054730A1
; GENERAL INFORMATION:
;  APPLICANT: Fu, Jin
;  APPLICANT:  Gaetani, Silvana
;  APPLICANT:  Piomelli, Daniele
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Compounds, Compositions and Treatments of
;  TITLE OF INVENTION:  Oleoylethanolamide-Like Modulators of PPARalpha
;  FILE REFERENCE: 02307E-133310US
;  CURRENT APPLICATION NUMBER: US/10/884,617
;  CURRENT FILING DATE:  2004-07-01
```

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;  PRIOR APPLICATION NUMBER: US 60/279,542
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: US 60/336,289
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: US 10/112,509
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: US 60/485,062
;  PRIOR FILING DATE: 2003-07-02
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Oligo(dT)-12-18
;   OTHER INFORMATION: primer for reverse transcription of total RNA
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (13)..(18)
;   OTHER INFORMATION: t at positions 13-18 may be present or absent
US-10-884-617-2

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 867
US-10-669-962-28/c
; Sequence 28, Application US/10669962
; Publication No. US20050081264A1
; GENERAL INFORMATION:
;  APPLICANT: Brugliera, Filippa
;  APPLICANT:  Holton, Timothy A.
;  APPLICANT:  Michael, Michael Z.
;  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 11658
;  CURRENT APPLICATION NUMBER: US/10/669,962
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: US/09/142,108C
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: PN8386
;  PRIOR FILING DATE: 1996-03-01
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-669-962-28

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 868
US-10-503-120-1/c
; Sequence 1, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-503-120-1

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 869
US-10-503-120-8/c
; Sequence 8, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(17)
;   OTHER INFORMATION: Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are 2'-O-methyl-D-uridi
;   OTHER INFORMATION: ne
US-10-503-120-8

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 870
US-10-503-120-9/c
; Sequence 9, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
```

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;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15)
;   OTHER INFORMATION: Residues 1-3, 7-9, and 13-15 are 2'-O-methyl-D-uridine
US-10-503-120-9

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 871
US-10-503-120-10/c
; Sequence 10, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine
US-10-503-120-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 872
US-10-503-120-21
; Sequence 21, Application US/10503120
; Publication No. US20050142535A1
; GENERAL INFORMATION:
;  APPLICANT: MCGILL UNIVERSITY ET AL.
;  TITLE OF INVENTION: OLIGONUCLEOTIDES COMPRISING ALTERNATING SEGMENTS AND USES THEREOF
;  FILE REFERENCE: 85827-63
;  CURRENT APPLICATION NUMBER: US/10/503,120
;  CURRENT FILING DATE:  2004-07-30
;  PRIOR APPLICATION NUMBER: US 60/352,873
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Target RNA oligonucleotide
US-10-503-120-21

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 873
US-10-775-973-10/c
; Sequence 10, Application US/10775973
; Publication No. US20050158729A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  Kapoun, Ann Marie
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.014A
;  CURRENT APPLICATION NUMBER: US/10/775,973
;  CURRENT FILING DATE:  2004-02-09
;  PRIOR APPLICATION NUMBER: US/09/665,976
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/156,280
;  PRIOR FILING DATE: 1999-09-27
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-775-973-10

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 874
US-10-959-440-84/c
; Sequence 84, Application US/10959440
; Publication No. US20050208605A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence W.
;  APPLICANT:  White, R. Tyler
;  TITLE OF INVENTION: SECRETED FACTORS
;  FILE REFERENCE: SCIOS.017A
;  CURRENT APPLICATION NUMBER: US/10/959,440
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: US/09/809,545
;  PRIOR FILING DATE: 2001-03-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-10-959-440-84
```

```
  Query Match          0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 875
US-11-024-428-7/c
; Sequence 7, Application US/11024428
; Publication No. US20050106676A1
; GENERAL INFORMATION:
;  APPLICANT: NAGAI, HIROSHI
;  APPLICANT:  KURODA, KYOKO
;  APPLICANT:  NAKAJIMA, TERUMI
;  TITLE OF INVENTION: NOVEL PROTEINS HAVING HEMOLYTIC ACTIVITY AND GENES
;  TITLE OF INVENTION:  ENCODING THE PROTEIN
;  FILE REFERENCE: 037181.50611US
;  CURRENT APPLICATION NUMBER: US/11/024,428
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: US/09/979,275
;  PRIOR FILING DATE: 2003-05-27
;  PRIOR APPLICATION NUMBER: PCT/JP01/02209
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: JP 2000-78967
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
;   FEATURE:
;   OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-11-024-428-7

  Query Match          0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 876
US-11-014-373-192
; Sequence 192, Application US/11014373
; Publication No. US20050196781A1
; GENERAL INFORMATION:
;  APPLICANT: Robin, Howard
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION
;  TITLE OF INVENTION:  USING SHORT INTERFERING NUCLEIC ACID (siNA)
;  FILE REFERENCE: 400/241 MBHB04-1067
;  CURRENT APPLICATION NUMBER: US/11/014,373
;  CURRENT FILING DATE:  2004-12-15
;  PRIOR APPLICATION NUMBER: PCT/US 04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Target Sequence/siNA sense region
US-11-014-373-192

  Query Match          0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   72.2%;  Pred. No. 8.8e+02;
  Matches   13;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAA 3617
              :|:  ||||||| |||||
Db          1 UCUCAAAAAAAAAAAAAA 18


RESULT 877
US-11-014-373-469/c
; Sequence 469, Application US/11014373
; Publication No. US20050196781A1
; GENERAL INFORMATION:
;  APPLICANT: Robin, Howard
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION
;  TITLE OF INVENTION:  USING SHORT INTERFERING NUCLEIC ACID (siNA)
;  FILE REFERENCE: 400/241 MBHB04-1067
;  CURRENT APPLICATION NUMBER: US/11/014,373
;  CURRENT FILING DATE:  2004-12-15
;  PRIOR APPLICATION NUMBER: PCT/US 04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 678
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 469
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Target Sequence/siNA sense region
US-11-014-373-469
```

```
  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAA 3617
              |||  ||||||| |||||
Db         19 TCTCAAAAAAAAAAAAAA 2


RESULT 878
US-10-205-309-325
; Sequence 325, Application US/10205309
; Publication No. US20030190635A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
;  TITLE OF INVENTION:  Interfering RNA
;  FILE REFERENCE: 900/033
;  CURRENT APPLICATION NUMBER: US/10/205,309
;  CURRENT FILING DATE:  2002-10-25
;  NUMBER OF SEQ ID NOS: 674
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 325
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-205-309-325

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          2 AAAAAAAAAAAAAAAAAA 19


RESULT 879
US-10-205-309-650/c
; Sequence 650, Application US/10205309
; Publication No. US20030190635A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
;  TITLE OF INVENTION:  Interfering RNA
;  FILE REFERENCE: 900/033
;  CURRENT APPLICATION NUMBER: US/10/205,309
;  CURRENT FILING DATE:  2002-10-25
;  NUMBER OF SEQ ID NOS: 674
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 650
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-205-309-650

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 880
US-10-619-253-151
; Sequence 151, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 151
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-151

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATATA 2410
              ||| ||||||  ||||||
Db          3 AATGTATATATGTATATA 20


RESULT 881
US-09-263-959-849
; Sequence 849, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  849:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-849

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
                || |||| ||||| ||||
Db          3 AAGAAAAAAAAAAAAGAA 20


RESULT 882
US-09-005-243-32/c
; Sequence 32, Application US/09005243
; Patent No. US20020018763A1
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/005,243
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/449,653
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/34465
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-005-243-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
                ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 883
US-09-224-683-32/c
; Sequence 32, Application US/09224683
; Patent No. US20020031491A1
;  GENERAL INFORMATION:
;    APPLICANT:  Zsebo, Krisztina M.
;    APPLICANT:  Bosselman, Robert A.
;    APPLICANT:  Suggs, Sidney V.
;    APPLICANT:  Martin, Francis H.
;    TITLE OF INVENTION:  Stem Cell Factor: Composition Claims
;    NUMBER OF SEQUENCES:  104
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/224,683
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/005,893
;      FILING DATE:  12-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/449,653
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,255
;      FILING DATE:  25-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/589,701
;      FILING DATE:  01-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/573,616
;      FILING DATE:  24-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/537,198
;      FILING DATE:  11-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/422,383
;      FILING DATE:  16-OCT-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  01017/35136
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-224-683-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
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```
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 884
US-10-671-395-654/c
; Sequence 654, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 654
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-654

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 885
US-10-175-608-32/c
; Sequence 32, Application US/10175608
; Publication No. US20040181044A1
;   GENERAL INFORMATION:
;        APPLICANT: Zsebo, Krisztina M.
;                   Bosselman, Robert A.
;                   Suggs, Sidney V.
;                   Martin, Francis H.
;        TITLE OF INVENTION: Stem Cell Factor
;        NUMBER OF SEQUENCES: 104
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: United States of America
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/175,608
;             FILING DATE: 16-Oct-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/635,249
;             FILING DATE: 07-AUG-2000
;             APPLICATION NUMBER: 09/486,546
;             FILING DATE: 24-MAY-1995
;             APPLICATION NUMBER: 08/172,329
;             FILING DATE: 21-DEC-1993
;             APPLICATION NUMBER: 07/982,255
;             FILING DATE: 25-NOV-1992
;             APPLICATION NUMBER: 07/684,535
;             FILING DATE: 10-APR-1991
;             APPLICATION NUMBER: 09/589,701
;             FILING DATE: 10-OCT-1991
;             APPLICATION NUMBER: 07/573,616
;             FILING DATE: 24-AUG-1990
;             APPLICATION NUMBER: 07/537,198
;             FILING DATE: 11-JUN-1990
;             APPLICATION NUMBER: 07/422,383
;             FILING DATE: 16-OCT-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Clough, David W.
;             REGISTRATION NUMBER: 36,107
;             REFERENCE/DOCKET NUMBER: 01017/35199
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 32:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-175-608-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 886
US-10-620-642-32/c
; Sequence 32, Application US/10620642
; Publication No. US20050080250A1
;   GENERAL INFORMATION:
;        APPLICANT: Zsebo, Krisztina M.
;                   Bosselman, Robert A.
;                   Suggs, Sidney V.
;                   Martin, Francis H.
;        TITLE OF INVENTION: Stem Cell Factor
;        NUMBER OF SEQUENCES: 104
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: United States of America
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/620,642
;             FILING DATE: 16-Jul-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/175,608
;             FILING DATE: 16-Oct-2002
;             APPLICATION NUMBER: 09/635,249
;             FILING DATE: 07-AUG-2000
```

XX
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI; 1999-257710/22.
XX
PT Labelling of an oligonucleotide - useful for detecting genes.
XX
PS Example 1; Page 7; 10pp; Japanese.
XX
CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1256
AAX19942/c
ID AAX19942 standard; DNA; 18 BP.
XX
AC AAX19942;
XX
DT 14-JUN-1999 (first entry)
XX
DE Primer SEQ ID NO:2 from JP11075880.
XX
KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS Synthetic.
XX
PN JP11075880-A.
XX
PD 23-MAR-1999.
XX
PF 10-JUL-1998; 98JP-00195719.
XX
PR 14-JUL-1997; 97JP-00205378.
XX
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI; 1999-257710/22.
XX
PT Labelling of an oligonucleotide - useful for detecting genes.
XX
PS Example 1; Page 7; 10pp; Japanese.
XX
CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1257
AAX18373
ID AAX18373 standard; DNA; 18 BP.
XX
AC AAX18373;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 14.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 11; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1258
AAX18372
ID AAX18372 standard; DNA; 18 BP.
XX
AC AAX18372;
XX
DT 11-MAY-1999 (first entry)
XX

DE RT-PCR primer of the invention SEQ ID 13.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 11; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1259
AAA40563/c
ID AAA40563 standard; cDNA; 18 BP.
XX
AC AAA40563;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human adult ovary cDNA fragment AQ2_1i #2.
XX
KW Secreted protein; cytostatic; immunostimulatory; antimicrobial;
KW antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;
KW cell proliferation; differentiation; regulator; treatment; tumor;
KW autoimmune disease; inflammatory disorder; wound; microbial infection;
KW viral disease; graft versus host reaction suppression; ss.
XX
OS Homo sapiens.
XX
PN WO200037630-A1.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-US031005.
XX
PR 23-DEC-1998; 98US-00220876.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
DR WPI; 2000-442661/38.
DR P-PSDB; AAB10274.
XX
PT Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors,
PT autoimmune diseases, inflammatory disorders, wounds, microbial infections
PT and viral diseases.
XX
PS Disclosure; Page 269; 293pp; English.
XX
CC This invention describes novel secreted human proteins (I) which have
CC cytostatic, immunostimulatory, antimicrobial, antiviral,
CC immunosuppressive, antiinflammatory and vulnerary activity and which act
CC as cytokine, cell proliferation or differentiation regulators. (I) is
CC useful for treating tumors, autoimmune diseases, inflammatory disorders,
CC wounds, microbial infections and viral diseases. (I) is also useful for
CC suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
CC fragments that encode the secreted proteins AAB10226-B10288 described in
CC the method of the invention
XX
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1260
AAA58385/c
ID AAA58385 standard; DNA; 18 BP.
XX
AC AAA58385;
XX
DT 01-NOV-2000 (first entry)
XX
DE Polynucleotide # 1 used in a biomolecule detection system.
XX
KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS Synthetic.
XX
PN WO200028088-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026612.
XX
PR 10-NOV-1998; 98US-0107828P.
PR 09-NOV-1999; 99US-00437076.
XX
PA (BIOC-) BIOCRYSTAL LTD.
XX
PI Barbera-Guillem E, Nelson MB, Castro S;
XX
DR WPI; 2000-376593/32.
XX
PT Functionalized nanocrystal carrying polynucleotide, used for detecting
PT target analyte, forms dendrimers with complementary nanocrystals to
PT amplify the fluorescent signal.
XX
PS Example 3; Page 68; 72pp; English.
XX
CC The present invention relates to functionalised nanocrystals for use in
CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands

CC attached to their surfaces with one end of the polynucleotide extending
CC outwardly from the nanocrystal. The present sequence is one such
CC polynucleotide. These nanocrystals are used with a second series of
CC nanocrystals, which have polynucleotides complementary to the first
CC polynucleotides, so that the respective complementary strands hybridise
CC to each other and form a dendrimer. This dendrimer produces a signal
CC which can then be detected e.g. fluorescence. The present sequence is
CC composed mainly of Adenine bases. This sequence may therefore be used
CC with a polynucleotide composed mainly of Thymine bases (AAA58386)
XX
SQ Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1261
AAZ87161/c
ID AAZ87161 standard; RNA; 18 BP.
XX
AC AAZ87161;
XX
DT 08-MAY-2000 (first entry)
XX
DE Oligoarabinonucleotide SEQ ID NO:2.
XX
KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW reverse transcription; viral replication; RNase H cleavage;
KW triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX
DR WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
PT include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 1; Page 29; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targetting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AAZ87160-Z87164 represent
CC oligoarabinonucleotides containing beta-D-arabinose used in an
CC exemplification of the present invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1262
AAZ87162
ID AAZ87162 standard; RNA; 18 BP.
XX
AC AAZ87162;
XX
DT 08-MAY-2000 (first entry)
XX
DE Oligoarabinonucleotide SEQ ID NO:3.
XX
KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW reverse transcription; viral replication; RNase H cleavage;
KW triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX
DR WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
PT include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 1; Page 29; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific

```
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   0.0%;  Pred. No. 8.8e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1263
AAZ87166
ID   AAZ87166 standard; DNA; 18 BP.
XX
AC   AAZ87166;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Deoxyarabinonucleotide SEQ ID NO:7.
XX
KW   2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW   transcription; expression; reverse transcription; viral replication;
KW   RNase H cleavage; triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT                    fluoro-beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 2; Page 31; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87165-Z87169 represent
CC   oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC   arabinose used in an exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1264
AAZ87167/c
ID   AAZ87167 standard; DNA; 18 BP.
XX
AC   AAZ87167;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Deoxyarabinonucleotide SEQ ID NO:8.
XX
KW   2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW   transcription; expression; reverse transcription; viral replication;
KW   RNase H cleavage; triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT                    fluoro-beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 2; Page 31; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
```

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CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87165-Z87169 represent
CC   oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC   arabinose used in an exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 1265
AAD03565
ID   AAD03565 standard; DNA; 18 BP.
XX
AC   AAD03565;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX
KW   Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
KW   antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
KW   antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
KW   antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
KW   nootropic; neuroprotective; congestive heart failure; myocarditis;
KW   hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
KW   kidney disease; acute renal failure; renal glucosuria; renal infarction;
KW   polycystic kidney disease; hereditary nephritis; inflammatory disease;
KW   tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
KW   stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
KW   ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX
OS   Rattus norvegicus.
XX
PN   WO200123564-A1.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026544.
XX
PR   27-SEP-1999;   99US-0156280P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  Kapoun AM;
XX
DR   WPI; 2001-266159/27.
XX
PT   Novel secreted factor encoded by clone P00188D12 which is differentially
PT   expressed in certain disease states, useful in diagnosing and treating
PT   cardiac, renal or inflammatory diseases.
XX
PS   Example 1; Page 42; 71pp; English.
XX
CC   The patent discloses novel secreted factor protein encoded by clone
CC   P00188_D12. The secreted factor is differentially expressed in certain
CC   disease states. Secreted protein, its antibodies, antagonists or
CC   compositions comprising them are useful in the diagnosis and treatment of
CC   cardiac diseases such as congestive heart failure, myocarditis,
CC   hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
CC   cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
CC   failure, renal glucosuria, renal infarction, nephrogenic diabetes
CC   insipidus, polycystic kidney disease, hereditary nephritis and
CC   inflammatory diseases such as asthma, autoimmune diabetes, tumour
CC   angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
CC   asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
CC   Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
CC   protein DNA is useful in antisense-mediated gene inhibition and in gene
CC   therapy. An array comprising one or more oligonucleotides complementary
CC   to reference RNA or DNA encoding the secreted factor is useful for
CC   detecting cardiac, kidney and inflammatory disease. The present DNA
CC   sequence is an oligonucleotide which is used in the preparation of a
CC   normalised cDNA library containing secreted factor DNAs. The normalised
CC   cDNA libraries are used in the identification of differentially expressed
CC   rat secreted factor P00188_D12 gene
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1266
AAD17014/c
ID   AAD17014 standard; DNA; 18 BP.
XX
AC   AAD17014;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Oligonucleotide A18-2PEG linker.
XX
KW   Scaffold protein; antibody mimic; fibronectin type III domain;
KW   randomised loop; randomised beta-sheet; diagnostic purpose;
KW   protein designing; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    18
FT                   /*tag=  a
FT                   /note= "Linked to (PEG)2CCPuromycin"
XX
PN   WO200164942-A1.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006414.
XX
PR   29-FEB-2000; 2000US-00515260.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lipovsek D,  Wagner RW,  Kuimelis RG;
XX
DR   WPI; 2001-557782/62.
XX
PT   Fibronectin scaffold protein array for obtaining a protein/compound which
PT   binds to a compound/protein, comprises a fibronectin type III domain
PT   having a randomized loop, a randomized beta-sheet or their combination.
XX
PS   Disclosure; Page 25; 67pp; English.
XX
CC   The present invention relates to an array of proteins (antibody mimics)
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CC   comprising a fibronectin type III domain having a randomised loop, a
CC   randomised beta-sheet, or their combination, and has the capacity to bind
CC   to a compound that is not bound by a corresponding naturally- occurring
CC   fibronectin, immobilised onto a solid support. The antibody mimics is
CC   useful for detecting a compound preferably a protein, in a biological
CC   sample. It is also useful to detect one or more different analytes
CC   simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC   is also useful for the purpose of designing proteins capable of binding
CC   to virtually any compound of interest. The present sequence is an
CC   oligonucleotide A18-2PEG linker used in an exemplification of the
CC   invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 1267
AAF75598
ID   AAF75598 standard; DNA; 18 BP.
XX
AC   AAF75598;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #3.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 101; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1268
AAD20091/c
ID   AAD20091 standard; mRNA; 18 BP.
XX
AC   AAD20091;
XX
DT   03-JAN-2002  (first entry)
XX
DE   mRNA fragment used in 3' end PCR/IVT method of the invention.
XX
KW   RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX
OS   Unidentified.
XX
PN   US6271002-B1.
XX
PD   07-AUG-2001.
XX
PF   04-OCT-1999;   99US-00411074.
XX
PR   04-OCT-1999;   99US-00411074.
XX
PA   (ROSE-) ROSETTA INPHARMATICS INC.
XX
PI   Linsley PS,  Schelter JM;
XX
DR   WPI; 2001-624273/72.
XX
PT   Amplifying and detecting RNA derived from a population of cells by
PT   employing a primer that contains an RNA polymerase promoter in a
PT   polymerase chain reaction.
XX
PS   Example 3; Fig 1; 29pp; English.
XX
CC   The invention relates to methods and kits for amplification of mRNA using
CC   a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
CC   invention provides methods for amplification and detection of RNA derived
CC   from a population of cells, preferably eukaryotic cells and most
CC   preferably mammalian cells, which methods preserve fidelity with respect
CC   to sequence and transcript representation and additionally enable
CC   amplification of extremely small amounts of mRNA. The method and kit are
CC   useful for amplifying and detecting RNA derived from a population of
CC   cells, especially eukaryotic cells like mammals. The RNAs generated are
CC   useful for profiling gene expression in different populations of cells.
CC   The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
CC   transcription) method of the invention
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 1269
AAF99708
ID   AAF99708 standard; DNA; 18 BP.
XX
AC   AAF99708;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #824.
```

XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1270
AAF99734
ID AAF99734 standard; DNA; 18 BP.
XX
AC AAF99734;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #850.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1271
AAF82472
ID AAF82472 standard; DNA; 18 BP.
XX
AC AAF82472;
XX
DT 29-JUN-2001 (first entry)
XX
DE Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX
KW Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;
KW renal disease; inflammatory disease; polylinker; ss.
XX
OS Synthetic.
XX
PN WO200123419-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026582.
XX
PR 27-SEP-1999; 99US-0156277P.
XX
PA (SCIO-) SCIOS INC.

XX
PI Stanton LW, Kapoun AM;
XX
DR WPI; 2001-328177/34.
XX
PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
PT treating and/or preventing various cardiac, renal and inflammatory
PT diseases.
XX
PS Example 1; Page 41; 69pp; English.
XX
CC The present sequence corresponds to polylinker DNA of the phagemid vector
CC pCR2.1. It was used in the construction of a normalised rat cDNA library,
CC which was used in an example demonstrating differential expression of a
CC rat gene referred to as clone P00210D09. The invention relates to a
CC polypeptide comprising a sequence of at least 80% identity to residues 22
CC -122 of the present sequence, or a sequence encoded by a nucleic acid
CC hybridising under stringent conditions to the complement of the coding
CC region comprising 1031 nucleotides, and having at least one biological
CC activity of the polypeptide encoded by clone P00210D09. The polypeptides
CC and polynucleotides of the invention are useful for the treatment of
CC cardiac, renal and inflammatory diseases. The polynucleotides are useful
CC in antisense mediated gene inhibition and in gene therapy. The
CC polypeptides are useful in assays for identifying lead compounds that may
CC be used as therapeutic agents in the treatment of cardiac, kidney or
CC inflammatory diseases
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1272
ABK51158
ID ABK51158 standard; DNA; 18 BP.
XX
AC ABK51158;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX
KW Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
KW cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
KW reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS Human cytomegalovirus.
XX
FH Key Location/Qualifiers
FT misc_difference 17
FT /*tag= a
FT /label= n
FT /note= "n= dATP, dCTP or dGTP"
XX
PN EP1201765-A2.
XX
PD 02-MAY-2002.
XX
PF 15-OCT-2001; 2001EP-00124604.
XX
PR 16-OCT-2000; 2000US-0240750P.
XX
PA (AXXI-) AXXIMA PHARM AG.
XX
PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
XX
DR WPI; 2002-373930/41.
XX
PT Identifying agents for treatment or prevention of cytomegalovirus
PT infection, comprises contacting test compound with cellular kinase and
PT detecting change in cellular kinase activity.
XX
PS Example 1; Page 13; 49pp; English.
XX
CC The present invention relates to a new method for identifying compounds
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC related diseases. The method of the invention comprises contacting a test
CC compound with at least one of the cellular kinases RICK, RIP, Nck-
CC Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
CC activity. The method of the invention can be used to treat and/or prevent
CC CMV infections and related diseases. Oligonucleotides that can detect the
CC specified kinases can also be used for diagnosis of infection. The
CC present nucleic acid sequence represents human CMV reverse transcriptase
CC (RT)-PCR primer TXN that was used in the methods of the invention for
CC preparation of radioactively labelled cDNA probes
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1273
AAS94743
ID AAS94743 standard; DNA; 18 BP.
XX
AC AAS94743;
XX
DT 12-MAR-2002 (first entry)
XX
DE Rat secreted factor DNA oligonucleotide probe #6.
XX
KW Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
KW renal infarction; hereditary nephritis; polycystic kidney disease;
KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;
KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
KW Alzheimer's disease; gene therapy.
XX
OS Synthetic.
XX
PN WO200174901-A2.
XX
PD 11-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-US009555.
XX
PR 31-MAR-2000; 2000US-0193548P.
PR 14-MAR-2001; 2001US-00809545.
XX
PA (SCIO-) SCIOS INC.
XX
PI Stanton LW, White RT;
XX
DR WPI; 2002-010779/01.
XX
PT Novel secreted factor polypeptide useful for treating cardiac diseases
PT such as arteriosclerosis, myocardial infarction, inflammatory diseases
PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.
XX
PS Example 1; Page 51; 189pp; English.

XX
CC The invention relates to rat secreted factor polypeptides and the
CC polynucleotides encoding them. The sequences are useful for treating
CC cardiac, renal or inflammatory diseases. These include cardiac diseases
CC such as congestive heart failure, myocarditis, dilated congestive
CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac
CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
CC syndrome, renal infarction, hereditary nephritis, polycystic kidney
CC disease, chronic renal failure, renal vein thrombosis and medullary
CC sponge kidney and inflammatory diseases such as asthma, rheumatoid
CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode
CC the secreted factor polypeptides of the invention, and oligonucleotide
CC probes and PCR primers
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1274
ABS78455
ID ABS78455 standard; DNA; 18 BP.
XX
AC ABS78455;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #939.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1275
ABS78429
ID ABS78429 standard; DNA; 18 BP.
XX
AC ABS78429;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #913.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 35; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1276
ABL39401
ID ABL39401 standard; DNA; 18 BP.
XX
AC ABL39401;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 837.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 308; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1277
AAD41497
ID AAD41497 standard; DNA; 18 BP.
XX
AC AAD41497;
XX
DT 30-OCT-2002 (first entry)
XX
DE Oligonucleotide used for amplifying sea hare cyplasin L DNA.
XX
KW Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;
KW heart disease; stroke; vascular disease; nootropic; neuroprotective;
KW cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.
XX
OS Unidentified.
XX
PN WO200231144-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-EP011837.
XX
PR 13-OCT-2000; 2000EP-00122466.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Butzke D, Machuy N, Rudel T, Meyer TF;
XX
DR WPI; 2002-537205/57.
XX
PT Novel polypeptide having cytotoxic activity obtainable from Aplysia,
PT useful for destroying tumors, for identifying novel targets for the
PT development of anti-tumor agents, and as specific ion channel modulators.
XX
PS Example 5; Page 37; 87pp; English.
XX
CC The present invention relates to novel polypeptides having cytotoxic
CC activity obtainable from sea hare Aplysia. Sequences of the invention are
CC useful for the manufacture of cytotoxic agents against apoptosis-
CC resistant cells, where the agents are useful for diagnosis, prevention,
CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
CC protein, factors for generating or detoxifying reactive oxygen species
CC (ROS) and factors for blocking and/or by-passing of caspases. They are
CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
CC for destroying tumours and/or selectively killing cells in tissues, for
CC identifying novel targets for the development of pharmaceutical agents,
CC preferably anti-tumour agents and as specific ion channel modulators,
CC e.g., blockers or openers for therapy, diagnostic or research. They are
CC useful for the diagnosis and therapy of hyperproliferative diseases,
CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
CC They are also useful for development of drugs for the treatment of
CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
CC present sequence is an oligonucleotide which is used for amplifying sea
CC hare cyplasin L DNA. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1278
ABS53437
ID   ABS53437 standard; DNA; 18 BP.
XX
AC   ABS53437;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Poly d(T) primer.
XX
KW   Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
KW   poly d(T).
XX
OS   Synthetic.
XX
PN   WO200265093-A2.
XX
PD   22-AUG-2002.
XX
PF   14-FEB-2002; 2002WO-US005713.
XX
PR   14-FEB-2001; 2001US-0268645P.
PR   14-FEB-2001; 2001US-0268664P.
PR   18-JUL-2001; 2001US-0306216P.
PR   07-NOV-2001; 2001US-0344557P.
PR   07-NOV-2001; 2001US-0348242P.
PR   09-NOV-2001; 2001US-0350176P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (REME-) RES FOUND MENTAL HYGIENE INC.
XX
PI   Ginsberg SD,  Che S;
XX
DR   WPI; 2002-567050/60.
XX
PT   Increasing efficiency of second strand cDNA synthesis using terminal
PT   continuation model before performing further RNA amplification by RNA
PT   transcription.
XX
PS   Example 7; Page 80; 128pp; English.
XX
CC   This invention relates to a novel method for increasing the efficiency of
CC   second strand cDNA synthesis through a mechanism of terminal
CC   continuation. In the method an RNA molecule is obtained and a first
CC   primer is added that comprises a region that hybridises to a
CC   complementary region of the molecule before a second primer is added
CC   comprising at least one riboguanine at the 3' end of the primer. A first
CC   complementary nucleic acid molecule is synthesised, the RNA molecule and
CC   second primer are removed and a second complementary nucleic acid
CC   molecule is synthesised to form a second hybrid with an extension product
CC   of the third primer bound to the first complementary molecule. The method
CC   of the invention is useful for increasing the efficiency of second strand
CC   cDNA synthesis and may be used for linear amplification of genetic
CC   signals from histologically stained tissue. The present sequence
CC   represents a poly d(T) PCR primer used in the method of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1279
ABA93239
ID   ABA93239 standard; DNA; 18 BP.
XX
AC   ABA93239;
XX
DT   18-APR-2002  (first entry)
XX
DE   Adaptor oligonucleotide SEQ ID NO:2.
XX
KW   Detection; comparative detection; adaptor; ss.
XX
OS   Synthetic.
XX
PN   JP2001333800-A.
XX
PD   04-DEC-2001.
XX
PF   30-MAY-2000; 2000JP-00160324.
XX
PR   30-MAY-2000; 2000JP-00160324.
XX
PA   (UNIT-) UNITECH CO LTD.
XX
DR   WPI; 2002-135950/18.
XX
PT   Comparative detection of the amounts of RNA and DNA.
XX
PS   Disclosure; Page 9; 9pp; Japanese.
XX
CC   The present invention describes a method for the comparative detection of
CC   the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC   transcribing respectively from at least two tissue RNAs are respectively
CC   fragmented by using a same restriction enzyme; (b) each different adaptor
CC   and a common adaptor are added to each of the cDNA fragments derived from
CC   the same or different tissues by the step (a); (c) the resultant adaptor-
CC   added cDNAs are mixed together; (d) an adaptor primer having the common
CC   sequence to said different adaptor and a gene-specific adaptor are used
CC   to amplify said adaptor-added cDNAs containing no region derived from
CC   polyadenylic acid of the mRNA before the addition of the adaptor among
CC   the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC   cDNA amounts are measured between the tissues; (f) the RNA is detected
CC   from the measured result; (g) each different adaptor and a common adaptor
CC   are added to each of the genomic DNA fragments derived from a same or
CC   different individuals; (h) the resultant adaptor-added genomic DNAs are
CC   mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC   an adaptor primer having the common sequence to the different adaptor and
CC   a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC   of the genomic DNAs are measured between the individuals. The method is
CC   used for the detection of the amounts of RNA and DNA. The present
CC   sequence represents an oligonucleotide which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1280
AAD52799
ID   AAD52799 standard; DNA; 18 BP.
XX
AC   AAD52799;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Primer used to prepare radioactively labelled cDNA probes from RNA.
```

```
XX
KW   Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW   cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW   prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW   CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW   TME; BSE; Gerstmann-Straussler-Scheinker syndrome; GSS; Alpers syndrome;
KW   fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic;
KW   Alzheimer's disease; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200293164-A2.
XX
PD   21-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-EP005420.
XX
PR   16-MAY-2001; 2001EP-00111858.
PR   29-MAY-2001; 2001US-0293528P.
PR   13-JUL-2001; 2001EP-00117113.
PR   18-JUL-2001; 2001US-0305898P.
XX
PA   (AXXI-) AXXIMA PHARM AG.
XX
PI   Stein-Gerlach M,  Salassidis K,  Bacher G,  Mueller S;
XX
DR   WPI; 2003-120714/11.
XX
PT   New pyridylpyrimidine derivatives useful in the treatment or prevention
PT   of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease
PT   (CJD).
XX
PS   Example; Page 38; 96pp; English.
XX
CC   The invention relates to novel pyridylpyrimidine derivatives and methods
CC   of detecting prion infections and/or prion disease in an individual or in
CC   cells, cell cultures and/or cell lysates. The method involves adding at
CC   least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-
CC   pyrimidine derivative to the sample or in cells, cell cultures and/or
CC   cell lysates and detecting the activity of at least one human cellular
CC   protein kinases (e.g., FGF-R1 (also known as flg, Fl-1, Flt-2, b-FGFR),
CC   Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also
CC   known as c-abl), clk1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also
CC   known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL
CC   (also known as MCP83) and PTP-zeta, the cellular signal transduction
CC   molecules HSP80 and GPIR-1. The invention is useful for regulating the
CC   production of prions in cells and in the manufacture of pharmaceutical
CC   composition for prophylaxis and/or treatment of infectious disease (e.g.
CC   Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy
CC   (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy
CC   (BSE), variant CJD, Gerstmann-Straussler-Scheinker syndrome (GSS), fatal
CC   familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,
CC   vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans
CC   or ruminants. The present DNA sequence is a primer used to prepare
CC   radioactively labelled cDNA probes from RNA. This sequence is used in the
CC   exemplification of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1281
AAD56466/c
ID   AAD56466 standard; RNA; 18 BP.
XX
AC   AAD56466;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Target RNA #1 used in the exemplification of the invention.
XX
KW   Acyclic linker; gene expression; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is a target RNA, used in the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 1282
AAD56440
ID   AAD56440 standard; DNA; 18 BP.
XX
AC   AAD56440;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
```

PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Fig 9; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1283
AAD56446
ID AAD56446 standard; DNA; 18 BP.
XX
AC AAD56446;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Fig 7; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1284
ACH03247
ID ACH03247 standard; DNA; 18 BP.
XX
AC ACH03247;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #882.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 33; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory

```
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1285
AAD57871
ID   AAD57871 standard; DNA; 18 BP.
XX
AC   AAD57871;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense oligo #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
XX
OS   Unidentified.
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense oligonucleotide used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1286
AAD57878
ID   AAD57878 standard; DNA; 18 BP.
XX
AC   AAD57878;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .3
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7. .9
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .15
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
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  Best Local Similarity   40.0%;  Pred. No. 8.8e+02;
  Matches    6;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::|||:::|||::: 
Db          1 UUUTTTUUUTTTUUU 15


RESULT 1287
AAD57879
ID   AAD57879 standard; DNA; 18 BP.
XX
AC   AAD57879;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .6
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .18
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   40.0%;  Pred. No. 8.8e+02;
  Matches    6;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::||||||::: 
Db          1 UUUUUUTTTTTTUUU 15


RESULT 1288
AAD57877
ID   AAD57877 standard; DNA; 18 BP.
XX
AC   AAD57877;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        3
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        5
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7
FT                   /*tag=  d
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        9
FT                   /*tag=  e
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        11
FT                   /*tag=  f
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13
FT                   /*tag=  g
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        15
FT                   /*tag=  h
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        17
FT                   /*tag=  i
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
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DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 8.8e+02;
Matches 7; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:|:|:|:|:|:|:|:
Db 1 UTUTUTUTUTUTUTU 15

RESULT 1289
AAD57890/c
ID AAD57890 standard; RNA; 18 BP.
XX
AC AAD57890;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target RNA #1 used in RNase H assay.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS Unidentified.
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CA000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA;
XX
DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 4; Page 38; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is a target RNA used in RNase H assay. This sequence is used in
CC the exemplification of the invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
|||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1290
ADB37210
ID ADB37210 standard; DNA; 18 BP.
XX
AC ADB37210;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
|||||||||||||||

```
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1291
ADB37236
ID   ADB37236 standard; DNA; 18 BP.
XX
AC   ADB37236;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #850.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 18; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1292
ADE77617/c
ID   ADE77617 standard; DNA; 18 BP.
XX
AC   ADE77617;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW   probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW   genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW   multiplexed elongation assay; enzymatic recognition;
KW   cystic fibrosis conductance transmembrane regulator.
XX
OS   Synthetic.
XX
OS   Homo sapiens.
XX
PN   WO2003034029-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US033012.
XX
PR   15-OCT-2001; 2001US-0329427P.
PR   15-OCT-2001; 2001US-0329428P.
PR   15-OCT-2001; 2001US-0329619P.
PR   15-OCT-2001; 2001US-0329620P.
PR   14-MAR-2002; 2002US-0364416P.
XX
PA   (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI   Li AX,  Hashmi G,  Seul M;
XX
DR   WPI; 2003-393553/37.
XX
PT   Concurrent interrogation of a number of polymorphic sites, useful for
PT   genetic testing, carrier screening, genetic profiling, and identity
PT   testing, comprises conducting a multiplexed elongation assay using
PT   probes.
XX
PS   Example 9; Page 46; 143pp; English.
XX
CC   This invention relates to a novel method for the concurrent interrogation
CC   of a number of polymorphic sites in the presence of, and without
CC   interference from, non-designated polymorphic sites. Specifically, it
CC   comprises conducting a multiplexed elongation assay by applying one or
CC   more temperature cycles to achieve linear amplification of the target or
CC   a combination of annealing and elongation steps under temperature-
CC   controlled conditions. Furthermore, this detection method uses probe
CC   extension or elongation and relies on enzymatic recognition, a superior
CC   technique that no longer depends on differential hybridisation. The
CC   present invention describes probes and methods useful for identifying or
CC   detecting polymorphisms at one or more designated sites, such that they
CC   can identify mutations within the cystic fibrosis conductance
CC   transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC   genes. In addition, concurrent interrogation of a multiplicity of
CC   polymorphic sites is useful for genetic testing, carrier screening,
CC   genotyping or genetic profiling, and identity testing. This
CC   oligonucleotide is the negative control probe used for the elongation
CC   mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC   invention.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 1293
ADI34489
ID   ADI34489 standard; DNA; 18 BP.
XX
AC   ADI34489;
XX
DT   22-APR-2004  (first entry)
XX
DE   Nucleotide sequence of an oligo dT18.
XX
KW   Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO2003102243-A1.
```

XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-US017103.
XX
PR 31-MAY-2002; 2002US-0384454P.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Kamme FC, Zhu JY;
XX
DR WPI; 2004-035466/03.
XX
PT Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT RNA transcription from a polynucleotide template, comprises eliminating
PT single-stranded oligonucleotide from the transcription sample.
XX
PS Example 1; SEQ ID NO 8; 26pp; English.
XX
CC The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction.
CC Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
CC transcription reaction.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||| |
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1294
ADH78590/c
ID ADH78590 standard; DNA; 18 BP.
XX
AC ADH78590;
XX
DT 22-APR-2004 (first entry)
XX
DE Test element oligonucleotide #2.
XX
KW Fluid functional property; fluid flow pattern;
KW fluid reagent distribution; time dependent fluid reactivity; ss.
XX
OS Synthetic.
XX
PN US2003232343-A1.
XX
PD 18-DEC-2003.
XX
PF 14-JUN-2002; 2002US-00172675.
XX
PR 14-JUN-2002; 2002US-00172675.
XX
PA (LEPR/) LEPROUST E M.
PA (AMOR/) AMORESE D A.
PA (PECK/) PECK B J.
XX
PI Leproust EM, Amorese DA, Peck BJ;
XX
DR WPI; 2004-061269/06.
XX
PT Determining a functional property of fluid in chamber by introducing a
PT support comprising test elements having reaction and detection domains,
PT introducing a test fluid, and detecting locations not reactive with the
PT fluid.
XX
PS Example 2; SEQ ID NO 2; 22pp; English.
XX
CC The invention relates to a method of determining a functional property of
CC a fluid in a chamber comprising introducing into the chamber a support to
CC which is bound several test elements, each of the test elements
CC comprising a reaction domain and a detection domain, introducing into the
CC chamber a fluid that is interactive with the reaction domains, removing
CC the fluid from the chamber, determining by means of the detection domains
CC the locations at which the fluid has not interacted with the reaction
CC domains, and relating the locations to the functional property of the
CC fluid. The reaction domains involves nucleotides. The detection domain
CC comprises a member of a specific binding pair. The determining of the
CC step involves treating the test elements to modify only those reaction
CC domains that have interacted with the fluid. The functional property is
CC chosen from the flow pattern of the fluid, reagent distribution within
CC the fluid and time dependent reactivity of the fluid. The method is
CC useful for determining a functional property of a fluid in a chamber and
CC for synthesising arrays of biopolymers e.g., arrays of polynucleotides.
CC The method provides for the characterisation of a new fluid in a known
CC flow cell, a known fluid in a new flow cell or a new fluid/flow cell
CC combination. This sequence represents a test element used in the method
CC of the invention.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||| |
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1295
ADL95318
ID ADL95318 standard; DNA; 18 BP.
XX
AC ADL95318;
XX
DT 01-JUL-2004 (first entry)
XX
DE Anti-proliferative oligonucleotide #9.
XX
KW ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
KW cancer; malignant tumour.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 8
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Optionally 32-P labelled"
FT
XX
PN US2004067197-A1.
XX
PD 08-APR-2004.
XX
PF 02-FEB-2001; 2001US-00775479.
XX
PR 26-NOV-1997; 97WO-CA000892.
PR 24-MAY-1999; 99US-00318106.
XX
PA (LECL/) LECLERC G.

PA (MART/) MARTEL R.
XX
PI Leclerc G, Martel R;
XX
DR WPI; 2004-314974/29.
XX
PT New anti-proliferative substance comprising a radiolabeled DNA carrier,
PT useful for preventing or treating uncontrolled cellular proliferation
PT e.g. restenosis, cancer or malignant tumors.
XX
PS Claim 13; SEQ ID NO 9; 28pp; English.
XX
CC The invention relates to an anti-proliferative substance for preventing
CC uncontrolled cellular proliferation comprising a radiolabelled DNA
CC carrier, where a radioisotope is located internally within the DNA
CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier
CC penetrates the cell membrane and is retained intracellularly for a time
CC sufficient for the radio-isotope to effect a dose therapy. The carrier in
CC the anti-proliferative substance is an oligonucleotide, which is linear
CC or a plasmid, which is circular. The plasmid is of viral or bacterial
CC origin. The oligonucleotide is a double- or a single-stranded DNA
CC sequence, which is conjugated with an antibody for cell-specific
CC delivery. The oligonucleotide is also conjugated to a stent surface,
CC cholesterol, oleic acid, linoleic acid, TGFalpha, antibody, TGFbeta,
CC cytokines or growth factors. The anti-proliferative substance is useful
CC for preventing or treating uncontrolled cellular proliferation. The
CC uncontrolled cell proliferation is a restenosis following angioplasty, or
CC cancer or a malignant tumour. The present sequence represents an
CC oligonucleotide carrier used in the invention.
XX
SQ Sequence 18 BP; 3 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1296
ADO28710/c
ID ADO28710 standard; DNA; 18 BP.
XX
AC ADO28710;
XX
DT 15-JUL-2004 (first entry)
XX
DE Single stranded cDNA production poly-A-tail seqid 6.
XX
KW single stranded cDNA; adaptor-mediated process; cDNA synthesis;
KW poly-A-tail; ss.
XX
OS Synthetic.
XX
PN US6706476-B1.
XX
PD 16-MAR-2004.
XX
PF 09-MAR-2001; 2001US-00803263.
XX
PR 22-AUG-2000; 2000US-0226954P.
XX
PA (AZIG-) AZIGN BIOSCIENCE AS.
XX
PI Thirstrup K, Warthoe P, Pettersson NB;
XX
DR WPI; 2004-326403/30.
XX
PT Synthesizing single stranded cDNA, involves annealing cDNA synthesis
PT primer to RNA and synthesizing first cDNA strand, ligating adaptor to
PT single stranded cDNA using DNA ligase, and amplifying ligated single
PT stranded cDNA fragment.
XX
PS Example 1; SEQ ID NO 6; 22pp; English.
XX
CC The invention describes a method of synthesising single stranded cDNA by
CC a 5'-ligated adaptor-mediated process involving: annealing a cDNA
CC synthesis primer to RNA, separating the cDNA strand from the RNA,
CC purifying the cDNA, contacting the cDNA with an adaptor, ligating the
CC adaptor through 5'-phosphate on strand (II) of the adaptor to single
CC stranded using DNA ligase, and amplifying the obtained ligated single
CC stranded fragment in an molecular amplification procedure. The method is
CC useful for: synthesising a single stranded cDNA by a 5'-ligated adaptor-
CC mediated process, where the source of nucleic acid is chosen from blood,
CC serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and
CC saliva. The tissue sample comprises a cell population which may be single
CC cell, 100-1000000 cells or more as desired; making a cDNA library from a
CC collection of mRNA molecules in a sample, where the method is applied to
CC amplify the cDNAs corresponding to the mRNAs by annealing one or more
CC cDNA synthesis primers to several mRNAs in the sample; producing a
CC subtractive hybridisation probe which involves synthesising a double-
CC stranded cDNA collection from a first mRNA population by the method,
CC where primer 1 is modified by biotin in the 5' end, isolating the biotin-
CC containing single stranded cDNA (sense) by use of streptavidin coated
CC magnetic beads, synthesising a double-stranded cDNA collection from a
CC second mRNA population according to the method, isolating the non-biotin-
CC containing single stranded cDNA (anti-sense) by use of streptavidin
CC coated magnetic beads, hybridising the sense to the anti-sense cDNA,
CC where an unhybridised sub-population of the anti-sense cDNA is found,
CC isolating the unhybridised sub-population of the antisense cDNA by use of
CC streptavidin coated cDNA, and generating a second double-stranded cDNA
CC collection from the unhybridised sub-population by PCR using primer 1 and
CC primer 2; and detecting expression of a gene in a pre-selected cell
CC population. The method is an improved method for producing amplified
CC heterogeneous populations of cDNA from limited quantities of RNA or other
CC nucleic acid. This sequence represents a poly-A-tail used to in the
CC production single stranded cDNA.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1297
ADO28711
ID ADO28711 standard; DNA; 18 BP.
XX
AC ADO28711;
XX
DT 15-JUL-2004 (first entry)
XX
DE Single stranded cDNA production poly-A-tail complement seqid 7.
XX
KW single stranded cDNA; adaptor-mediated process; cDNA synthesis;
KW poly-A-tail; ss.
XX
OS Synthetic.
XX
PN US6706476-B1.
XX
PD 16-MAR-2004.
XX
PF 09-MAR-2001; 2001US-00803263.
XX
PR 22-AUG-2000; 2000US-0226954P.
XX
PA (AZIG-) AZIGN BIOSCIENCE AS.
XX

PI Thirstrup K, Warthoe P, Pettersson NB;
XX
DR WPI; 2004-326403/30.
XX
PT Synthesizing single stranded cDNA, involves annealing cDNA synthesis
PT primer to RNA and synthesizing first cDNA strand, ligating adaptor to
PT single stranded cDNA using DNA ligase, and amplifying ligated single
PT stranded cDNA fragment.
XX
PS Example 1; SEQ ID NO 7; 22pp; English.
XX
CC The invention describes a method of synthesising single stranded cDNA by
CC a 5'-ligated adaptor-mediated process involving: annealing a cDNA
CC synthesis primer to RNA, separating the cDNA strand from the RNA,
CC purifying the cDNA, contacting the cDNA with an adaptor, ligating the
CC adaptor through 5'-phosphate on strand (II) of the adaptor to single
CC stranded using DNA ligase, and amplifying the obtained ligated single
CC stranded fragment in an molecular amplification procedure. The method is
CC useful for: synthesising a single stranded cDNA by a 5'-ligated adaptor-
CC mediated process, where the source of nucleic acid is chosen from blood,
CC serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and
CC saliva. The tissue sample comprises a cell population which may be single
CC cell, 100-1000000 cells or more as desired; making a cDNA library from a
CC collection of mRNA molecules in a sample, where the method is applied to
CC amplify the cDNAs corresponding to the mRNAs by annealing one or more
CC cDNA synthesis primers to several mRNAs in the sample; producing a
CC subtractive hybridisation probe which involves synthesising a double-
CC stranded cDNA collection from a first mRNA population by the method,
CC where primer 1 is modified by biotin in the 5' end, isolating the biotin-
CC containing single stranded cDNA (sense) by use of streptavidin coated
CC magnetic beads, synthesising a double-stranded cDNA collection from a
CC second mRNA population according to the method, isolating the non-biotin-
CC containing single stranded cDNA (anti-sense) by use of streptavidin
CC coated magnetic beads, hybridising the sense to the anti-sense cDNA,
CC where an unhybridised sub-population of the anti-sense cDNA is found,
CC isolating the unhybridised sub-population of the antisense cDNA by use of
CC streptavidin coated cDNA, and generating a second double-stranded cDNA
CC collection from the unhybridised sub-population by PCR using primer 1 and
CC primer 2; and detecting expression of a gene in a pre-selected cell
CC population. The method is an improved method for producing amplified
CC heterogeneous populations of cDNA from limited quantities of RNA or other
CC nucleic acid. This sequence represents the complement of a poly-A-tail
CC used to in the production single stranded cDNA.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1298
ADO26684
ID ADO26684 standard; DNA; 18 BP.
XX
AC ADO26684;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:77.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
DR WPI; 2004-411519/38.
DR P-PSDB; ADO26685.
XX
PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 77; 86pp; English.
XX
CC The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1299
ADO26682/c
ID ADO26682 standard; DNA; 18 BP.
XX
AC ADO26682;

```
XX
DT   12-AUG-2004  (first entry)
XX
DE   Synthetic leader sequence encoding DNA SEQ ID NO:75.
XX
KW   phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS   Synthetic.
XX
PN   WO2004042059-A1.
XX
PD   21-MAY-2004.
XX
PF   10-NOV-2003; 2003WO-AU001487.
XX
PR   08-NOV-2002; 2002US-0425163P.
XX
PA   (UYQU ) UNIV QUEENSLAND.
XX
PI   Frazer IH;
XX
DR   WPI; 2004-411519/38.
DR   P-PSDB; ADO26683.
XX
PT   Constructing synthetic polynucleotide for modulating the quality of a
PT   selected phenotype displayed by an organism comprises replacing a first
PT   codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS   Example 1; SEQ ID NO 75; 86pp; English.
XX
CC   The present invention describes a method for constructing a synthetic
CC   polynucleotide from which a polypeptide is producible to confer a
CC   selected phenotype to an organism of interest or part in a different
CC   quality than that conferred by a parent polynucleotide that encodes the
CC   same polypeptide. The method comprises: (a) selecting a first codon of
CC   the parent polynucleotide for replacement with a synonymous codon, where
CC   the synonymous codon is selected on the basis that it exhibits a
CC   different phenotypic preference than the first codon in a comparison of
CC   phenotypic preferences in test organisms or parts, where the test
CC   organism are selected from organisms of the same species as the organism
CC   of interest and organisms that are related to the organisms of interest;
CC   and (b) replacing the first codon with the synonymous codon to construct
CC   the synthetic polynucleotide. Also described: (1) a method for
CC   determining the phenotypic preference of a first codon in an organism of
CC   interest or its parts; (2) a synthetic polynucleotide constructed from
CC   the method above; (3) an organism or interest or part containing a
CC   synthetic polynucleotide constructed from the method above; (4) an
CC   organism or interest or part containing a synthetic construct that
CC   comprises a regulatory polynucleotide operably linked to a tandem repeat
CC   of a first codon fused in frame with a reporter polynucleotide that
CC   encodes a reporter protein, which produces, or is predicted to produce a
CC   selected phenotype or a phenotype of the same class as the selected
CC   phenotype in the organism or part; (5) a method of modulating the quality
CC   of a selected phenotype that is displayed by an organism of interest or
CC   part and that results from the expression of a parent polynucleotide that
CC   encodes the polypeptide; (6) a method of enhancing the quality of a
CC   selected phenotype that is displayed by an organism of interest or part
CC   and that results from the expression of a parent polynucleotide that
CC   encodes the polypeptide; and (7) a method of reducing the quality of a
CC   selected phenotype that is displayed by an organism of interest or part
CC   and that results from the expression of a parent polynucleotide that
CC   encodes the polypeptide. The method is useful for constructing a
CC   synthetic polynucleotide from which a polypeptide is producible to confer
CC   a selected phenotype to an organism of interest or part in a different
CC   quality than that conferred by a parent polynucleotide that encodes the
CC   same polypeptide. It is useful for modulating the quality of a selected
CC   phenotype displayed by an organism or part. The present sequence encodes
CC   a synthetic leader sequence, which is used in an example from the present
CC   invention.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4


RESULT 1300
ADP86130
ID   ADP86130 standard; DNA; 18 BP.
XX
AC   ADP86130;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #1.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 1; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1301
ADR32355
ID   ADR32355 standard; DNA; 18 BP.
XX
AC   ADR32355;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Rat KDR cytosolic domain cloning RT-PCR primer.
XX
KW   Rat; receptor tyrosine kinase; KDR; therapy; cancer;
KW   ischaemic ocular disease; proliferative retinopathy; inflammation;
KW   reverse transcription; RT; PCR; primer; ss.
XX
OS   Rattus norvegicus.
XX
PN   WO2004070004-A2.
XX
PD   19-AUG-2004.
XX
PF   23-JAN-2004; 2004WO-US001928.
XX
PR   29-JAN-2003; 2003US-0443335P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Thomas RA,  Pan B,  Mcgaughey GB;
XX
DR   WPI; 2004-604429/58.
XX
PT   New nucleic acid molecules encoding rat KDR protein, useful for
PT   identifying inhibitors of KDR activity for treating cancer, ischemic
PT   ocular diseases, and inflammation.
XX
PS   Example 2; Page 30; 77pp; English.
XX
CC   The invention relates to rat receptor tyrosine kinase (KDR) and its
CC   corresponding nucleic acid sequence. The nucleic acid molecules of the
CC   invention are useful for identifying compounds that modulate wild-type
CC   rat KDR activity to evaluate the safety and efficacy of specific
CC   inhibitors of KDR in rats. KDR inhibitors are useful for treating cancer,
CC   ischaemic ocular diseases such as proliferative retinopathy and
CC   inflammation. The present sequence is a reverse transcription (RT) PCR
CC   primer used for cloning rat KDR cytosolic domain. This sequence is used
CC   in the exemplification of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1302
ADR57967
ID   ADR57967 standard; DNA; 18 BP.
XX
AC   ADR57967;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Nucleotide #4 for signal amplification method.
XX
KW   ss; signal amplification method; gene expression; reverse transcription;
KW   self-assembly reaction; DNA chip.
XX
OS   Unidentified.
XX
PN   WO2004072302-A1.
XX
PD   26-AUG-2004.
XX
PF   13-FEB-2004; 2004WO-JP001588.
XX
PR   14-FEB-2003; 2003JP-00037212.
XX
PA   (PALM-) PALMA BEEZ RES INST CO LTD.
XX
PI   Usui M,  Fujikawa T;
XX
DR   WPI; 2004-642306/62.
XX
PT   Signal amplification method for detecting expressed gene, by using
PT   reverse transcription reaction and self-assembly reaction of
PT   oligonucleotide probes.
XX
PS   Disclosure; SEQ ID NO 4; 27pp; Japanese.
XX
CC   The invention relates to a signal amplification method (M1) for detecting
CC   expressed gene using reverse transcription reaction and a self-assembly
CC   reaction of forming a self assembly of oligonucleotide probes, thus
CC   improving detection sensitivity of the expressed gene in a DNA chip. (M1)
CC   is useful for signal amplification method (M1) for detecting expressed
CC   gene (claimed). (M1) improves detection sensitivity of the expressed gene
CC   in a DNA chip (claimed). (M1) does not require use of expensive enzymes
CC   and enables detection corresponding to the original RNA length or
CC   expression amount because of using neither linear amplification nor PCR.
CC   This sequence corresponds to a nucleotide used in the method of the
CC   invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1303
ADE27471
ID   ADE27471 standard; RNA; 19 BP.
XX
AC   ADE27471;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:415.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
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PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 415; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   80.0%;  Pred. No. 9.2e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2217 AGCAGCTCATGGAAT 2231
                ||||||:||:||||:
Db          1 AGCAGCUCAUGGAAU 15


RESULT 1304
ADE27181/c
ID   ADE27181 standard; RNA; 19 BP.
XX
AC   ADE27181;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:125.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 125; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2217 AGCAGCTCATGGAAT 2231
                |||||||||||||||
Db         19 AGCAGCTCATGGAAT 5


RESULT 1305
ADE27470
ID   ADE27470 standard; RNA; 19 BP.
XX
AC   ADE27470;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:414.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
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PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 414; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 9.2e+02;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2239 ATTCCATGAGCTGCT 2253
              |::|||:||||:||:
Db          5 AUUCCAUGAGCUGCU 19


RESULT 1306
ADE27180/c
ID   ADE27180 standard; RNA; 19 BP.
XX
AC   ADE27180;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:124.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 124; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2239 ATTCCATGAGCTGCT 2253
              |||||||||||||||
Db         15 ATTCCATGAGCTGCT 1


RESULT 1307
AAQ20109
ID   AAQ20109 standard; DNA; 18 BP.
XX
AC   AAQ20109;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 943 to target human TNF Receptor mRNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW   cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
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```
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 27; 42pp; English.
XX
CC   The oligomer was designed to target human TNF receptor mRNA beginning at
CC   nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC   ethanocytosine group. See also AAQ20108
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTC 2141
              |||| |||| ||||||||
Db          1 TTTTATTTTTTTTTTTTC 18


RESULT 1308
AAQ30448
ID   AAQ30448 standard; DNA; 18 BP.
XX
AC   AAQ30448;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N6 methyl-8-oxo-2' deoxyadenine"
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTC 2141
              |||| |||| ||||||||
Db          1 TTTTATTTTTTTTTTTTC 18


RESULT 1309
AAX15198
ID   AAX15198 standard; DNA; 18 BP.
XX
AC   AAX15198;
XX
DT   25-MAR-2003  (revised)
DT   28-APR-1999  (first entry)
XX
DE   Triple helix forming oligonucleotide.
XX
KW   Double-stranded DNA; triple helix; quinoline;
KW   quinazoline-based structure; hydrogen bonding; ss.
XX
OS   Synthetic.
XX
PN   WO9623777-A1.
XX
PD   08-AUG-1996.
XX
PF   29-JAN-1996;   96WO-US001473.
XX
PR   01-FEB-1995;   95US-00384324.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold BI;
XX
DR   WPI; 1996-371338/37.
XX
PT   New substd. quinoline and quinazoline cpds. - are monomers for triple
PT   helix-forming oligo:nucleotide analogues useful e.g. for treating tumours
PT   or viral infection.
XX
PS   Disclosure; Fig 2; 102pp; English.
XX
```

CC The present sequence represents a triple helix forming oligonucleotide
CC that form a triple helix with the double-stranded DNA sequence described
CC in AAX15197. The specification describes novel monomeric compositions
CC which are substituted quinoline or quinazoline-based structures capable
CC of hydrogen bonding specifically with interstrand purine-pyrimidine pairs
CC in a double stranded Watson-Crick DNA molecule to form a triple-helix.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 18 BP; 0 A; 3 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2127 TCTTTTCTTTTTTTCTTT 2144
||||| |||||||||||
Db 1 TCTTTCTTTTTTTTCTTT 18

RESULT 1310
AAV21969
ID AAV21969 standard; DNA; 18 BP.
XX
AC AAV21969;
XX
DT 14-JUL-1998 (first entry)
XX
DE Nuclease resistant antisense oligo NBT 142 targeted against (TC)9.
XX
KW Nuclease resistant; bacterial infection; antibiotic; target;
KW veterinary medicine; treatment; human; industrial process;
KW bacterial control; ss.
XX
OS Synthetic.
XX
PN WO9803533-A1.
XX
PD 29-JAN-1998.
XX
PF 23-JUL-1997; 97WO-US012961.
XX
PR 24-JUL-1996; 96US-00685575.
XX
PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI Arrow A, Dale RMK, Thompson TL;
XX
DR WPI; 1998-120687/11.
XX
PT Treating bacterial infections in humans or animals with
PT oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT with antibiotics.
XX
PS Claim 49; Page 87; 163pp; English.
XX
CC This antisense oligonucleotide is nuclease resistant and can be used in
CC the treatment of animals, including humans, having a bacterial infection.
CC The treatment comprises administration of such nuclease resistant
CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC and formulated with a carrier. A compound comprising this nuclease
CC resistant oligonucleotide can be covalently linked to an antibiotic. The
CC method is used to treat infections by a wide variety of Gram-positive and
CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC The methods are particularly used in immuno-compromised individuals (e.g.
CC patients with acquired immunodeficiency syndrome or those receiving
CC chemotherapy or radiation therapy), optionally in combination with, or
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC therapeutic use, the oligonucleotides can be used to control bacteria in
CC laboratory cultures, foods, beverages and industrial processes. The
CC oligonucleotides are specific for bacteria, without affecting metabolism
CC in mammalian cells. They may also activate RNase H and have a general,
CC non-specific immune-stimulating effect. The oligonucleotides can be
CC administered orally, intranasally, rectally, topically or by injection,
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC enhances cellular uptake
XX
SQ Sequence 18 BP; 0 A; 9 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3182 TCTCTCTCCCTCCCTCTC 3199
|||||||| ||| |||||
Db 1 TCTCTCTCTCTCTCTCTC 18

RESULT 1311
AAX91065
ID AAX91065 standard; RNA; 18 BP.
XX
AC AAX91065;
XX
DT 15-NOV-1999 (first entry)
XX
DE CAT gene target RNA fragment.
XX
KW Phosphonate internucleosidyl linkage; chirality; hybridization; racemic;
KW binding affinity; ss.
XX
OS Synthetic.
XX
PN US5955597-A.
XX
PD 21-SEP-1999.
XX
PF 30-JUN-1997; 97US-00885126.
XX
PR 16-NOV-1993; 93US-00154013.
PR 21-NOV-1994; 94US-00343018.
XX
PA (GENT-) GENTA INC.
XX
PI Schwartz DA, Vaghefi MM, Riley TA, Arnold LJ, Reynolds MA;
XX
DR WPI; 1999-539600/45.
XX
PT Oligomers made using chirally pure nucleoside dimers, trimers, or
PT tetramers with enhanced binding affinities.
XX
PS Example 19; Col 41-42; 30pp; English.
XX
CC The invention provides methods for preparing oligomers having phosphonate
CC internucleosidyl linkages of a preselected chirality which hybridize to a
CC target RNA sequence. The method of making comprises: (a) synthesizing a
CC nucleoside dimer, trimer, or tetramer with racemic internucleosidyl
CC phosphonate linkages; (b) purifying the racemic nucleoside to a chirally
CC pure nucleoside; and (c) sequentially linking at least 2 of the chirally
CC pure nucleosides to form a synthetic oligomer that is enriched for
CC phosphonate internucleosidyl linkages of a preselected chirality and is
CC complementary to an RNA target sequence. The methods are useful for
CC providing chirally enriched synthetic oligomers. Rp chirally enriched
CC synthetic oligomers have enhanced binding affinities for RNA compared to
CC oligomers with racemic all methylphosphonate internucleosidyl linkages.
CC Sequences AAX91054-75 represent oligomers chemically synthesised using
CC the method of the invention
XX
SQ Sequence 18 BP; 0 A; 9 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCT 3198
|:|:|:|:| |:| |:|:

```
Db          1 CUCUCUCUCUCUCUCUCU 18


RESULT 1312
AAH63154
ID   AAH63154 standard; DNA; 18 BP.
XX
AC   AAH63154;
XX
DT   06-AUG-2003  (revised)
DT   11-SEP-2001  (first entry)
XX
DE   Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 315.
XX
KW   Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW   antiviral agent; gene expression; antisense construct; probe; primer;
KW   transgenic viral resistant shrimp; ss.
XX
OS   Shrimp white spot syndrome virus.
XX
PN   WO200138351-A2.
XX
PD   31-MAY-2001.
XX
PF   08-NOV-2000; 2000WO-US028888.
XX
PR   24-NOV-1999;   99CN-00124717.
XX
PA   (PENY-) PE CORP NY.
PA   (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA   (SINO-) SINOGENOMAX CO LTD.
XX
PI   Xu X,  Yang F,  He J,  Pham L,  He M,  Ye Y,  Shen Y,  Kodira C;
XX
DR   WPI; 2001-355877/37.
XX
PT   Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PT   (WSBV), useful for producing viral polypeptides that can be used to
PT   screen for agents that are useful for treating WSBV infection.
XX
PS   Disclosure; Fig 3; 626pp; English.
XX
CC   The invention provides the primary nucleotide sequence of the WSBV genome
CC   (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
CC   encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
CC   (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
CC   molecules and proteins of the invention are useful for diagnosis and
CC   monitoring viral infection, in screens for antiviral agents and for
CC   monitoring viral gene expression or activity during a treatment regimen.
CC   The nucleic acid molecules are also useful as antisense constructs to
CC   control viral gene expression in infected cells and tissues and to create
CC   transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
CC   field.)
XX
SQ   Sequence 18 BP; 6 A; 9 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1124 TTCCACAACTACCACCAC 1141
              ||||||||| ||||| ||
Db          1 TTCCACAACCACCACTAC 18


RESULT 1313
AAD14847
ID   AAD14847 standard; DNA; 18 BP.
XX
AC   AAD14847;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human PS-133 EST-specific clones sequencing primer, PS133.F1-5 #1.
XX
KW   PS133; prostate disease; cancer; immunogen; gene therapy; cytostatic;
KW   human; primer; ds.
XX
OS   Homo sapiens.
XX
PN   US6232456-B1.
XX
PD   15-MAY-2001.
XX
PF   06-OCT-1997;   97US-00944483.
XX
PR   06-OCT-1997;   97US-00944483.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Cohen M,  Colpitts TL,  Friedman PN,  Granados E,  Klass MR;
PI   Russell JC,  Stewart KD,  Stroupe SD;
XX
DR   WPI; 2001-366357/38.
XX
PT   New PS133 polynucleotides, useful for detecting, diagnosing, staging,
PT   monitoring, prognosing, preventing, treating or determining the
PT   predisposition of an individual to a prostate disease, e.g. cancer.
XX
PS   Example 2; Col 75; 93pp; English.
XX
CC   The patent discloses PS-133 polynucleotides and polypeptides which are
CC   indicative of prostate disease. The patent also provides a method for
CC   detecting PS133 protein in a test sample. The polynucleotides of the
CC   invention are useful for detecting, diagnosing, staging, monitoring,
CC   prognosing, preventing, treating or determining the predisposition of an
CC   individual to prostate diseases such as cancer. PS133-derived
CC   polynucleotides are used for the detection of normal or altered gene
CC   expression, in assays for detecting, amplifying or quantifying genes or
CC   nucleic acids relating to prostate tissue diseases and conditions, and to
CC   produce probes which can be used in the detection of nucleic acids in a
CC   sample. PS-133 proteins are used as immunogens for the production of
CC   antibodies. PS-133 sequences are also used in gene therapy. The present
CC   DNA sequence is primer, PS133.F1-5 which is used for sequencing PS-133
CC   EST-specific clones
XX
SQ   Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1960 TCAAGCCCCACCACATAG 1977
              ||||||||| | ||||||
Db          1 TCAAGCCCCGCTACATAG 18


RESULT 1314
AAI64450/c
ID   AAI64450 standard; DNA; 18 BP.
XX
AC   AAI64450;
XX
DT   23-NOV-2001  (first entry)
XX
DE   SSR motif #10.
XX
KW   Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
KW   trait mapping; marker-assisted selection; gene selection; legume;
KW   DNA profiling; breeding; ds.
XX
OS   Unidentified.
XX
PN   NZ509194-A.
XX
PD   25-MAY-2001.
```

```
XX
PF   03-JAN-2001; 2001NZ-00509194.
XX
PR   24-DEC-1999;   99AU-00004907.
PR   28-MAR-2000; 2000AU-00006520.
XX
PA   (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX
PI   Koelliker R,  Forster JW;
XX
DR   WPI; 2001-431058/46.
XX
PT   Novel simple sequence repeats in clover species useful for selection of
PT   genes in legume breeding, for profiling legume species varieties and for
PT   testing the purity of legume seed batches.
XX
PS   Claim 6; Page 35; 52pp; English.
XX
CC   The present invention relates to Simple Sequence Repeats (SSRs) from
CC   clover species. SSRs, also called microsatellites, are based on a 1-7
CC   nucleotide core element which is tandemly repeated. The SSR array is
CC   embedded in complex flanking DNA. SSRs are ideal markers for genome
CC   mapping, trait mapping and marker-assisted selection. The SSRs may be
CC   used in methods for selecting genes in clover/ legume breeding. The SSRs
CC   are also useful for DNA profiling of clover varieties and for testing the
CC   purity of legume seed batches. The present sequence is a SSR motif, which
CC   was used in the present invention
XX
SQ   Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTG 4099
              ||||||| |||| |||||
Db         18 TGTGTGGGTGTGTGTGTG 1


RESULT 1315
ABT21493
ID   ABT21493 standard; DNA; 18 BP.
XX
AC   ABT21493;
XX
DT   16-APR-2003  (first entry)
XX
DE   Multiplex group PCR primer #240.
XX
KW   Racing potential; horse; grandpaternal DNA; over-represented; breeding;
KW   grandmother; performance; progeny horse; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200292851-A2.
XX
PD   21-NOV-2002.
XX
PF   15-MAY-2002; 2002WO-GB002273.
XX
PR   15-MAY-2001; 2001GB-00011886.
XX
PA   (ANIM-) ANIMAL HEALTH TRUST.
PA   (BRHO-) BRITISH HORSERACING BOARD.
XX
PI   Binns MM,  Swinburne JE;
XX
DR   WPI; 2003-129314/12.
XX
PT   Determining the racing potential of a horse comprises measuring whether
PT   grandpaternal or grandmaternal DNA from the selected grandmother DNA is
PT   over-represented in the genome of the horse.
XX
PS   Example 2; Page 24; 49pp; English.
XX
CC   The invention relates to a novel method for determining racing potential
CC   of a horse. The method comprises measuring: whether grandpaternal DNA is
CC   over-represented in the genome of the horse; or in the case where one of
CC   the grandmothers was selected for breeding on the basis of racing
CC   performance, whether grandmaternal DNA from the selected grandmother is
CC   over-represented in the genome of the horse which indicates that the
CC   horse has good racing potential. The method of the invention is useful
CC   for determining the racing potential of a horse or for obtaining a
CC   progeny horse with good racing potential. This polynucleotide sequence
CC   represents a PCR primer used in the detection method of over-
CC   representation of DNA from male grandparents of the invention
XX
SQ   Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4693 ACTTGCTGTGTGACCCTG 4710
              |||||||||| ||| |||
Db          1 ACTTGCTGTGCGACTCTG 18


RESULT 1316
ABZ10686
ID   ABZ10686 standard; DNA; 18 BP.
XX
AC   ABZ10686;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Haematopoietic cell proliferation disorder related oligonucleotide #826.
XX
KW   Human; haematopoietic cell proliferation disorder; cytostatic;
KW   gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW   cytosine methylation state; probe; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200277272-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003401.
XX
PR   26-MAR-2001; 2001US-0278333P.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Berlin K,  Braun A,  Distler J,  Guetig D,  Howe A,  Mueller J;
PI   Olek A,  Piepenbrock C,  Adorjan P,  Grabs G,  Lesche R,  Leu E;
PI   Lewin A,  Lipscher E,  Maier S,  Model F,  Mueller V,  Otto T,  Pelet C;
PI   Schwope I,  Ziebarth H;
XX
DR   WPI; 2003-018942/01.
XX
PT   Detecting and differentiating between hematopoietic cell proliferative
PT   disorders, comprises contacting a target nucleic acid with a reagent that
PT   distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS   Claim 15; Page 57; 117pp; English.
XX
CC   The present invention describes a method for detecting and
CC   differentiating between haematopoietic cell proliferative disorders
CC   associated with at least 1 gene and/or their regulatory regions in a
CC   subject. The method comprises contacting a target nucleic acid in a
CC   biological sample obtained from the subject with at least 1 reagent,
CC   which distinguishes between methylated and non-methylated CpG
CC   dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC   represent specifically claimed nucleotide sequences from the present
```

CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5056 TGATTGGGTGGGATTTTT 5073
|||| ||||||||||
Db 1 TGATGTGGTGGGATTTTT 18

RESULT 1317
ABZ11102
ID ABZ11102 standard; DNA; 18 BP.
XX
AC ABZ11102;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #1242.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 15; Page 69; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTGGG 4518
||| ||||| ||||||||
Db 1 TTTATTTTGTTTTTGGG 18

RESULT 1318
ABZ10510
ID ABZ10510 standard; DNA; 18 BP.
XX
AC ABZ10510;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #650.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 15; Page 47; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG

CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||| ||||| |||||||| |
Db 1 TTTATTTTGTTTTTGGG 18

RESULT 1319
ADB54892
ID ADB54892 standard; DNA; 18 BP.
XX
AC ADB54892;
XX
DT 04-DEC-2003 (first entry)
XX
DE Hybridisation oligonucleotide 428 used to analyse genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
KW probe.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP002035.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
XX
DR WPI; 2003-731620/69.
XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
PS Claim 36; Page 39; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the hybridisation
CC oligonucleotide of the invention which was used to analyse the genomic
CC DNA region.
XX
SQ Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5056 TGATTGGGTGGGATTTTT 5073
|||| |||||||||||
Db 1 TGATGTGGTGGGATTTTT 18

RESULT 1320
ADC70239
ID ADC70239 standard; DNA; 18 BP.
XX
AC ADC70239;
XX
DT 18-DEC-2003 (first entry)
XX
DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 729).
XX
KW PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
KW adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
KW cytosine methylation state.
XX
OS Unidentified.
XX
PN WO2003052135-A2.
XX
PD 26-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP014026.
XX
PR 14-DEC-2001; 2001DE-01061625.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;
PI Nimmrich I;
XX
DR WPI; 2003-533029/50.
XX
PT Detecting and differentiating cytosine methylation state of genomic DNA,
PT useful for diagnosing, treating prognosticating and/or monitoring lung
PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
PT carcinoma.
XX
PS Claim 15; SEQ ID NO 729; 58pp; English.
XX
CC This invention relates to a novel method for detecting and
CC differentiating between lung cell proliferative disorders associated with
CC at least one gene and/or their regulatory regions. Specifically, it
CC refers to a method comprising contacting a target nucleic acid in a
CC biological sample with at least one reagent, wherein the reagent is able
CC to distinguish between methylated and non-methylated CpG dinucleotides
CC present in the target DNA. As such, it is possible to further
CC differentiate and diagnose medical conditions including adenocarcinoma
CC and squamous cell carcinoma, and their respective adjacent lung tissue.
CC The present invention describes cytostatic oligomers and PNA-oligomers
CC that are useful as probes for determining the cytosine methylation state
CC or single nucleotide polymorphisms (SNPs) of the target sequence. This
CC oligonucleotide sequence is a primer oligomer used for the analysis of
CC CpG positions within genomic DNA, used in an exemplification of the
CC invention.

```
XX
SQ   Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              |||| ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 1321
ADC70018
ID   ADC70018 standard; DNA; 18 BP.
XX
AC   ADC70018;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Primer oligo used for analysing CpG islands in genomic DNA (SeqID 507).
XX
KW   PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
KW   adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
KW   cytosine methylation state.
XX
OS   Unidentified.
XX
PN   WO2003052135-A2.
XX
PD   26-JUN-2003.
XX
PF   10-DEC-2002; 2002WO-EP014026.
XX
PR   14-DEC-2001; 2001DE-01061625.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Burger M,  Field JK,  Genc B,  Liloglou T,  Lipscher E,  Maier S;
PI   Nimmrich I;
XX
DR   WPI; 2003-533029/50.
XX
PT   Detecting and differentiating cytosine methylation state of genomic DNA,
PT   useful for diagnosing, treating prognosticating and/or monitoring lung
PT   cell proliferative disorders e.g. adenocarcinoma and squamous cell
PT   carcinoma.
XX
PS   Claim 15; SEQ ID NO 507; 58pp; English.
XX
CC   This invention relates to a novel method for detecting and
CC   differentiating between lung cell proliferative disorders associated with
CC   at least one gene and/or their regulatory regions. Specifically, it
CC   refers to a method comprising contacting a target nucleic acid in a
CC   biological sample with at least one reagent, wherein the reagent is able
CC   to distinguish between methylated and non-methylated CpG dinucleotides
CC   present in the target DNA. As such, it is possible to further
CC   differentiate and diagnose medical conditions including adenocarcinoma
CC   and squamous cell carcinoma, and their respective adjacent lung tissue.
CC   The present invention describes cytostatic oligomers and PNA-oligomers
CC   that are useful as probes for determining the cytosine methylation state
CC   or single nucleotide polymorphisms (SNPs) of the target sequence. This
CC   oligonucleotide sequence is a primer oligomer used for the analysis of
CC   CpG positions within genomic DNA, used in an exemplification of the
CC   invention.
XX
SQ   Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTTGTTTTTGGG 18


RESULT 1322
ADE84378
ID   ADE84378 standard; DNA; 18 BP.
XX
AC   ADE84378;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human lymphoid cell proliferative disorder gene CpG analysis oligo #84.
XX
KW   lymphoid cell proliferative disorder; methylation;
KW   methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW   diffuse large B-cell lymphoma; mantle cell lymphoma;
KW   chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW   follicular lymphoma; diagnosis; prognosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003044226-A2.
XX
PD   30-MAY-2003.
XX
PF   25-NOV-2002; 2002WO-EP013265.
XX
PR   23-NOV-2001; 2001DE-01057491.
PR   28-DEC-2001; 2001DE-01064501.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Burger M,  Caldwell C,  Genc B,  Becker E,  Maier S,  Nimmrich I;
XX
DR   WPI; 2003-457621/43.
XX
PT   Detecting and differentiating between lymphoid cell proliferative
PT   disorders comprises contacting a target nucleic acid with at least one
PT   reagent that distinguishes between methylated and non-methylated CpG
PT   dinucleotides.
XX
PS   Claim 30; SEQ ID NO 374; 448pp; English.
XX
CC   The invention relates to a method of detecting and differentiating
CC   between lymphoid cell proliferative disorders associated with at least
CC   one gene and/or their regulatory regions in a subject by contacting a
CC   target nucleic acid in a biological sample obtained from the subject with
CC   at least one reagent or series of reagents that distinguish between
CC   methylated and non-methylated CpG dinucleotides within the target nucleic
CC   acid. The genes and/or their regulatory regions are preferably selected
CC   from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3,
CC   MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
CC   GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC,
CC   GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC   acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC   of the genes are useful for detecting the methylation state of all the
CC   CpG dinucleotides within one or more the sequences, or their complements,
CC   for determining the cytosine methylation state and or single nucleotide
CC   polymorphisms (SNPs), and for differentiating at least two of the medical
CC   conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC   chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC   lymphoma. They are also useful for detecting of a predisposition to,
CC   differentiation between subclasses, diagnosis, prognosis, treating and/or
CC   monitoring of lymphoid cell proliferative disorder. This sequence
CC   represents an oligonucleotide used to analyse of CpG positions within the
CC   above mentioned genes.
XX
SQ   Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||| ||||| ||||||||
Db          1 TTTATTTTTGTTTTTGGG 18
```

RESULT 1323
ADE84488
ID ADE84488 standard; DNA; 18 BP.
XX
AC ADE84488;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human lymphoid cell proliferative disorder gene CpG analysis oligo #194.
XX
KW lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003044226-A2.
XX
PD 30-MAY-2003.
XX
PF 25-NOV-2002; 2002WO-EP013265.
XX
PR 23-NOV-2001; 2001DE-01057491.
PR 28-DEC-2001; 2001DE-01064501.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX
DR WPI; 2003-457621/43.
XX
PT Detecting and differentiating between lymphoid cell proliferative
PT disorders comprises contacting a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated CpG
PT dinucleotides.
XX
PS Claim 30; SEQ ID NO 484; 448pp; English.
XX
CC The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least
CC one gene and/or their regulatory regions in a subject by contacting a
CC target nucleic acid in a biological sample obtained from the subject with
CC at least one reagent or series of reagents that distinguish between
CC methylated and non-methylated CpG dinucleotides within the target nucleic
CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3,
CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC,
CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC CpG dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and or single nucleotide
CC polymorphisms (SNPs), and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting of a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents an oligonucleotide used to analyse of CpG positions within the
CC above mentioned genes.
XX
SQ Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match 0.3%; Score 14.8; DB 1; Length 18;
  Best Local Similarity 88.9%; Pred. No. 9.4e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18
```

RESULT 1324
ADF92108/c
ID ADF92108 standard; DNA; 18 BP.
XX
AC ADF92108;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human cytokeratin 18-related R3 PCR primer - SEQ ID 196.
XX
KW human; cytokeratin; CK; LAMP; loop mediated isothermal amplification;
KW tumour metastasis; prostate cancer; lymphoma; human; CK18; ss; primer;
KW PCR; R3.
XX
OS Homo sapiens.
XX
PN WO2003097878-A1.
XX
PD 27-NOV-2003.
XX
PF 20-MAY-2003; 2003WO-JP006256.
XX
PR 21-MAY-2002; 2002JP-00145689.
PR 17-JUN-2002; 2002JP-00175271.
PR 09-JUL-2002; 2002JP-00199759.
XX
PA (SYSM-) SYSMEX CORP.
XX
PI Tada S, Akai Y, Imura Y, Abe S, Minekawa H;
XX
DR WPI; 2004-012543/01.
XX
PT LAMP nucleic acid amplification primers for detection of cytokeratin
PT expression as indicator in diagnosis of tumour metastasis.
XX
PS Claim 3; SEQ ID NO 196; 266pp; Japanese.
XX
CC The invention relates to novel nucleic acid amplification primers for the
CC detection of human cytokeratin (CK) 18, 19 or 20 expression by the LAMP
CC (loop mediated isothermal amplification) method. The primers of the
CC invention may be useful for the detecting cytokeratin 18-20 expression as
CC an indicator for the diagnosis of tumour metastasis, particularly
CC prostate cancer and lymphoma. The amplification using the primers is
CC highly efficient and allows very sensitive detection of tumour
CC metastasis. The current sequence is that of the human CK18-related PCR
CC primer of the invention.
XX
SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match 0.3%; Score 14.8; DB 1; Length 18;
  Best Local Similarity 88.9%; Pred. No. 9.4e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        893 CCTGGCTTGCTGCTGATG 910
              || | ||||||||||||||
Db         18 CCCGTCTTGCTGCTGATG 1
```

RESULT 1325
ADH70321/c
ID ADH70321 standard; DNA; 18 BP.
XX
AC ADH70321;
XX
DT 25-MAR-2004 (first entry)

XX
DE Human Vbeta gene repeat sequence #111.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 515; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 18 BP; 9 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCT 3198
||||||||| ||| ||||
Db 18 CTCTCTCTCTCTCTCTCT 1

RESULT 1326
ADH70679/c
ID ADH70679 standard; DNA; 18 BP.
XX
AC ADH70679;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #469.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 873; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 18 BP; 9 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;

```
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTC 3199
              ||||||||  |||  |||||
Db         18 TCTCTCTCTCTCTCTCTC 1
```

RESULT 1327
ADQ15984/c
ID ADQ15984 standard; DNA; 18 BP.
XX
AC ADQ15984;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human HES-6 transcriptional modulator reverse PCR primer.
XX
KW Human; transcriptional modulator; splice variant; tumour-specific;
KW tumour-enriched; differential expression; expression pattern; cancer;
KW diagnosis; NRSF; MDM2 TSG; RREB; ZNF207; TTF-1; GTFIIIA; HES-6; HRY;
KW Msx2; neuralised-1; Neu; NeuroD1; Mash-1; Irx-2;
KW variant-specific antibody; autoantibody; diagnostic array; prognosis;
KW lung cancer; gastrointestinal cancer; breast cancer; prostate cancer;
KW skin cancer; sarcoma; endocrine cancer; neural cancer; bladder cancer;
KW cervical cancer; renal cancer; haematopoietic cancer; cytostatic;
KW transcription modulator inhibitor; gene therapy; antibody detection;
KW expression analysis; small cell lung cancer; SCLC; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2004060302-A2.
XX
PD 22-JUL-2004.
XX
PF 24-DEC-2003; 2003WO-US041253.
XX
PR 26-DEC-2002; 2002US-0436693P.
XX
PA (CEMI-) CEMINES LLC.
XX
PI Neuman T, Palm K;
XX
DR WPI; 2004-534307/51.
XX
PT Transcription modulator splice variants, useful in diagnosing or treating
PT cancers such as lung, gastrointestinal, breast, prostate, skin,
PT endocrine, cervical and renal cancer.
XX
PS Example 6; Page 42; 59pp; English.
XX
CC The invention relates to tumour-specific or tumour-enriched splice
CC variants of the human transcription modulators neuralised-1 (hNeu delta
CC NHR1), NeuroD1 (hNeuroD1), Irx-2 (Irx-2A) and Mash-1 (hMash-1-deltaN76)
CC and nucleic acids encoding these splice variants. The invention also
CC relates to a method of diagnosing cancer by determining the expression of
CC at least one splice variant of each of a plurality of transcription
CC modulators, or a plurality of splice variants of at least one
CC transcription modulator, where the splice variants are differentially
CC expressed compared to the wild-type isoform of the corresponding
CC transcription modulator, and where the expression pattern of the splice
CC variants is indicative of cancer. In this method, the transcription
CC modulators whose splice variant expression is analysed are selected from
CC NRSF, MDM2 TSG, RREB, ZNF207, TTF-1, GTFIIIA, HES-6, HRY, Msx2, Neu,
CC NeuroD1, Mash-1 and Irx-2. The invention further relates to a method for
CC the treatment of cancer by administration of a bioactive agent capable of
CC inhibiting the activity of one or more of the transcriptional modulator
CC splice variants; an antibody which binds to a transcription modulator
CC splice variant but not to the wild-type isoform; a peptide which binds to
CC the splice variant-specific antibody; and a diagnostic array for the
CC diagnosis of cancer comprising peptides which are capable of binding to
CC splice variant-specific autoantibodies but not to wild-type isoform-
CC specific autoantibodies. The methods and compositions of the present
CC invention are useful for the diagnosis, prognosis and/or treatment of
CC cancer, such as lung cancer, gastrointestinal cancer, breast cancer,
CC prostate cancer, skin cancer, sarcoma, endocrine cancer, neural cancer,
CC bladder cancer, cervical cancer, renal cancer and haematopoietic cancer.
CC Sequences ADQ15948-ADQ15988 represent PCR primers used in an example of
CC the invention to analyse the expression of various transcription
CC modulator splice variants in small cell lung cancer (SCLC) cells.
XX
SQ Sequence 18 BP; 5 A; 0 C; 12 G; 1 T; 0 U; 0 Other;

```
  Query Match              0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3184 TCTCTCCCTCCCTCTCTC 3201
              ||||||||||||  | |||
Db         18 TCTCTCCCTCCCACCCTC 1
```

RESULT 1328
ADS90292
ID ADS90292 standard; DNA; 18 BP.
XX
AC ADS90292;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:1308.
XX
KW ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Unidentified.
XX
PN WO2004035803-A2.
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
DR WPI; 2004-348468/32.
XX
PT Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
PS Disclosure; SEQ ID NO 1308; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX

```
SQ   Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5056 TGATTGGGTGGGATTTTT 5073
              ||||  ||||||||||||
Db          1 TGATGTGGTGGGATTTTT 18


RESULT 1329
ADS90530/c
ID   ADS90530 standard; DNA; 18 BP.
XX
AC   ADS90530;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Oligonucleotide of the invention SEQ ID NO:1546.
XX
KW   ss; cell proliferative disorder; breast; methylation; cytostatic;
KW   gene therapy; single nucleotide polymorphism; SNP.
XX
OS   Unidentified.
XX
PN   WO2004035803-A2.
XX
PD   29-APR-2004.
XX
PF   01-OCT-2003; 2003WO-EP010881.
XX
PR   01-OCT-2002; 2002DE-01045779.
PR   07-JAN-2003; 2003DE-01000096.
PR   17-APR-2003; 2003DE-01017955.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Foekens J,  Harbeck N,  Koenig T,  Maier S,  Martens J,  Model F;
PI   Nimmrich I,  Rujan T,  Schmitt A,  Schmitt M,  Look MP,  Marx A;
XX
DR   WPI; 2004-348468/32.
XX
PT   Predicting responsiveness of a subject with breast cell proliferative
PT   disorder, useful for treating or differentiating breast cell
PT   proliferative disorders comprises analyzing methylation pattern of a
PT   genomic DNA from the subject.
XX
PS   Disclosure; SEQ ID NO 1546; 104pp; English.
XX
CC   The invention relates to a novel method for predicting the responsiveness
CC   of a subject with a cell proliferative disorder of the breast tissues to
CC   a therapy comprising analysing the methylation pattern of a target
CC   nucleic acid by contacting at least one of the target nucleic acids in a
CC   biological sample obtained from the subject prior to or during treatment.
CC   The method of the invention has cytostatic activity, and may have a use
CC   in gene therapy. The set of oligonucleotides comprising at least two of
CC   the oligomers are useful for detecting the cytosine methylation state
CC   and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC   methods, nucleic acid, oligonucleotide, and kit are useful for the
CC   treatment, characterisation, classification and/or differentiation, of
CC   breast cell proliferative disorders. The method is also useful for
CC   predicting the responsiveness of a subject with a cell proliferative
CC   disorder of the breast tissues to a therapy. The present sequence is used
CC   in the exemplification of the invention.
XX
SQ   Sequence 18 BP; 3 A; 0 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2336 TTCCAAACATCCAAAAAA 2353
              | ||||||||||||||| |
Db         18 TACCAAACATCCAAAATA 1


RESULT 1330
ADB25743/c
ID   ADB25743 standard; DNA; 20 BP.
XX
AC   ADB25743;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Mouse connective tissue growth factor antisense oligo DNA (SeqID 136).
XX
KW   antisense; mouse; murine; ss; connective tissue growth factor; CTGF;
KW   chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW   fisp-12; NOV2;
KW   insulin-like growth factor binding protein-related protein 2; IGFBP-rP2;
KW   IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW   hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW   scleroderma; atherosclerosis; cytostatic; dermatological;
KW   antiarteriosclerotic.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT                    16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT                    5-methylcytidines"
XX
PN   WO2003053340-A2.
XX
PD   03-JUL-2003.
XX
PF   09-DEC-2002; 2002WO-US038618.
XX
PR   10-DEC-2001; 2001US-00006191.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Gaarde WA,  Watt AT;
XX
DR   WPI; 2003-559091/52.
XX
PT   New antisense oligonucleotides for modulating connective tissue growth
PT   factor expression, particularly useful for treating cancers (e.g. breast
PT   or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT   atherosclerosis.
XX
PS   Claim 3; Page 89; 139pp; English.
XX
CC   This invention relates to novel methods for modulating the expression of
CC   connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC   CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC   as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC   insulin-like growth factor binding protein-related protein 2, IGFBP-rP2,
CC   IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC   promote chemotaxis of fibroblasts, however, it is also upregulated in
CC   acute lymphoblastic leukaemia and in tumour or endothelial cells
CC   associated with the vasculature. Accordingly, antisense oligonucleotides
CC   that inhibit the expression of CTGF in cells or tissues can be used in
CC   gene therapy to treat various conditions including hyperproliferative
CC   disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC   pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC   such, the present invention describes these antisense oligos as having
CC   cytostatic, dermatological and antiarteriosclerotic activities. This
CC   oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC   with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC   mouse CTGF of the invention.
XX
```

```
SQ   Sequence 20 BP; 11 A; 1 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACATT 2414
              |||||| ||||||| |||
Db         20 TATATATATATATATATT 3


RESULT 1331
AAD55499
ID   AAD55499 standard; DNA; 20 BP.
XX
AC   AAD55499;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human FGFR-3 antisense oligonucleotide, ISIS #125205.
XX
KW   Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
KW   developmental disorder; hyperproliferative disorder; antisense therapy;
KW   FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidine residues
FT                   are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2 -methoxyethyl (2'-MOE) nucleotides"
FT
XX
PN   WO2003023004-A2.
XX
PD   20-MAR-2003.
XX
PF   06-SEP-2002; 2002WO-US028549.
XX
PR   10-SEP-2001; 2001US-00953047.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Wyatt JR;
XX
DR   WPI; 2003-313244/30.
XX
PT   Novel compound targeted to a nucleic acid molecule encoding fibroblast
PT   growth factor receptor 3, useful for inhibiting the expression of the
PT   receptor and for treating an animal having cancer or developmental
PT   disorder.
XX
PS   Example 15; Page 79; 120pp; English.
XX
CC   The invention relates to antisense compounds targetted to a nucleic acid
CC   molecule encoding fibroblast growth factor (FGF) receptor 3 (also known
CC   as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense
CC   compounds of the invention are useful for treating diseases or conditions
CC   associated with FGFR-3 such as developmental disorders or
CC   hyperproliferative disorders, especially cancer of colorectal, bladder,
CC   bone, lung, cervical, breast or skin. They are useful as research
CC   reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools
CC   in differential and/or combinatorial analyses to elucidate expression
CC   patterns of a portion of the genes expressed within cells and tissues.
CC   They are also useful in antisense therapy. The present sequence is an
CC   antisense oligonucleotide targetted to human FGFR-3
XX
SQ   Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATAC 2411
              ||||||||  ||||||||
Db          1 ATATATATGTATATATAC 18


RESULT 1332
ADG75988/c
ID   ADG75988 standard; DNA; 24 BP.
XX
AC   ADG75988;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Immunostimulatory non-CpG oligonucleotide IMT 037 SeqID 100.
XX
KW   ss; non-CpG; immunostimulatory; non-palindromic; immune response;
KW   proliferation; differentiation; cytokine; antibody production; B-cell;
KW   plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW   chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
KW   renal cell carcinoma.
XX
OS   Synthetic.
XX
PN   WO2003101375-A2.
XX
PD   11-DEC-2003.
XX
PF   30-MAY-2003; 2003WO-EP005691.
XX
PR   30-MAY-2002; 2002CA-02388049.
XX
PA   (IMMU-) IMMUNOTECH SA.
XX
PI   Lopez RA;
XX
DR   WPI; 2004-053333/05.
XX
PT   New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT   acid sequence motif, useful for inducing B-cell activation, treating,
PT   preventing or ameliorating immune system disorder or tumoral disease e.g.
PT   melanoma.
XX
PS   Disclosure; Fig 3; 139pp; English.
XX
CC   This invention relates to novel immunostimulatory oligonucleotides that
CC   contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC   oligonucleotides (without a CpG motif), which can stimulate an immune
CC   response in animals of the order of primate, including humans. The immune
CC   response is characterised by the proliferation, differentiation, cytokine
CC   and antibody production in B-cells, as well as cell differentiation and
CC   cytokine production in plasmacytoid dendritic cells. The present
CC   invention describes immunomodulator compositions that also comprise an
CC   antigen selected from, for example, viruses, bacteria, parasites, tumour
CC   cells and glycolipids. As such, these DNA oligos can be used in gene
CC   therapy for inducing B-cell activation, treating, preventing or
CC   ameliorating an immune system disorder or a tumoural disease including
CC   chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC   carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG
CC   variant DNA oligo, used in an exemplification of the invention.
XX
SQ   Sequence 24 BP; 0 A; 3 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.8;  DB 1;  Length 24;
```

```
  Best Local Similarity   88.9%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| |||
Db         22 GAAAAAAAGAAAAAAAGA 5


RESULT 1333
AAS99971
ID   AAS99971 standard; DNA; 15 BP.
XX
AC   AAS99971;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human NPR1 gene allele-specific oligonucleotide probe #13.
XX
KW   Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
KW   atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
KW   haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
KW   drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200179231-A2.
XX
PD   25-OCT-2001.
XX
PF   16-APR-2001; 2001WO-US012300.
XX
PR   14-APR-2000; 2000US-0197330P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Kliem SE,  Nandabalan K;
XX
DR   WPI; 2002-066340/09.
XX
PT   Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
PT   an individual, involves determining identity of nucleotide pair at
PT   specific polymorphic sites for two copies of the gene.
XX
PS   Claim 15; Page 14; 96pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding the human natriuretic peptide receptor A/guanylate cyclase A
CC   (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for
CC   haplotyping the NPR1 gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the NPR1 haplotypes given
CC   in the specification or whether both copies are defined by a haplotype
CC   pair. This method is useful in genotyping, whereby all possible haplotype
CC   pairs can be assigned to specific genotypes. An association between a
CC   trait and a haplotype or haplotype pair of the NPR1 gene can be
CC   identified by comparing the frequency of the haplotype or haplotype pair
CC   in a population exhibiting the trait with the frequency of the haplotype
CC   or haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. NPR1 and its corresponding DNA are used
CC   for studying the expression and function of NPR1, for use in screening
CC   for candidate drugs to treat diseases related to NPR1 activity, such as
CC   hypertension. The sequences are also useful for studying the effect of
CC   variation on the biological activity of NPR1 as well as on the binding
CC   affinity of candidate drugs targeting NPR1. Sequences AAS99959-AAS99990
CC   and ABK09390-ABK09462 represent probes, sequencing primers and PCR
CC   primers used to detect NPR1 gene polymorphisms
XX
SQ   Sequence 15 BP; 2 A; 4 C; 3 G; 5 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.6;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 8.6e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4693 ACTTGCTGTGTGACC 4707
              |||||||:|||||||
Db          1 ACTTGCTRTGTGACC 15


RESULT 1334
ABK32799/c
ID   ABK32799 standard; DNA; 15 BP.
XX
AC   ABK32799;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human APPBP1 gene, allele-specific oligonucleotide #29.
XX
KW   Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;
KW   Alzheimer's disease; transgenic animal; platelet aggregation;
KW   single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO200202820-A1.
XX
PD   10-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-US020951.
XX
PR   30-JUN-2000; 2000US-0215511P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Chew A,  Choi JY,  Kazemi A,  Koshy B,  Sausker EA;
PI   Stephens CJ;
XX
DR   WPI; 2002-164539/21.
XX
PT   Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene
PT   polymorphic variants, useful e.g. in studying the expression and function
PT   of APPBP1 and screening candidate drugs for treating Alzheimer's disease.
XX
PS   Claim 17; Page 13; 104pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising a sequence
CC   which is a polymorphic variant of a reference sequence for the amyloid
CC   beta precursor protein binding protein 1, 59kD (APPBP1) protein or its
CC   fragment. The polymorphic variants are useful in studying the expression
CC   and function of APPBP1, in expressing APPBP1 protein for use in screening
CC   for candidate drugs to treat diseases related to APPBP1 activity, in
CC   studying the effect of the variation on the biological activity of
CC   APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for
CC   the treatment of disorders such as Alzheimer's disease. The haplotyping
CC   methods are useful in validating APPBP1 as a candidate target for
CC   treating a specific condition or disease predicted to be associated with
CC   APPBP1 activity, or in the design of clinical trials of candidate drugs
CC   for treating a specific condition or disease associated with APPBP1
CC   activity. The transgenic animals are useful for studying expression of
CC   the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs
CC   targeted against APPBP1 protein, and for testing the efficacy of
CC   therapeutic agents and compounds for disorders related to platelet
CC   aggregation in a biological system. ABK32771-ABK32327 represent human
CC   APPBP1 gene allele-specific oligonucleotides used in the method of the
CC   invention
XX
SQ   Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.6;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 8.6e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              |:|||||||||||||
Db         15 TYTTTTTTTTTTTTG 1
```

```
RESULT 1335
AAQ83416/c
ID   AAQ83416 standard; DNA; 16 BP.
XX
AC   AAQ83416;
XX
DT   25-MAR-2003  (revised)
DT   20-SEP-1995  (first entry)
XX
DE   c-fos antisense oligonucleotide.
XX
KW   c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
KW   phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO9502051-A2.
XX
PD   19-JAN-1995.
XX
PF   06-JUL-1994;   94WO-EP002218.
XX
PR   10-JUL-1993;   93EP-00111059.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen G,  Schlingensiepen R,  Schlingensiepen K,  Brysch W;
XX
DR   WPI; 1995-066896/09.
XX
PT   Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
PT   treating neuronal injury, degeneration, cell death and/or neoplasms.
XX
PS   Claim 2; Page 61; 86pp; English.
XX
CC   Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
CC   comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC   causal role in neuronal injury, degeneration, cell death and/ or
CC   neoplasms, can be used to prevent and treat such conditions. c-jun
CC   antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC   antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC   fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC   Preferably the antisense sequences are phosphorothioate oligonucleotides
CC   since these are not destroyed as fast by endogenous factors as naturally
CC   occuring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 16 BP; 3 A; 6 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2314 AGTAATAAGATGGCTG 2329
              || |||||||||||||
Db         16 AGGAATAAGATGGCTG 1


RESULT 1336
AAX18360
ID   AAX18360 standard; DNA; 16 BP.
XX
AC   AAX18360;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 1.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTTCG 16


RESULT 1337
AAX18368
ID   AAX18368 standard; DNA; 16 BP.
XX
AC   AAX18368;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 9.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
```

```
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||
Db          1 TTTTTTTTTTTTTTAG 16


RESULT 1338
AAX82792
ID   AAX82792 standard; DNA; 16 BP.
XX
AC   AAX82792;
XX
DT   29-JUN-2000  (first entry)
XX
DE   Chicken cytochrome b PCR primer 1R.
XX
KW   Cytochrome b; chicken; PCR primer; forensic; raw materials; cosmetic;
KW   contamination; ss.
XX
OS   Gallus sp.
XX
PN   DE19842991-A1.
XX
PD   23-MAR-2000.
XX
PF   21-SEP-1998;   98DE-01042991.
XX
PR   21-SEP-1998;   98DE-01042991.
XX
PA   (BEHR/) BEHRENS M.
PA   (UNTH/) UNTHAN M.
PA   (LATU/) LATUS N.
XX
PI   Behrens M,  Unthan M,  Latus N;
XX
DR   WPI; 2000-257940/23.
XX
PT   Novel methods and primers for genetic analysis of biological material by
PT   polymerase chain reaction using specific primer pairs useful in, e.g.
PT   forensic medicine.
XX
PS   Claim 2; Col 5; 10pp; German.
XX
CC   This invention describes a novel method for determining the origin of
CC   biological material by PCR using specific primers pairs, which are
CC   exclusively complementary to the respective animal or plant DNA. The
CC   method and primers are useful in forensic medicine or in purity testing
CC   raw materials, end products, cosmetics or pharmaceuticals. The methods
CC   are useful for determining if there has been contamination of biological
CC   materials. AAX82791-X82812 represent the PCR primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 16 BP; 4 A; 1 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3379 CTTGTAGAAGTAGGAG 3394
              ||||||| |||||||
Db          1 CTTGTAGAGGTAGGAG 16


RESULT 1339
AAX82793/c
ID   AAX82793 standard; DNA; 16 BP.
XX
AC   AAX82793;
XX
DT   29-JUN-2000  (first entry)
XX
DE   Chicken cytochrome b PCR primer 2U.
XX
KW   Cytochrome b; chicken; PCR primer; forensic; raw materials; cosmetic;
KW   contamination; ss.
XX
OS   Gallus sp.
XX
PN   DE19842991-A1.
XX
PD   23-MAR-2000.
XX
PF   21-SEP-1998;   98DE-01042991.
XX
PR   21-SEP-1998;   98DE-01042991.
XX
PA   (BEHR/) BEHRENS M.
PA   (UNTH/) UNTHAN M.
PA   (LATU/) LATUS N.
XX
PI   Behrens M,  Unthan M,  Latus N;
XX
DR   WPI; 2000-257940/23.
XX
PT   Novel methods and primers for genetic analysis of biological material by
PT   polymerase chain reaction using specific primer pairs useful in, e.g.
PT   forensic medicine.
XX
PS   Claim 2; Col 5; 10pp; German.
XX
CC   This invention describes a novel method for determining the origin of
CC   biological material by PCR using specific primers pairs, which are
CC   exclusively complementary to the respective animal or plant DNA. The
CC   method and primers are useful in forensic medicine or in purity testing
CC   raw materials, end products, cosmetics or pharmaceuticals. The methods
CC   are useful for determining if there has been contamination of biological
CC   materials. AAX82791-X82812 represent the PCR primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 16 BP; 4 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3379 CTTGTAGAAGTAGGAG 3394
              ||||||| |||||||
Db         16 CTTGTAGAGGTAGGAG 1


RESULT 1340
ABL57076
ID   ABL57076 standard; DNA; 16 BP.
XX
AC   ABL57076;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence (single mismatch).
```

XX
KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 9
FT /*tag= a
FT /note= "mismatch site"
XX
PN WO200218951-A2.
XX
PD 07-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US041941.
XX
PR 29-AUG-2000; 2000US-0228728P.
PR 30-MAR-2001; 2001US-0280350P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Dubertret B, Calame M, Libchaber A;
XX
DR WPI; 2002-404569/43.
XX
PT Sensitively detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.
XX
PS Example 3; Page 30; 62pp; English.
XX
CC The present sequence is that of a single mismatch target sequence for a
CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC a nanoparticle. In the native state, the probe forms a hairpin
CC conformation with hybridised termini. The proximity of the fluorophore
CC and quencher (gold nanoparticle) in the molecular beacon results in
CC little or no detectable fluorescence. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, such as the
CC present sequence, the hairpin undergoes a conformational change resulting
CC in an increase in fluorescence, the extent of which is proportional to
CC the amount of target sequence present. Experiments with the present
CC sequence and a perfectly-matched target (see ABL57071) showed that
CC hybridisation was very specific to the matched target. The invention
CC relates generally to the use of metal surface quenchers such as particles
CC or films for high sensitivity applications in, for example, detection and
CC diagnostic systems
XX
SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACA 3619
||||||||||||| |
Db 1 GAAAAAAACAAAAAAA 16

RESULT 1341
ABK90419
ID ABK90419 standard; DNA; 16 BP.
XX
AC ABK90419;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human UGT1a1 promoter polymorphism (TA)8 repeat.
XX
KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
KW TAS-103; xenobiotic.
XX
OS Homo sapiens.
XX
PN US6395481-B1.
XX
PD 28-MAY-2002.
XX
PF 16-FEB-1999; 99US-00251274.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Di Rienzo A, Iyer L, Ratain MJ;
XX
DR WPI; 2002-588597/63.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient,
PT comprises determining the presence of five thymidine-adenine repeats in
PT the promoter.
XX
PS Claim 7; Col 17; 13pp; English.
XX
CC The invention relates to detecting (M1) polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
CC the presence of five thymidine-adenine (TA) repeats in the promoter,
CC where the presence of the five TA repeats correlates with increased
CC expression of the gene. The method is used for detecting polymorphisms in
CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is
CC useful for screening individuals for variation in glucuronidation
CC activity, for optimising drug dosages for a patient, where the drugs
CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
CC UGT1A1) and the activity of the drug is effected by its level of
CC glucurodination. The method preferably involves obtaining DNA from an
CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
CC promoter) contained in the DNA and determining the number of TA repeats
CC in the promoter. Thus the DNA being amplified comprises all or part of
CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
CC the number of TA repeats is determined by gel electrophoresis or by
CC sequencing the amplified DNA. The polymorphism comprises an allele
CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
CC (TA)8/(TA)8. (M1) is also useful for predicting an individuals
CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
CC UGT1A1) gene product, the method comprising determining the number of TA
CC repeats in a UGT gene promoter, where the number of TA repeats correlates
CC with expression of the UGT gene, and the individuals sensitivity to
CC xenobiotics is effected by glucuronidation activity. The methods
CC preferably involve determining the presence of five, six or seven TA
CC repeats in the promoter. Defects in glucurodination is associated with
CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
CC present sequence is the UGT1A1 promoter (TA)8 repeat
XX
SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
|||||||| |||||||
Db 1 TATATATATATATATA 16

RESULT 1342
ABK90419/c
ID ABK90419 standard; DNA; 16 BP.
XX
AC ABK90419;
XX
DT 05-NOV-2002 (first entry)

XX
DE Human UGT1a1 promoter polymorphism (TA)8 repeat.
XX
KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
KW TAS-103; xenobiotic.
XX
OS Homo sapiens.
XX
PN US6395481-B1.
XX
PD 28-MAY-2002.
XX
PF 16-FEB-1999; 99US-00251274.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Di Rienzo A, Iyer L, Ratain MJ;
XX
DR WPI; 2002-588597/63.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient,
PT comprises determining the presence of five thymidine-adenine repeats in
PT the promoter.
XX
PS Claim 7; Col 17; 13pp; English.
XX
CC The invention relates to detecting (M1) polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
CC the presence of five thymidine-adenine (TA) repeats in the promoter,
CC where the presence of the five TA repeats correlates with increased
CC expression of the gene. The method is used for detecting polymorphisms in
CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is
CC useful for screening individuals for variation in glucuronidation
CC activity, for optimising drug dosages for a patient, where the drugs
CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
CC UGT1A1) and the activity of the drug is effected by its level of
CC glucurodination. The method preferably involves obtaining DNA from an
CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
CC promoter) contained in the DNA and determining the number of TA repeats
CC in the promoter. Thus the DNA being amplified comprises all or part of
CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
CC the number of TA repeats is determined by gel electrophoresis or by
CC sequencing the amplified DNA. The polymorphism comprises an allele
CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
CC (TA)8/(TA)8. (M1) is also useful for predicting an individuals
CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
CC UGT1A1) gene product, the method comprising determining the number of TA
CC repeats in a UGT gene promoter, where the number of TA repeats correlates
CC with expression of the UGT gene, and the individuals sensitivity to
CC xenobiotics is effected by glucuronidation activity. The methods
CC preferably involve determining the presence of five, six or seven TA
CC repeats in the promoter. Defects in glucurodination is associated with
CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
CC present sequence is the UGT1A1 promoter (TA)8 repeat
XX
SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
||||||| |||||||
Db 16 TATATATATATATATA 1

RESULT 1343
AAL50677
ID AAL50677 standard; DNA; 16 BP.
XX
AC AAL50677;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #11.
XX
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
OS Homo sapiens.
XX
PN US2002115097-A1.
XX
PD 22-AUG-2002.
XX
PF 01-FEB-2002; 2002US-00061693.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Rienzo AD, Iyer L, Ratain MJ;
XX
DR WPI; 2002-740095/80.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
PS Claim 7; Page 9; 13pp; English.
XX
CC The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
||||||| |||||||
Db 1 TATATATATATATATA 16

RESULT 1344
AAL50677/c
ID AAL50677 standard; DNA; 16 BP.
XX
AC AAL50677;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #11.
XX
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
OS Homo sapiens.

XX
PN US2002115097-A1.
XX
PD 22-AUG-2002.
XX
PF 01-FEB-2002; 2002US-00061693.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Rienzo AD, Iyer L, Ratain MJ;
XX
DR WPI; 2002-740095/80.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
PS Claim 7; Page 9; 13pp; English.
XX
CC The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
||||||||.|||||||
Db 16 TATATATATATATATA 1

RESULT 1345
ABL45022/c
ID ABL45022 standard; DNA; 16 BP.
XX
AC ABL45022;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:2066.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 45; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 16 BP; 5 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4696 TGCTGTGTGACCCTGG 4711
||||||||.|||||||
Db 16 TGCTGTGTCACCCTGG 1

RESULT 1346
AAD44147
ID AAD44147 standard; DNA; 16 BP.
XX
AC AAD44147;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #7 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
OS Unidentified.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broaddus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Fig 1C; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed

```
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              | ||||||||||||||
Db          1 GVTTTTTTTTTTTTT 16


RESULT 1347
AAD57846
ID   AAD57846 standard; DNA; 16 BP.
XX
AC   AAD57846;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #3 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20-B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||||||||||  |
Db          1 GAAAAAAACAAAAAAA 16


RESULT 1348
ADF23332
ID   ADF23332 standard; DNA; 16 BP.
XX
AC   ADF23332;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Binding partner sceening method molecular beacon analogue #3.
XX
KW   binding partner screening; light beam; nonlinear optical light beam; ss;
KW   molecular beacon analogue.
XX
OS   Synthetic.
XX
PN   US2003148391-A1.
XX
PD   07-AUG-2003.
XX
PF   06-JUN-2002; 2002US-00164915.
XX
PR   24-JAN-2002; 2002US-0351879P.
PR   06-FEB-2002; 2002US-0354668P.
PR   06-FEB-2002; 2002US-0354679P.
PR   05-MAR-2002; 2002US-0362003P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-897567/82.
XX
PT   Screening of candidate binding partners for binding to test molecule
PT   comprises illuminating sample with light beams and measuring physical
PT   properties of nonlinear optical light beam emanating from sample.
XX
PS   Disclosure; SEQ ID NO 3; 58pp; English.
XX
CC   The invention describes screening a candidate binding partner by
CC   illuminating the sample with light beams at fundamental frequencies to
CC   binding partners, and measuring physical properties of a nonlinear
CC   optical light beam emanating from sample. On binding to the test molecule
CC   the properties change relative to that in absence of exposure of the test
CC   molecule. The invention is used in the screening of candidate binding
CC   partners for binding to test molecule. This sequence represents a
CC   molecular beacon analogue, an exemplary test molecule of the invention.
XX
SQ   Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||||||||||  |
Db          1 GAAAAAAACAAAAAAA 16


RESULT 1349
ADI20623
ID   ADI20623 standard; DNA; 16 BP.
XX
AC   ADI20623;
XX
DT   15-APR-2004  (first entry)
XX
DE   Putative eRNA sequence #32.
XX
KW   ds; eRNA.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO2003025229-A1.
```

XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-AU001286.
XX
PR 19-SEP-2001; 2001US-0324127P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Mattick J, Gagen M, Stanley S;
XX
DR WPI; 2003-371830/35.
XX
PT Identifying an eRNA or a DNA sequence comprising an eRNA-encoding
PT sequence in the nucleome of a eukaryotic cell, comprising identifying non
PT -protein-encoding nucleotide sequences within an mRNA transcript or a DNA
PT sequence.
XX
PS Example 14; SEQ ID NO 113; 137pp; English.
XX
CC The present invention relates to identifying an eRNA or a DNA sequence
CC comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell
CC comprises identifying non-protein-encoding nucleotide sequences within an
CC mRNA transcript or a DNA sequence encoding same in the nucleome. The
CC methods are useful for identifying an eRNA or DNA for modifying a genetic
CC network in cell to alter the cells phenotype. The present sequence
CC represents a putative eRNA sequence of the invention.
XX
SQ Sequence 16 BP; 0 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||| ||||||
Db 1 TTTTTTTTTGTTTTTG 16

RESULT 1350
ADH70346
ID ADH70346 standard; DNA; 16 BP.
XX
AC ADH70346;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #136.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 540; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2394 ATATATATACATATAT 2409
||||||||| ||||||
Db 1 ATATATATATATATAT 16

RESULT 1351
ADH70346/c
ID ADH70346 standard; DNA; 16 BP.
XX
AC ADH70346;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #136.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX

PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 540; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2394 ATATATATACATATAT 2409
||||||||| ||||||
Db 16 ATATATATATATATAT 1

RESULT 1352
ADH70379
ID ADH70379 standard; DNA; 16 BP.
XX
AC ADH70379;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #169.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 573; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 16 BP; 0 A; 9 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCT 3196
||||||||||||| ||
Db 1 CTCTCTCTCCCTCTCT 16

RESULT 1353
ADH70276
ID ADH70276 standard; DNA; 16 BP.
XX
AC ADH70276;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #66.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;

KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 470; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 16 BP; 0 A; 3 C; 0 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTTCTTTTTT 2139
||||||||||||| |
Db 1 TTTTCTTTTCTTTTCT 16

RESULT 1354
ADH70347
ID ADH70347 standard; DNA; 16 BP.
XX
AC ADH70347;
XX

DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #137.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 541; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 16 BP; 8 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2397 TATATACATATATACA 2412
||||||||||||| |
Db 1 TATATACATATATATA 16

```
RESULT 1355
ADR33544
ID   ADR33544 standard; DNA; 16 BP.
XX
AC   ADR33544;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent target DNA #1085.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 1; Page 89; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. This sequence
CC   corresponds to nucleic acid used in the method of the invention.
XX
SQ   Sequence 16 BP; 8 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2071 TAAAGAAAAGACATTT 2086
              ||||||||||||  |||
Db          1 TAAAGAAAAGACGTTT 16


RESULT 1356
ADR33311/c
ID   ADR33311 standard; DNA; 16 BP.
XX
AC   ADR33311;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent target DNA #852.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 1; Page 85; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. This sequence
CC   corresponds to nucleic acid used in the method of the invention.
XX
SQ   Sequence 16 BP; 4 A; 3 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2071 TAAAGAAAAGACATTT 2086
              ||||||||||| |||
Db         16 TAAAGAAAAGACGTTT 1
```

RESULT 1357
ADS15827
ID ADS15827 standard; DNA; 16 BP.
XX
AC ADS15827;
XX
DT 02-DEC-2004 (first entry)
XX
DE Control probe targeted to labelled/bound oligo in binding analysis.
XX
KW binding; sequence detection; reaction kinetics; ss; probe.
XX
OS Synthetic.
XX
PN DE10307801-A1.
XX
PD 09-SEP-2004.
XX
PF 24-FEB-2003; 2003DE-01007801.
XX
PR 24-FEB-2003; 2003DE-01007801.
XX
PA (ADVA-) ADVALYTIX AG.
XX
PI Kirchner R, Gauer C;
XX
DR WPI; 2004-654186/64.
XX
PT Analyzing binding between macromolecules, useful for detecting nucleic
PT acids by hybridization, where a labeled detector molecule is immobilized
PT and becomes fluorescent only after specific binding.
XX
PS Example; Page 6; 11pp; German.
XX
CC The invention relates to a novel analytical method for examining binding
CC events between first and second macromolecules. The method comprises
CC preparing a surface on which a fluorescently-labelled first macromolecule
CC is bound and which is at least partly fitted with a fluorescence-
CC suppressing layer. A sample liquid containing the second macromolecule is
CC applied and fluorescence is measured. The first macromolecule has a
CC secondary structure such that its fluorescence is suppressed by the
CC suppressing layer when it is not specifically bound to the second
CC macromolecule, but fluorescence is not suppressed when the two
CC macromolecules are specifically bound. The method of the invention may be
CC used to detect hybridisation of RNA or, particularly DNA, especially for
CC detecting the presence of particular sequences in samples, but also for
CC studying reaction kinetics. The method allows the use of molecular
CC beacons that are simple to prepare or synthesise, particularly because
CC they do not require incorporation of a quencher. The current sequence is
CC that of the control probe of the invention which is targeted to the
CC fluorescent-labelled and bound DNA oligonucleotide in the binding
CC analysis method.
XX
SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match   0.3%; Score 14.4; DB 1; Length 16;
  Best Local Similarity   93.8%; Pred. No. 9.8e+02;
  Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||||||||||  |
Db          1 GAAAAAAACAAAAAAA 16
```

RESULT 1358
AAT81559
ID AAT81559 standard; RNA; 17 BP.
XX
AC AAT81559;
XX
DT 14-DEC-1997 (first entry)
XX
DE Human c-myb hammerhead ribozyme target sequence (nt. position 2898).
XX
KW Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
KW coronary angioplasty; ss.
XX
OS Homo sapiens.
XX
PN WO9531541-A2.
XX
PD 23-NOV-1995.
XX
PF 18-MAY-1995; 95WO-US006368.
XX
PR 18-MAY-1994; 94US-00245466.
PR 13-JAN-1995; 95US-00373124.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
XX
DR WPI; 1996-010927/01.
XX
PT New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
PT for treating restenosis or cancer.
XX
PS Claim 1; Page 78; 128pp; English.
XX
CC The present sequence represents the preferred target sequence for an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the human c-myb sequence at the base position indicated in the descriptor
CC line. The c-myb sequence was screened for optimal ribozyme target sites
CC using a computer folding algorithm, and regions of the mRNA which did not
CC form secondary folding structures and contained potential ribozyme
CC cleavage sites were identified. Ribozymes were synthesised and their
CC activities optimised by either varying the length of the binding arms or
CC by modification to prevent degradation by nucleases. The ribozymes cleave
CC the c-myb sequence and can be used to prevent smooth muscle cell
CC hyperproliferation in restenosis, especially after coronary angioplasty,
CC and in cancers
XX
SQ Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

  Query Match   0.3%; Score 14.4; DB 1; Length 17;
  Best Local Similarity   50.0%; Pred. No. 1e+03;
  Matches   8; Conservative   7; Mismatches   1; Indels   0; Gaps   0;

```
Qy       2399 TATACATATATACATT 2414
              :|:| |:|:|:|||::
Db          2 UAUAUAUAUAUACAUU 17
```

RESULT 1359
AAX69798
ID AAX69798 standard; RNA; 17 BP.
XX
AC AAX69798;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1093.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.

XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 6.2%; Pred. No. 1e+03;
Matches 1; Conservative 14; Mismatches 1; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTT 4514
| ::::::::::::::
Db 2 ACUUUUUUUUUUUUUU 17

RESULT 1360
AAX69804/c
ID AAX69804 standard; RNA; 17 BP.
XX
AC AAX69804;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3602 TGGAAAAAAACAAAAA 3617
||||||||| |||||
Db 16 TGGAAAAAAAAAAAAA 1

RESULT 1361
AAX69803/c
ID AAX69803 standard; RNA; 17 BP.
XX
AC AAX69803;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.

```
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAA 3617
              |||||||||| |||||
Db         17 TGGAAAAAAAAAAAAA 2


RESULT 1362
AAX73165/c
ID   AAX73165 standard; RNA; 17 BP.
XX
AC   AAX73165;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #598.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Mus sp.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 142; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3471 GTCAGGGTGAACTGCA 3486
              ||||| ||||||||||
Db         17 GTCAGCGTGAACTGCA 2


RESULT 1363
AAA19027
ID   AAA19027 standard; RNA; 17 BP.
XX
AC   AAA19027;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human TIE-2 substrate sequence SEQ ID NO:2253.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  Mcswiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or stability
PT   of an mRNA encoding an angiogenic factors.
XX
PS   Claim 56; Page 132; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
```

```
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ   Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 1e+03;
  Matches    2;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTT 2139
              :::|::::|:::: :
Db          1 UUUUCUUUUCUUUUCU 16


RESULT 1364
AAA22602
ID   AAA22602 standard; RNA; 17 BP.
XX
AC   AAA22602;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Integrin subunit beta 3 substrate sequence SEQ ID NO:5828.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  Mcswiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or stability
PT   of an mRNA encoding an angiogenic factors.
XX
PS   Claim 54; Page 230; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ   Sequence 17 BP; 0 A; 3 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 1e+03;
  Matches    2;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2129 TTTTCTTTTTTTCTTT 2144
              ::::|::: :::|:::
Db          2 UUUUCUUUCUUUCUUU 17


RESULT 1365
AAA22593
ID   AAA22593 standard; RNA; 17 BP.
XX
AC   AAA22593;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Integrin subunit beta 3 substrate sequence SEQ ID NO:5819.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  Mcswiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or stability
PT   of an mRNA encoding an angiogenic factors.
XX
PS   Claim 54; Page 230; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
```

CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 0 A; 3 C; 0 G; 0 T; 14 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 12.5%; Pred. No. 1e+03;
Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

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Qy       2124 TTTTCTTTTCTTTTTT 2139
              ::::|::: |::::::
Db          2 UUUUCUUUCCUUUUUU 17
```

RESULT 1366
AAA19024
ID AAA19024 standard; RNA; 17 BP.
XX
AC AAA19024;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:2250.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
DR WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 131; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 2 C; 3 G; 0 T; 11 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 1e+03;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

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Qy       2121 GGGTTTTCTTTTCTTT 2136
              || ::::|::::|:::
Db          2 GGAUUUUCUUUUCUUU 17
```

RESULT 1367
AAA22603
ID AAA22603 standard; RNA; 17 BP.
XX
AC AAA22603;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5829.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
DR WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 231; 305pp; English.
XX

```
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ   Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 1e+03;
  Matches    2;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2129 TTTTCTTTTTTTCTTT 2144
              :::: ::: :::|:::
Db          1 UUUUCUUUCUUUCUUU 16


RESULT 1368
AAA22594
ID   AAA22594 standard; RNA; 17 BP.
XX
AC   AAA22594;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Integrin subunit beta 3 substrate sequence SEQ ID NO:5820.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  Mcswiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or stability
PT   of an mRNA encoding an angiogenic factors.
XX
PS   Claim 54; Page 230; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ   Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 1e+03;
  Matches    2;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTT 2139
              :::: ::: |::::::
Db          1 UUUUCUUUCCUUUUUU 16


RESULT 1369
AAA19026
ID   AAA19026 standard; RNA; 17 BP.
XX
AC   AAA19026;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human TIE-2 substrate sequence SEQ ID NO:2252.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
```

XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
DR WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 132; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 3 C; 0 G; 0 T; 13 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 12.5%; Pred. No. 1e+03;
Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTTCTTTTTT 2139
:::: |:::: |:::: :
Db 2 UUUUCUUUUCUUUUCU 17

RESULT 1370
AAA19025
ID AAA19025 standard; RNA; 17 BP.
XX
AC AAA19025;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:2251.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
DR WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 132; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 3 C; 1 G; 0 T; 12 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 1e+03;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 2122 GGTTTTCTTTTCTTTT 2137
| :::: |:::: |::::
Db 1 GAUUUUCUUUUCUUUU 16

RESULT 1371
AAZ21177
ID AAZ21177 standard; DNA; 17 BP.
XX
AC AAZ21177;
XX
DT 23-NOV-1999 (first entry)
XX
DE Mouse inhibitor for caspase-activating DNase PCR primer #2.
XX
KW Mouse; caspase activating DNase; CAD; inhibitor; ICAD; ICAD-L; ICAD-S;
KW cell death; PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN JP11239495-A.
XX
PD 07-SEP-1999.
XX
PF 25-DEC-1998; 98JP-00369222.

```
XX
PR   25-DEC-1997;   97JP-00369356.
XX
PA   (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.
XX
DR   WPI; 1999-554024/47.
XX
PT   Inhibitor for caspase-activating DNase - useful for preventing cell death
PT   and is useful as reagent for cell death.
XX
PS   Example 2; Page 10; 26pp; Japanese.
XX
CC   The present invention describes an inhibitor (ICAD) for caspase-
CC   activating DNase (CAD). Two ICAD's are specifically claimed: a long chain
CC   form (ICAD-L) and a short chain form (ICAD-S). ICAD and ICAD cDNA can be
CC   used in the prevention of cell death, and can be used as a research
CC   reagent for cell death. The present sequence represent a PCR primer for
CC   mouse ICAD, which is used in an example from the present invention
XX
SQ   Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4173 GATAAACTCAGATCTG 4188
              ||||||||||| ||||
Db          1 GATAAACTCAGCTCTG 16


RESULT 1372
AAA25445
ID   AAA25445 standard; DNA; 17 BP.
XX
AC   AAA25445;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1943.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4497 TAAGTTTTTTTTTTTT 4512
              | ||||||||||||||
Db          2 TTAGTTTTTTTTTTTT 17


RESULT 1373
ABK02864/c
ID   ABK02864 standard; RNA; 17 BP.
XX
AC   ABK02864;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human CD20 Hammerhead ribozyme #163.
XX
KW   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW   cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW   muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW   DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW   B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW   human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW   MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW   inflammatory arthropathy; central nervous system injury;
KW   cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW   chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW   Parkinson's disease; ataxia; Huntington's disease;
KW   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US004273.
XX
PR   11-FEB-2000; 2000US-0181797P.
PR   28-FEB-2000; 2000US-0185516P.
PR   06-MAR-2000; 2000US-0187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (CHOW/) CHOWRIRA B M.
XX
PI   Blatt L,  Mcswiggen J,  Chowrira BM;
XX
DR   WPI; 2001-607195/69.
XX
```

PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 30; Page 142; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^2^+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targetting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg^2^+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
XX
SQ Sequence 17 BP; 7 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5120 TTGGAATAATTTCTAT 5135
||||||||||||| ||
Db 16 TTGGAATAATTTCAAT 1

RESULT 1374
ABK90422
ID ABK90422 standard; DNA; 17 BP.
XX
AC ABK90422;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human UGT1a1 promoter polymorphism (TA)7 repeat region.
XX
KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
KW TAS-103; xenobiotic.
XX
OS Homo sapiens.
XX
PN US6395481-B1.
XX
PD 28-MAY-2002.
XX
PF 16-FEB-1999; 99US-00251274.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Di Rienzo A, Iyer L, Ratain MJ;
XX
DR WPI; 2002-588597/63.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient,
PT comprises determining the presence of five thymidine-adenine repeats in
PT the promoter.
XX
PS Example 6; Col 11; 13pp; English.
XX
CC The invention relates to detecting (M1) polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
CC the presence of five thymidine-adenine (TA) repeats in the promoter,
CC where the presence of the five TA repeats correlates with increased
CC expression of the gene. The method is used for detecting polymorphisms in
CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is
CC useful for screening individuals for variation in glucuronidation
CC activity, for optimising drug dosages for a patient, where the drugs
CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
CC UGT1A1) and the activity of the drug is effected by its level of
CC glucurodination. The method preferably involves obtaining DNA from an
CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
CC promoter) contained in the DNA and determining the number of TA repeats
CC in the promoter. Thus the DNA being amplified comprises all or part of
CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
CC the number of TA repeats is determined by gel electrophoresis or by
CC sequencing the amplified DNA. The polymorphism comprises an allele
CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
CC (TA)8/(TA)8. (M1) is also useful for predicting an individuals
CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
CC UGT1A1) gene product, the method comprising determining the number of TA
CC repeats in a UGT gene promoter, where the number of TA repeats correlates
CC with expression of the UGT gene, and the individuals sensitivity to
CC xenobiotics is effected by glucuronidation activity. The methods
CC preferably involve determining the presence of five, six or seven TA
CC repeats in the promoter. Defects in glucurodination is associated with
CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
CC present sequence is the UGT1A1 promoter (TA)7 repeat region
XX
SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
|||||||| |||||||
Db 1 TATATATATATATATA 16

RESULT 1375
ABK90422/c
ID ABK90422 standard; DNA; 17 BP.
XX
AC ABK90422;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human UGT1a1 promoter polymorphism (TA)7 repeat region.
XX
KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
KW TAS-103; xenobiotic.
XX
OS Homo sapiens.

XX
PN US6395481-B1.
XX
PD 28-MAY-2002.
XX
PF 16-FEB-1999; 99US-00251274.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Di Rienzo A, Iyer L, Ratain MJ;
XX
DR WPI; 2002-588597/63.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient,
PT comprises determining the presence of five thymidine-adenine repeats in
PT the promoter.
XX
PS Example 6; Col 11; 13pp; English.
XX
CC The invention relates to detecting (M1) polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
CC the presence of five thymidine-adenine (TA) repeats in the promoter,
CC where the presence of the five TA repeats correlates with increased
CC expression of the gene. The method is used for detecting polymorphisms in
CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is
CC useful for screening individuals for variation in glucuronidation
CC activity, for optimising drug dosages for a patient, where the drugs
CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
CC UGT1A1) and the activity of the drug is effected by its level of
CC glucurodination. The method preferably involves obtaining DNA from an
CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
CC promoter) contained in the DNA and determining the number of TA repeats
CC in the promoter. Thus the DNA being amplified comprises all or part of
CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
CC the number of TA repeats is determined by gel electrophoresis or by
CC sequencing the amplified DNA. The polymorphism comprises an allele
CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
CC (TA)8/(TA)8. (M1) is also useful for predicting an individuals
CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
CC UGT1A1) gene product, the method comprising determining the number of TA
CC repeats in a UGT gene promoter, where the number of TA repeats correlates
CC with expression of the UGT gene, and the individuals sensitivity to
CC xenobiotics is effected by glucuronidation activity. The methods
CC preferably involve determining the presence of five, six or seven TA
CC repeats in the promoter. Defects in glucurodination is associated with
CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
CC present sequence is the UGT1A1 promoter (TA)7 repeat region
XX
SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
||||||| |||||||
Db 16 TATATATATATATATA 1

RESULT 1376
AAL50679
ID AAL50679 standard; DNA; 17 BP.
XX
AC AAL50679;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.
XX
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
OS Homo sapiens.
XX
PN US2002115097-A1.
XX
PD 22-AUG-2002.
XX
PF 01-FEB-2002; 2002US-00061693.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Rienzo AD, Iyer L, Ratain MJ;
XX
DR WPI; 2002-740095/80.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
PS Example 6; Page 2; 13pp; English.
XX
CC The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
||||||| |||||||
Db 1 TATATATATATATATA 16

RESULT 1377
AAL50679/c
ID AAL50679 standard; DNA; 17 BP.
XX
AC AAL50679;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.
XX
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
OS Homo sapiens.
XX
PN US2002115097-A1.
XX
PD 22-AUG-2002.
XX
PF 01-FEB-2002; 2002US-00061693.
XX
PR 16-FEB-1999; 99US-00251274.
XX

PA (ARCH-) ARCH DEV CORP.
XX
PI Rienzo AD, Iyer L, Ratain MJ;
XX
DR WPI; 2002-740095/80.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
PS Example 6; Page 2; 13pp; English.
XX
CC The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATA 2410
||||||||| |||||||
Db 16 TATATATATATATATA 1

RESULT 1378
ABK49298
ID ABK49298 standard; DNA; 17 BP.
XX
AC ABK49298;
XX
DT 15-JUL-2002 (first entry)
XX
DE Norwalk-like virus genogroup II (GII) cDNA probe #2.
XX
KW Norwalk-like virus genogroup II; GII; probe; ss; viral food poisoning;
KW non-bacterial gastroenteritis; fish; shellfish; polluted water system.
XX
OS Norwalk-like virus.
XX
PN WO200229120-A1.
XX
PD 11-APR-2002.
XX
PF 28-MAR-2001; 2001WO-JP002542.
XX
PR 29-SEP-2000; 2000JP-00300724.
XX
PA (BMLB-) BML INC.
XX
PI Kageyama T, Kojima S, Fukushi S, Hoshino F, Katayama K;
XX
DR WPI; 2002-340118/37.
XX
PT Detecting Norwalk-like virus (GII) with kits based on nucleic acids of
PT both complementary base sequences of highly conserved domain in cDNA of
PT its prototype, useful in diagnosis of viral food poisoning.
XX
PS Example; Page 49; 52pp; Japanese.
XX
CC The invention relates to a method of detecting a virus, particularly of
CC Norwalk-like viruses, using as an indication the nucleic acids of both
CC complementary base sequences corresponding to positions 4851-5450 in the
CC base sequence of cDNA of the prototype of Norwalk-like virus genogroup II
CC (GII). Detection of Norwalk-like virus (GII) is useful in diagnosis of
CC viral food poisoning e.g. non-bacterial gastroenteritis, and for
CC examining foods, particularly fish and shellfish, and infectivity of
CC polluted water systems and other contamination sources like work clothes.
CC This sequence represents a probe for Norwalk-like virus (GII) cDNA, used
CC in the method of the invention
XX
SQ Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1562 ATTGCTATCGCCCTCC 1577
||||| ||||||||||
Db 1 ATTGCGATCGCCCTCC 16

RESULT 1379
ABK19272
ID ABK19272 standard; RNA; 17 BP.
XX
AC ABK19272;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 1919.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 124; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour

```
CC   angiogenesis is treated by administering (I) to the patient in
CC   conjunction with one or more of other therapies such as radiation or
CC   chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC   cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC   ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC   cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC   diseases related to the expression of ERG, and as diagnostic tool to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of ERG RNA in a cell. (I) is useful for specifically
CC   targeting genes that share homology with ERG gene or ERG fusion genes.
CC   ABK17354-ABK22719 represent nucleic acids, including antisense and
CC   enzymatic nucleic acid molecules which regulate expression of ERG, and
CC   related PCR primers of the invention
XX
SQ   Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 1e+03;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1061 TATGACAAGAACATTA 1076
              :|:||||||||||: |
Db          1 UAUGACAAGAACAUCA 16


RESULT 1380
ABS75218
ID   ABS75218 standard; DNA; 17 BP.
XX
AC   ABS75218;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 17-mer SEQ ID 744.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 173; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 1 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3057 GCTAGCTGCCACTTTC 3072
              |||||||||| |||||
Db          2 GCTAGCTGCCTCTTTC 17


RESULT 1381
ABS75219
ID   ABS75219 standard; DNA; 17 BP.
XX
AC   ABS75219;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 17-mer SEQ ID 745.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 173; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 1 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3057 GCTAGCTGCCACTTTC 3072
              |||||||||| |||||
Db          1 GCTAGCTGCCTCTTTC 16
```

```
RESULT 1382
ABK55689/c
ID   ABK55689 standard; RNA; 17 BP.
XX
AC   ABK55689;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human CLCA1 gene enzymatic nucleic acid #60.
XX
KW   Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW   antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW   chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW   oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW   acetylcysteine.
XX
OS   Homo sapiens.
XX
PN   WO200211674-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US024970.
XX
PR   09-AUG-2000; 2000US-0224383P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (SYNT ) SYNTEX USA LLC.
PA   (THOM/) THOMPSON J.
XX
PI   Thompson J,  Mcswiggen J,  Mckenzie T,  Ayers D,  Szymkowski DE;
PI   Grupe A;
XX
DR   WPI; 2002-217145/27.
XX
PT   Enzymatic polynucleotide that down regulates expression of chloride
PT   channel calcium activated gene, useful for treating Chronic obstructive
PT   pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS   Claim 4; Page 54; 152pp; English.
XX
CC   The invention relates to enzymatic nucleic acid molecules that down
CC   regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC   by cleaving RNA derived from the genes. The nucleic acid sequences are
CC   useful as pharmaceutical agents for treating conditions such as chronic
CC   obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC   fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC   that are related to or will respond to the levels of CLCA1 in a cell or
CC   tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC   hence, are useful for treatment of a patient having a condition
CC   associated with the level of CLCA1, where the invention further comprises
CC   the use of one or more therapies under conditions suitable for the
CC   treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC   antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC   nucleic acids of the invention are also used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of CLCA1 RNA in a cell. This sequence represents an
CC   enzymatic nucleic acid molecule of the invention
XX
SQ   Sequence 17 BP; 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATAT 2409
              ||||||||||| ||||
Db         16 ATATATATACAGATAT 1


RESULT 1383
ADB04275
ID   ADB04275 standard; DNA; 17 BP.
XX
AC   ADB04275;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5261.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5261; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGGG 4518
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTGAG 16


RESULT 1384
ACD65318/c
ID   ACD65318 standard; RNA; 17 BP.
XX
AC   ACD65318;
XX
DT   30-SEP-2003  (first entry)
XX
DE   HCV minus strand DNAzyme substrate sequence #2005.
XX
```

```
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 310; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 8 A; 3 C; 5 G; 0 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2271 CTTTCTGCTCTGCCAT 2286
                ||||||||||||| ||
Db         16 CTTTCTGCTCTGCTAT 1


RESULT 1385
ACC66072/c
ID   ACC66072 standard; DNA; 17 BP.
XX
AC   ACC66072;
XX
DT   01-JUL-2003  (first entry)
XX
DE   Murine oligonucleotide associated with tumour supression, SEQ ID 3319.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; ss.
XX
OS   Mus musculus.
XX
PN   WO2003025176-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004210.
XX
PR   17-SEP-2001; 2001FR-00011979.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-333167/31.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; Page 419; 738pp; French.
XX
CC   The present invention relates to murine oligonucleotides (ACC62754-
CC   ACC68806), which are associated with tumour suppression, tumour
CC   reversion, apoptosis and virus resistance. The oligonucleotides are
CC   useful as (1) as probes and primers for detecting, identifying,
CC   quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC   gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC   recombinant polypeptides. The oligonucleotides are useful for preparation
CC   of pharmaceuticals for prevention and/or treatment of viral diseases that
CC   are characterised by development of tumours or cell degeneration,
CC   specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ   Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2583 CACATAGGAAGGGATC 2598
                || ||||||||||||
Db         16 CATATAGGAAGGGATC 1


RESULT 1386
ACC65071/c
ID   ACC65071 standard; DNA; 17 BP.
XX
AC   ACC65071;
XX
DT   01-JUL-2003  (first entry)
XX
DE   Murine oligonucleotide associated with tumour supression, SEQ ID 2318.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
```

KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 302; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 2 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2541 GCTGAGGGACAGGATC 2556
||||| |||||||||||
Db 16 GCTGAAGGACAGGATC 1

RESULT 1387
ABZ23260
ID ABZ23260 standard; DNA; 17 BP.
XX
AC ABZ23260;
XX
DT 24-MAR-2003 (first entry)
XX
DE PCR primer used to test semen samples for presence of Ureaplasma sp.
XX
KW Reproduction; sperm; infertility; pregnancy; male infertility;
KW miscarriage; PCR; primer; ss.
XX
OS Ureaplasma sp.
XX
PN WO200295410-A1.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-AU000611.
XX
PR 18-MAY-2001; 2001AU-00005124.
XX
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
PI Knox CL, Timms P;
XX
DR WPI; 2003-148488/14.
XX
PT Detecting presence of a reproductive function-modulating organism, for
PT treating e.g. infertility, or assisted reproductive technology outcome,
PT comprises detecting organism capable of adhering to sperm.
XX
PS Example 8; Page 67; 97pp; English.
XX
CC The specification describes a method for detecting the presence of a
CC reproductive function-modulating organism. The method comprises detecting
CC an organism that is capable of adhering to sperm and that correlates with
CC the presence or risk of a condition such as infertility, adverse
CC pregnancy outcome or adverse assisted reproductive technology (ART)
CC outcome. The method is useful for the treatment and prophylaxis of male
CC infertility, adverse pregnancy outcome (e.g. miscarriage, pre-term
CC delivery, premature onset of labour, prolonged rupture of membrane,
CC neonatal morbidity or mortality) or adverse ART outcome (e.g reduced
CC embryonic development, reduced implantation rate, reduced fertilization
CC rate, reduced clinical pregnancy rate, reduced viable pregnancy rate,
CC reduced blastocyst culture rate or increased miscarriage rate). The
CC present PCR primer was used to detect the presence of Ureaplasma organism
CC in semen samples, in the course of the invention
XX
SQ Sequence 17 BP; 5 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4866 ATTTTTTATAATAGGA 4881
|||||||||| |||||
Db 1 ATTTTTTATATTAGGA 16

RESULT 1388
ACC53486/c
ID ACC53486 standard; DNA; 17 BP.
XX
AC ACC53486;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #2253.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 560; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%

```
CC   identity to them, and polypeptides encoded by the sequences or
CC   polypeptides having 80% identity to the polypeptide sequences. The
CC   invention is used to diagnose or treat viral disease or disease
CC   characterized by development of tumour cells or cellular degeneration
XX
SQ   Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3682 TTTGCTCTATTAAGAT 3697
              ||||||||||| ||||
Db         17 TTTGCTCTATTTAGAT 2


RESULT 1389
ADH70415/c
ID   ADH70415 standard; DNA; 17 BP.
XX
AC   ADH70415;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #205.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 609; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 17 BP; 13 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2125 TTTCTTTTCTTTTTTT 2140
              ||||||||||||  |||
Db         16 TTTCTTTTCTTTCTTT 1


RESULT 1390
ADI87036/c
ID   ADI87036 standard; RNA; 17 BP.
XX
AC   ADI87036;
XX
DT   03-JUN-2004  (first entry)
XX
DE   HCV DNAzyme substrate sequence #4282.
XX
KW   ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW   HCV infection; type I interferon; DNAzyme.
XX
OS   Hepatitis C virus.
XX
PN   US2003125270-A1.
XX
PD   03-JUL-2003.
XX
PF   18-DEC-2000; 2000US-00740332.
XX
PR   18-DEC-2000; 2000US-00740332.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (ROBE/) ROBERTS E.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen J,  Roberts E,  Pavco PA,  Macejack D;
XX
DR   WPI; 2004-031273/03.
XX
PT   Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT   from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT   especially in combination with type I interferon therapy.
XX
PS   Claim 1; SEQ ID NO 4282; 198pp; English.
XX
CC   The invention relates to an enzymatic nucleic acid molecule which
CC   specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC   the binding arms of the enzymatic nucleic acid molecule comprises
CC   sequences complementary to any of the defined substrate sequences given
CC   in the specification. The nucleic acid molecule may be administered for
CC   the treatment of HCV infections, especially in combination with type I
CC   interferons. The present sequence represents a HCV DNAzyme substrate
CC   sequence.
XX
SQ   Sequence 17 BP; 8 A; 3 C; 5 G; 0 T; 1 U; 0 Other;
```

```
  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2271 CTTTCTGCTCTGCCAT 2286
              ||||||||||||| ||
Db         16 CTTTCTGCTCTGCTAT 1


RESULT 1391
ADP86138/c
ID   ADP86138 standard; DNA; 17 BP.
XX
AC   ADP86138;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #9.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 9; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 14 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              ||||||||||||||| |
Db         17 TTTTTTTTTTTTTTCG 2


RESULT 1392
ADP86139
ID   ADP86139 standard; DNA; 17 BP.
XX
AC   ADP86139;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #10.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 10; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1e+03;
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```
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              | ||||||||||||||
Db          2 GCTTTTTTTTTTTTT 17


RESULT 1393
ABX79779
ID   ABX79779 standard; cDNA; 18 BP.
XX
AC   ABX79779;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #104.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 385; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              |||||||| |||||||
Db          2 TATATATATATATATA 17


RESULT 1394
AAQ38707
ID   AAQ38707 standard; RNA; 18 BP.
XX
AC   AAQ38707;
XX
DT   25-MAR-2003  (revised)
DT   15-JUL-1993  (first entry)
XX
DE   First chimeric primer for adding poly A tails.
XX
KW   oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;
KW   treatment; diagnosis; testing; assay; Candida; papillomavirus;
KW   cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;
KW   liver disease; human immunodeficiency virus; herpes simplex virus; HSV;
KW   human immunodeficiency virus; HIV; AIDS; influenza virus;
KW   genetic disease; genetic abnormalities.
XX
OS   Synthetic.
XX
PN   WO9305182-A1.
XX
PD   18-MAR-1993.
XX
PF   04-SEP-1992;   92WO-US007489.
XX
PR   05-SEP-1991;   91US-00755485.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bruice TW;
XX
DR   WPI; 1993-101001/12.
XX
PT   Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule
PT   - for use in therapeutics, diagnostics and research reagents.
XX
PS   Disclosure; Page 27; 61pp; English.
XX
CC   This sequence was used as a PCR primer in order to add a polyA tail to
CC   the 3'end of the highest specific activity selected oligonucleotide in
CC   order to form a first strand. The primer is comprised of a 5'known
CC   sequence and a 3' polynucleotide portion corresp. to the polynucleotide
CC   tail of the first strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4513
              | ||||||||||||||
Db          3 ATGTTTTTTTTTTTT 18


RESULT 1395
AAX70270/c
ID   AAX70270 standard; RNA; 18 BP.
XX
AC   AAX70270;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hairpin ribozyme substrate #38.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
```

OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 93; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 18 BP; 5 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3655 GCTCAGTCATCAAAGC 3670
||||||||||| |||
Db 18 GCTCAGTCATCAGAGC 3

RESULT 1396
AAT96107
ID AAT96107 standard; DNA; 18 BP.
XX
AC AAT96107;
XX
DT 31-MAR-1998 (first entry)
XX
DE First chimeric primer.
XX
KW Determination; oligonucleotide; specific activity; therapy;
KW target biomolecule; randomised oligonucleotide; diagnosis; research; PCR;
KW chimeric; primer; ss.
XX
OS Synthetic.
XX
PN US5686242-A.
XX
PD 11-NOV-1997.
XX
PF 27-OCT-1994; 94US-00330000.
XX
PR 05-SEP-1991; 91US-00755485.
PR 04-SEP-1992; 92WO-US007489.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Lima WF, Bruice TW;
XX
DR WPI; 1997-558135/51.
XX
PT Determination of oligo-nucleotide with specific activity for target bio-
PT molecule - using set of randomised oligo-nucleotide(s).
XX
PS Disclosure; Col 27-28; 22pp; English.
XX
CC The present sequence was used in the development of a method of
CC determining an oligonucleotide having specific activity for a target
CC biomolecule. The method comprises assaying a set of randomised
CC oligonucleotides for activity against a target biomolecule, separating
CC active from inactive oligonucleotides and recovering, amplifying and
CC determining the nucleic acid sequence of the active oligonucleotides. The
CC oligonucleotides can be used for therapeutic, diagnostic and research
CC purposes
XX
SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTT 4513
| |||||||||||||
Db 3 ATGTTTTTTTTTTTT 18

RESULT 1397
AAT49044/c
ID AAT49044 standard; DNA; 18 BP.
XX
AC AAT49044;
XX
DT 10-OCT-1997 (first entry)
XX
DE Rapamycin-dependent activation of signal transduction oligonucleotide.
XX
KW Rapamycin; responsive transfected cell; recombinant DNA; fusion protein;
KW rapamycin binding domain; RBD; FKBP; FK506-binding protein; FRB domain;
KW genetic engineering; regulation; transcription; signal transduction;
KW apoptosis; inhibition; virus; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO9641865-A1.
XX
PD 27-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009948.
XX
PR 07-JUN-1995; 95US-00481941.
PR 09-FEB-1996; 96US-00598776.
XX
PA (ARIA-) ARIAD GENE THERAPEUTICS INC.
XX
PI Clackson T, Holt DA, Gilman MZ;
XX
DR WPI; 1997-065453/06.
XX
PT New rapamycin-responsive transfected cells - contg. recombinant DNA
PT encoding fusion proteins which act as biological switches for regulating
PT biological events.
XX
PS Example 8; Page 102; 149pp; English.
XX
CC The present sequence represents an oligonucleotide which is involved in
CC the rapamycin-dependent activation of signal transduction. This is
CC involved in the construction of transcription factor fusion proteins,
CC which in turn are involved in the production of animal cells containing
CC at least two recombinant DNAs. One DNA should encode a chimeric protein
CC which is capable of binding to rapamycin, or a rapamycin analogue, and

```
CC   comprises at least one rapamycin binding domain (RBD) and at least one
CC   protein domain heterologous to it; the second recombinant DNA should
CC   encode a second chimeric protein which is capable of forming a complex
CC   with rapamycin, or a rapamycin analogue, and the first chimeric protein
CC   and comprises at least one FKBP:rapamycin binding (FRB) domain and at
CC   least one domain heterologous to it. Contacting these genetically
CC   engineered cells with rapamycin or analogues results in the formation of
CC   a complex (between the fusion proteins, and the rapamycin), and
CC   initiation of a biological response. The products can be used for
CC   regulating biological events such as gene transcription, activation of an
CC   intracellular signal transduction pathway leading to e.g. gene expression
CC   or apoptotic cell death, gene knock-out, blockade of a gene or inhibition
CC   of function of a gene product. They are used particularly for regulated
CC   gene therapy and for production of recombinant proteins and viruses
XX
SQ   Sequence 18 BP; 6 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1313 TGAGTTTGGGGTCCCT 1328
              ||||||||||| ||||
Db         17 TGAGTTTGGGGACCCT 2


RESULT 1398
AAA06980
ID   AAA06980 standard; DNA; 18 BP.
XX
AC   AAA06980;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Human Smad5 phosphorothioate antisense oligonucleotide, SEQ ID NO:14.
XX
KW   Smad5; MADH5; Dwarfin-C; JV5-1; TGF-beta signalling pathway;
KW   transcription factor; expression inhibition; tumour formation;
KW   inflammation; antisense; ss.
XX
OS   Homo sapiens.
XX
PN   US6040178-A.
XX
PD   21-MAR-2000.
XX
PF   23-FEB-1999;   99US-00256492.
XX
PR   23-FEB-1999;   99US-00256492.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-270139/23.
XX
PT   Novel antisense compounds useful for inhibiting the expression of Smad5
PT   in human cells or tissues and treating inflammation and tumor formation.
XX
PS   Example 15; Col 38; 31pp; English.
XX
CC   Sequences AAA06974-A07013 represent antisense oligonucleotides targetted
CC   to the human Smad5 gene, which inhibit its expression. The antisense
CC   oligonucleotides were designed to target different regions of the human
CC   Smad5 RNA, and were analysed for their effect on Smad5 mRNA levels by
CC   quantitative real-time PCR. The Smad proteins are a family of cytosolic
CC   proteins which are involved in TGF-beta superfamily signal transduction.
CC   On ligand binding, TGF-beta superfamily proteins (such as bone
CC   morphogenetic protein (BMP), activin and TGF-betas themselves)
CC   phosphorylate Smad proteins, which then homo- or heterodimerise and
CC   translocate to the nucleus to activate target gene transcription. Smad5
CC   (also known as MADH5, Dwarfin-C and JV5-1) is a member of the subgroup of
CC   Smad family transcription factors which mediate signal transduction from
CC   BMPs. Smad5 is activated by BMP-2 through the BMP type Ia or Ib
CC   receptors, causing it to heterodimerise with the common mediator Smad4
CC   (US6013787; AAY69622) and translocate to the nucleus. The antisense
CC   oligonucleotides of the invention are useful for diagnosis, prevention
CC   and treatment of conditions associated with Smad5 expression, such as
CC   tumour formation, inflammation and certain infections
XX
SQ   Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1825 TTTGACACAAAGCTTC 1840
              ||||||||||| ||||
Db          1 TTTGACACAAATCTTC 16


RESULT 1399
AAZ69782
ID   AAZ69782 standard; DNA; 18 BP.
XX
AC   AAZ69782;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker upstream amplification primer SEQ ID NO:4138.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 1113; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 18 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
```

```
  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3998 ATTGTAATCGTGTGCC 4013
              ||||||||||| ||||
Db          2 ATTGTAATCGTATGCC 17


RESULT 1400
AAZ88678
ID   AAZ88678 standard; DNA; 18 BP.
XX
AC   AAZ88678;
XX
DT   11-MAY-2000  (first entry)
XX
DE   Chimeric primer #1.
XX
KW   Primer; detection; diagnosis; ss.
XX
OS   Unidentified.
XX
PN   US6022691-A.
XX
PD   08-FEB-2000.
XX
PF   07-NOV-1997;   97US-00965908.
XX
PR   05-SEP-1991;   91US-00755485.
PR   04-SEP-1992;   92WO-US007489.
PR   27-OCT-1994;   94US-00330000.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Lima WF,  Bruice TW;
XX
DR   WPI; 2000-170669/15.
XX
PT   Assay for a chemical or drug in a sample comprises detecting binding of
PT   an oligonucleotide selected from a set of randomized oligonucleotides.
XX
PS   Disclosure; Col 27-28; 20pp; English.
XX
CC   This invention describes a novel method (I) for specifically detecting a
CC   chemical or drug in a sample comprises contacting the sample with an
CC   oligonucleotide having specific activity for a target biomolecule and
CC   detecting the presence or absence of binding where the presence of
CC   binding indicates the presence of the chemical or drug in the sample. The
CC   oligonucleotide is identified by: (a) assaying a prepared set of
CC   randomized oligonucleotides for activity against a target biomolecule;
CC   (b) separating active from inactive oligonucleotides; (c) recovering the
CC   active oligonucleotides; and (d) characterizing the recovered
CC   oligonucleotides by microanalytical structure determination. The method
CC   can be used for diagnostic or research purposes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4513
              | |||||||||||||
Db          3 ATGTTTTTTTTTTTT 18


RESULT 1401
AAZ93494/c
ID   AAZ93494 standard; DNA; 18 BP.
XX
AC   AAZ93494;
XX
DT   24-JUL-2000  (first entry)
XX
DE   TRADD antisense oligonucleotide.
XX
KW   TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;
KW   programmed cell death; antisense; inhibition; treatment; therapy;
KW   septic shock; inflammation; cancer; antiinflammatory; human; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    complement(1. .18)
FT                   /*tag=  a
FT                   /note= "Complementary to bases 947-930 of the human TRADD
FT                   sequence described in GENESEQ record AAZ93431"
XX
PN   WO200012527-A1.
XX
PD   09-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019614.
XX
PR   28-AUG-1998;   98US-00143212.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-237846/20.
XX
PT   New antisense compounds that limit the expression of human TRADD protein,
PT   useful in the treatment and diagnosis of cancer, inflammation and septic
PT   shock.
XX
PS   Claim 3; Page 52; 85pp; English.
XX
CC   The intracellular protein TRADD has been identified as a critical link
CC   between tumour necrosis factor (TNF) receptor binding and downstream
CC   activation of NF-kappa-B. Overexpression of native TRADD activates NF-
CC   kappa-B in the absence of TNF and dominant negative mutants of TRADD
CC   block TNF-induced NF-kappa-B activation. A second effect of TNF in many
CC   cell types is the induction of apoptosis (programmed cell death). TRADD
CC   overexpression has been shown to mimic TNF induction of apoptosis as
CC   well. Data indicates that TRADD and other downstream effector proteins
CC   are the rate limiting step of TNF action and would therefore serve as the
CC   most efficient targets for inhibition of TNF-induced events. Antisense
CC   oligonucleotides capable of inhibiting TRADD function may therefore be
CC   useful in a number of therapeutic, diagnostic and research applications.
CC   Inhibiting expression of TRADD by contacting human cells or tissues with
CC   the antisense compound may be used to treat a disease or condition
CC   associated with TRADD expression, for example, septic shock,
CC   inflammation, or cancer. TRADD antisense oligonucleotides of varying
CC   inhibitory capabilities are listed in GENESEQ records AAZ93438-Z93517.
CC   The antisense oligonucleotides exhibit enhanced inhibitory capabilities
CC   when they have 2'-MOE wings and a deoxy gap
XX
SQ   Sequence 18 BP; 1 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1348 ACCAGCCAGGCAGAGG 1363
              ||||||| ||||||||
Db         17 ACCAGCCTGGCAGAGG 2


RESULT 1402
AAC70742
ID   AAC70742 standard; DNA; 18 BP.
XX
AC   AAC70742;
```

XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #382.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1251 TCTCCAAGGCCGCCAT 1266
||||||||||||| ||
Db 2 TCTCCAAGGCCGCAAT 17

RESULT 1403
AAC70757
ID AAC70757 standard; DNA; 18 BP.
XX
AC AAC70757;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #392.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1251 TCTCCAAGGCCGCCAT 1266
||||||||||||| ||
Db 2 TCTCCAAGGCCGCAAT 17

RESULT 1404
AAC70760
ID AAC70760 standard; DNA; 18 BP.
XX
AC AAC70760;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #394.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.

```
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 TCTCCAAGGCCGCCAT 1266
              ||||||||||||| ||
Db          2 TCTCCAAGGCCGCAAT 17


RESULT 1405
AAC70748
ID   AAC70748 standard; DNA; 18 BP.
XX
AC   AAC70748;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #386.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 TCTCCAAGGCCGCCAT 1266
              ||||||||||||| ||
Db          2 TCTCCAAGGCCGCAAT 17


RESULT 1406
AAC70745
ID   AAC70745 standard; DNA; 18 BP.
XX
AC   AAC70745;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #384.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 TCTCCAAGGCCGCCAT 1266
              ||||||||||||| ||
```

```
Db          2 TCTCCAAGGCCGCAAT 17


RESULT 1407
AAC70730
ID   AAC70730 standard; DNA; 18 BP.
XX
AC   AAC70730;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #374.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 TCTCCAAGGCCGCCAT 1266
              ||||||||||||| ||
Db          2 TCTCCAAGGCCGCAAT 17


RESULT 1408
AAC70733
ID   AAC70733 standard; DNA; 18 BP.
XX
AC   AAC70733;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #376.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 TCTCCAAGGCCGCCAT 1266
              ||||||||||||| ||
Db          2 TCTCCAAGGCCGCAAT 17


RESULT 1409
AAC70754
ID   AAC70754 standard; DNA; 18 BP.
XX
AC   AAC70754;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #390.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
```

XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1251 TCTCCAAGGCCGCCAT 1266
||||||||||||| ||
Db 2 TCTCCAAGGCCGCAAT 17

RESULT 1410
ABL57542
ID ABL57542 standard; DNA; 18 BP.
XX
AC ABL57542;
XX
DT 26-JUL-2002 (first entry)
XX
DE Nucleic acid probe g.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; probe; ss.
XX
OS Unidentified.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a nucleic acid probe of the
CC invention that was used for investigating the base selectivity of a
CC target nucleic acid
XX
SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2386 AAAATAAAATATATAT 2401
|||| ||||||||||
Db 3 AAAAAAAAATATATAT 18

RESULT 1411
ABL56899
ID ABL56899 standard; DNA; 18 BP.
XX
AC ABL56899;
XX
DT 26-JUL-2002 (first entry)
XX
DE Nucleic acid probe b.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; probe; ss.
XX
OS Unidentified.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX

```
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a nucleic acid probe of the
CC   invention that was used for investigating the base selectivity of a
CC   target nucleic acid
XX
SQ   Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2386 AAAATAAAATATATAT 2401
              |||| ||||||||||
Db          3 AAAAAAAAATATATAT 18


RESULT 1412
AAD24812/c
ID   AAD24812 standard; DNA; 18 BP.
XX
AC   AAD24812;
XX
DT   12-MAR-2002  (first entry)
XX
DE   B. thuringiensis cryET70 and cry22Aa DNA amplifying PCR primer, 2270-9.
XX
KW   Coleopteran insect infestation; insecticidal; crystal protein; tIC851;
KW   cryET70; cry22Aa; plant protection; cotton boll weevil; transgenic plant;
KW   PCR primer; ss.
XX
OS   Bacillus thuringiensis.
XX
PN   WO200187940-A2.
XX
PD   22-NOV-2001.
XX
PF   30-APR-2001; 2001WO-US013879.
XX
PR   15-MAY-2000; 2000US-0204367P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Isaac BC,  Krieger EK,  Mettus Light A,  Sivasupramaniam S;
PI   Moshiri F;
XX
DR   WPI; 2002-055684/07.
XX
PT   Novel polypeptide and polynucleotide compositions toxic to Anthonomus
PT   insects, useful in insecticidal formulations and for the development of
PT   transgenic insect-resistant plants.
XX
PS   Example 5; Page 64; 133pp; English.
XX
CC   The present invention relates to novel genes encoding Coleopteran
CC   inhibitory Bacillus thuringiensis insecticidal crystal proteins, tIC851,
CC   cryET70 and cry22Aa. These proteins are insecticidally active and provide
CC   plant protection from coleopteran insects such as cotton boll weevil
CC   (Anthonomus grandis Bohemian). Compositions containing proteins of the
CC   invention are useful for making transgenic plants resistant to
CC   coleopteran insect infestation. The present DNA sequence is a PCR primer
CC   which is used for amplifying B. thuringiensis cryET70 and cry22Aa DNA
XX
SQ   Sequence 18 BP; 8 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              |||||||||||| |||
Db         17 TATTTCTAATTCAACA 2


RESULT 1413
AAD24813
ID   AAD24813 standard; DNA; 18 BP.
XX
AC   AAD24813;
XX
DT   12-MAR-2002  (first entry)
XX
DE   B. thuringiensis cryET70 and cry22Aa DNA amplifying PCR primer, 2270-10.
XX
KW   Coleopteran insect infestation; insecticidal; crystal protein; tIC851;
KW   cryET70; cry22Aa; plant protection; cotton boll weevil; transgenic plant;
KW   PCR primer; ss.
XX
OS   Bacillus thuringiensis.
XX
PN   WO200187940-A2.
XX
PD   22-NOV-2001.
XX
PF   30-APR-2001; 2001WO-US013879.
XX
PR   15-MAY-2000; 2000US-0204367P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Isaac BC,  Krieger EK,  Mettus Light A,  Sivasupramaniam S;
PI   Moshiri F;
XX
DR   WPI; 2002-055684/07.
XX
PT   Novel polypeptide and polynucleotide compositions toxic to Anthonomus
PT   insects, useful in insecticidal formulations and for the development of
PT   transgenic insect-resistant plants.
XX
PS   Example 5; Page 64; 133pp; English.
XX
CC   The present invention relates to novel genes encoding Coleopteran
CC   inhibitory Bacillus thuringiensis insecticidal crystal proteins, tIC851,
CC   cryET70 and cry22Aa. These proteins are insecticidally active and provide
CC   plant protection from coleopteran insects such as cotton boll weevil
CC   (Anthonomus grandis Bohemian). Compositions containing proteins of the
CC   invention are useful for making transgenic plants resistant to
CC   coleopteran insect infestation. The present DNA sequence is a PCR primer
CC   which is used for amplifying B. thuringiensis cryET70 and cry22Aa DNA
XX
SQ   Sequence 18 BP; 6 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3923 TATTTCTAATTCCACA 3938
              |||||||||||| |||
Db          2 TATTTCTAATTCAACA 17
```

```
RESULT 1414
ABA99596
ID   ABA99596 standard; DNA; 18 BP.
XX
AC   ABA99596;
XX
DT   14-JUN-2002  (first entry)
XX
DE   Canine epididymis-specific CE12 PCR primer SEQ ID 16.
XX
KW   Canine; epididymis-specific protein; CE12; antiinfertility; primer;
KW   contraceptive; heparin binding; apolipoprotein A-I binding; PCR;
KW   sperm capacitance; male infertility; post-testicular; ss.
XX
OS   Canis sp.
XX
PN   WO200194387-A2.
XX
PD   13-DEC-2001.
XX
PF   08-JUN-2001; 2001WO-EP006554.
XX
PR   08-JUN-2000; 2000DE-01028376.
XX
PA   (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.
XX
PI   Kirchhoff C,  Ivell R;
XX
DR   WPI; 2002-179467/23.
XX
PT   New epididymis-specific protein, also related nucleic acid and
PT   antibodies, useful for diagnosis and treatment of male infertility and as
PT   reversible contraceptive.
XX
PS   Example 1; Page 60; 63pp; German.
XX
CC   This invention describes a novel epididymis-specific human protein HE12
CC   which has antiinfertility and contraceptive activity. The products of the
CC   invention modulate heparin and apolipoprotein A-I binding in the
CC   epididymis and thus capacitance of sperm. The protein of the invention,
CC   also similar sequences from other animals, their derivatives and
CC   fragments, are useful for diagnosis of male infertility. Antibodies (Ab)
CC   directed against the protein and nucleic acid that encodes it, are useful
CC   for treatment of male infertility and as reversible contraceptives since
CC   they have a post-testicular site of action and do not interfere with
CC   hormone metabolism. This sequence represents a PCR primer used in the
CC   amplification of the canine epididymis-specific polynucleotide described
CC   in the method of the invention
XX
SQ   Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match                 0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4001 GTAATCGTGTGCCATG 4016
             ||||||||  |||||||
Db          2 GTAATCGTCTGCCATG 17


RESULT 1415
ABT43442/c
ID   ABT43442 standard; DNA; 18 BP.
XX
AC   ABT43442;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Neuroblastoma-related DNA sequence #357.
XX
KW   Neuroblastoma; prognosis; ds; oligonucleotide.
XX
OS   Unidentified.
XX
PN   WO2002103017-A1.
XX
PD   27-DEC-2002.
XX
PF   30-MAY-2002; 2002WO-JP005295.
XX
PR   31-MAY-2001; 2001JP-00163666.
PR   24-AUG-2001; 2001JP-00255260.
XX
PA   (CHIB-) CHIBA PREFECTURE.
PA   (HISM ) HISAMITSU PHARM CO LTD.
XX
PI   Nakagawara A;
XX
DR   WPI; 2003-167523/16.
XX
PT   Nucleic acids isolated from neuroblastoma showing enhanced expression in
PT   human neuroblastoma with good prognosis, useful in clarifying good/poor
PT   prognosis of neuroblastoma and providing genetic data.
XX
PS   Example 5; Page 26; 444pp; Japanese.
XX
CC   The invention comprises DNA sequences that show enhanced expression in
CC   human neuroblastoma with good prognosis. The DNA sequences of the
CC   invention are useful in clarifying good/poor prognosis of neuroblastoma.
CC   The present DNA sequence was used in the exemplification of the invention
XX
SQ   Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match                 0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 TTCATCCTGCCCACGC 929
              ||||||||||||| ||
Db         16 TTCATCCTGCCCAAGC 1


RESULT 1416
ABT43153/c
ID   ABT43153 standard; DNA; 18 BP.
XX
AC   ABT43153;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Neuroblastoma-related DNA sequence #68.
XX
KW   Neuroblastoma; prognosis; ds; oligonucleotide.
XX
OS   Unidentified.
XX
PN   WO2002103017-A1.
XX
PD   27-DEC-2002.
XX
PF   30-MAY-2002; 2002WO-JP005295.
XX
PR   31-MAY-2001; 2001JP-00163666.
PR   24-AUG-2001; 2001JP-00255260.
XX
PA   (CHIB-) CHIBA PREFECTURE.
PA   (HISM ) HISAMITSU PHARM CO LTD.
XX
PI   Nakagawara A;
XX
DR   WPI; 2003-167523/16.
XX
PT   Nucleic acids isolated from neuroblastoma showing enhanced expression in
PT   human neuroblastoma with good prognosis, useful in clarifying good/poor
PT   prognosis of neuroblastoma and providing genetic data.
```

```
XX
PS   Example 5; Page 23(1); 444pp; Japanese.
XX
CC   The invention comprises DNA sequences that show enhanced expression in
CC   human neuroblastoma with good prognosis. The DNA sequences of the
CC   invention are useful in clarifying good/poor prognosis of neuroblastoma.
CC   The present DNA sequence was used in the exemplification of the invention
XX
SQ   Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 TTCATCCTGCCCACGC 929
              ||||||||||||| ||
Db         16 TTCATCCTGCCCAAGC 1


RESULT 1417
ABT32308/c
ID   ABT32308 standard; DNA; 18 BP.
XX
AC   ABT32308;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Neuroblastoma-related oligonucleotide #85.
XX
KW   Neuroblastoma; prognosis; spontaneous regression; primer; probe; ds;
KW   high malignancy.
XX
OS   Unidentified.
XX
PN   WO200297093-A1.
XX
PD   05-DEC-2002.
XX
PF   30-MAY-2002; 2002WO-JP005294.
XX
PR   30-MAY-2001; 2001JP-00162775.
PR   24-AUG-2001; 2001JP-00255226.
XX
PA   (CHIB-) CHIBA PREFECTURE.
PA   (HISM ) HISAMITSU PHARM CO LTD.
XX
PI   Nakagawara A;
XX
DR   WPI; 2003-140476/13.
XX
PT   Nucleic acids having higher expression in human neuroblastoma with poor
PT   prognosis for diagnostic prediction of neuroblastoma prognosis.
XX
PS   Example 5; Page 26; 111pp; Japanese.
XX
CC   The invention comprises nucleic acids that show increased expression in
CC   human neuroblastomas with poor prognosis over those with a good
CC   prognosis. The nucleic acids of the invention are useful as a tool for
CC   distinguishing neuroblastomas with a favourable prognosis (spontaneous
CC   regression) from neuroblastomas with a poor prognosis (high malignancy).
CC   The DNA sequences ABT32224 - ABT32571 represent oligonucleotides used in
CC   an example of the invention
XX
SQ   Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 TTCATCCTGCCCACGC 929
              ||||||||||||| ||
Db         16 TTCATCCTGCCCAAGC 1


RESULT 1418
ADE13403/c
ID   ADE13403 standard; DNA; 18 BP.
XX
AC   ADE13403;
XX
DT   29-JAN-2004  (first entry)
XX
DE   HLA class I allele specific primer #19.
XX
KW   ss; primer; PCR; human; Human Leukocyte Antigen; HLA; genotype.
XX
OS   Homo sapiens.
XX
PN   US2003165884-A1.
XX
PD   04-SEP-2003.
XX
PF   25-APR-2002; 2002US-00133779.
XX
PR   20-DEC-1999;   99US-0172768P.
PR   20-DEC-2000; 2000US-00747391.
XX
PA   (STEM-) STEMCYTE INC.
XX
PI   Chow R,  Tonai R;
XX
DR   WPI; 2003-874916/81.
XX
PT   Identifying class I or II Human Leukocyte Antigen genotypes using
PT   hybridization and amplification assays.
XX
PS   Claim 7; SEQ ID NO 19; 66pp; English.
XX
CC   The invention relates to a method of identifying a class I or II Human
CC   Leukocyte Antigen (HLA) genotype of a subject using hybridisation and
CC   amplification assay. The method is used for determining the HLA genotype
CC   of a subject. The present sequence represents a HLA class I allele
CC   specific primer.
XX
SQ   Sequence 18 BP; 4 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3492 TTGGCTGAGACCTGGG 3507
              ||||||| ||||||||
Db         18 TTGGCTGCGACCTGGG 3


RESULT 1419
ADE43545/c
ID   ADE43545 standard; DNA; 18 BP.
XX
AC   ADE43545;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human IDE sequencing primer, SEQ ID 150.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003054143-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002; 2002WO-US034679.
```

XX
PR 25-OCT-2001; 2001US-0339525P.
PR 08-NOV-2001; 2001US-0336929P.
PR 08-NOV-2001; 2001US-0338010P.
PR 09-NOV-2001; 2001US-0338363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR WPI; 2003-559131/52.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative
PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT the presence or absence of an allelic variant of one or more polymorphic
PT regions.
XX
PS Example 3; Page 275; 848pp; English.
XX
CC The present invention relates to a method (M1) for determining a
CC predisposition for or the occurrence of neurodegenerative disease in a
CC subject. The method comprises detecting in a target nucleic acid obtained
CC from the subject the presence or absence of an allelic variant of one or
CC more polymorphic regions of one or more genes selected from uPA
CC (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC presence of at least one of the allelic variant of one or more
CC polymorphic regions is indicative of a predisposition for or the
CC occurrence of neurodegenerative disease. The genes are all located on
CC chromosome 10. M1 is useful for determining a predisposition for or the
CC occurrence of, and for treating neurodegenerative disease, particularly
CC Alzheimer's disease. The present sequence is a PCR primer, which was used
CC in the method of the invention.
XX
SQ Sequence 18 BP; 9 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2262 TTCTTTCCTCTTTCTG 2277
||||||||| |||||||
Db 16 TTCTTTCCCCTTTCTG 1

RESULT 1420
ADG76788/c
ID ADG76788 standard; DNA; 18 BP.
XX
AC ADG76788;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human olfactory receptor gene identification oligonucleotide SEQ ID:65.
XX
KW identification; olfactory receptor gene; allelic variant; chromosome 17;
KW 17p13.3; male infertility; reduced sperm motility; human; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003091388-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003WO-IL000336.
XX
PR 23-APR-2002; 2002US-0374508P.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Lancet D, Menashe I, Man O, Gilad Y;
XX
DR WPI; 2004-108244/11.
XX
PT New oligonucleotides for identifying olfactory receptor genes, useful in
PT designing pleasing scents and flavors, and in diagnosing male
PT infertility.
XX
PS Claim 4; SEQ ID NO 65; 97pp; English.
XX
CC The present invention describes an oligonucleotide (I) comprising a
CC nucleic acid sequence suitable for identifying an olfactory receptor gene
CC selected from a group comprising SEQ ID Nos. 79-104, or an allelic
CC variant. Also described: (1) a kit for identifying an olfactory receptor
CC gene comprising at least one oligonucleotide (I); (2) an array suitable
CC for detecting the presence of at least one allelic variant of an
CC olfactory receptor gene, comprising at least one oligonucleotide (I)
CC contained in or attached to a support; (3) typing (M1) a subject
CC according to presence or absence of allelic variants of olfactory
CC receptor genes comprising detecting the presence or absence of at least
CC one olfactory receptor gene in a biological sample; (4) a nucleic acid
CC construct comprising a polynucleotide encoding an olfactory receptor
CC gene, or an allelic variant, selected from SEQ ID Nos. 79-104, and a
CC promoter for directing transcription; and (5) a cell comprising the
CC nucleic acid construct. The oligonucleotide (I) can be useful in
CC detecting olfactory receptor genes, and in typing a subject according to
CC the presence or absence of olfactory receptor genes. The olfactory
CC receptor gene cluster is located on human chromosome 17p13.3. The
CC oligonucleotides (I) may also be used to detect/diagnose male
CC infertility, specifically that associated with reduced sperm motility or
CC to detect specific odorants that may enhance or suppress sperm motility.
CC The present sequence represents a specifically claimed oligonucleotide
CC used in the identification of an olfactory receptor gene, which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 18 BP; 8 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 906 TGATGTGCTTCATCCT 921
|| ||||||||||||
Db 18 TGGTGTGCTTCATCCT 3

RESULT 1421
ADH70777/c
ID ADH70777 standard; DNA; 18 BP.
XX
AC ADH70777;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #567.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.

XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 971; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2398 ATATACATATATACAT 2413
||||||||||||| ||
Db 18 ATATACATATATATAT 3

RESULT 1422
ADH54023/c
ID ADH54023 standard; DNA; 18 BP.
XX
AC ADH54023;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human neurodegenerative disease-related sequencing primer SeqID150.
XX
KW human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW gamma-synuclein; SNCG; insulin degrading enzyme; IDE;
KW kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA;
KW tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; PCR;
KW primer; ss; sequencing.
XX
OS Homo sapiens.

XX
PN US2003224380-A1.
XX
PD 04-DEC-2003.
XX
PF 25-OCT-2002; 2002US-00282174.
XX
PR 25-OCT-2001; 2001US-0339525P.
PR 25-OCT-2001; 2001US-0348065P.
PR 02-NOV-2001; 2001US-0336983P.
PR 08-NOV-2001; 2001US-0336929P.
PR 08-NOV-2001; 2001US-0338010P.
PR 09-NOV-2001; 2001US-0338363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelebi G, Ellliott KJ, Wang X, Tanzi RE;
PI Bertram L, Saunders AJ, Mullin KM, Sampson AJ;
XX
DR WPI; 2004-060538/06.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative
PT disease, particularly Alzheimer's disease, comprises determining the
PT presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6
PT gene.
XX
PS Example 3; SEQ ID NO 150; 205pp; English.
XX
CC This invention relates to a novel method of determining a predisposition
CC for or the occurrence of neurodegenerative disease comprising detecting
CC in a target nucleic acid obtained from the subject the presence of an
CC allelic variant of polymorphic regions of human genes selected from
CC urokinase plasminogen activator (uPA), gamma-synuclein (SNCG), insulin
CC degrading enzyme (IDE), kinesin-like protein 1 (KNSL1), lysosomal acid
CC lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The
CC method is useful in determining the presence or predisposition to a
CC neurodegenerative disease, particularly Alzheimer's disease. The present
CC sequence is that of a sequencing primer which was used for sequencing of
CC a region of the human IDE gene in the exemplification of the invention.
XX
SQ Sequence 18 BP; 9 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2262 TTCTTTCCTCTTTCTG 2277
|||||||| |||||||
Db 16 TTCTTTCCCCTTTCTG 1

RESULT 1423
ADL09253/c
ID ADL09253 standard; DNA; 18 BP.
XX
AC ADL09253;
XX
DT 06-MAY-2004 (first entry)
XX
DE HLA locus-specific capture oligonucleotide #19.
XX
KW ss; primer; human leukocyte antigen; HLA; HLA genotyping; human; PCR.
XX
OS Homo sapiens.
XX
PN US6670124-B1.
XX
PD 30-DEC-2003.
XX
PF 20-DEC-2000; 2000US-00747391.
XX

PR 20-DEC-1999; 99US-0172768P.
XX
PA (STEM-) STEMCYTE INC.
XX
PI Chow R, Tonai R;
XX
DR WPI; 2004-068584/07.
XX
PT Identifying an HLA genotype of a subject by hybridizing the amplification
PT products with an HLA locus-specific capture oligonucleotide and detecting
PT the detectable complexes to identify the HLA genotype of the subject.
XX
PS Example 1; SEQ ID NO 19; 68pp; English.
XX
CC The invention describes a method of identifying a human leukocyte antigen
CC (HLA) genotype of a subject comprising: obtaining a sample comprising a
CC template nucleic acid from the subject; amplifying the template nucleic
CC acid with HLA allele-specific forward primers and HLA allele-specific
CC reverse primers to form amplification products; hybridising the
CC amplification products with an HLA locus-specific capture oligonucleotide
CC ; and detecting the detectable complexes to identify the HLA genotype of
CC the subject. The present sequence represents one of 276 HLA locus-
CC specific capture oligonucleotides of the invention.
XX
SQ Sequence 18 BP; 4 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3492 TTGGCTGAGACCTGGG 3507
||||||| ||||||||
Db 18 TTGGCTGCGACCTGGG 3

RESULT 1424
ADO56496
ID ADO56496 standard; DNA; 18 BP.
XX
AC ADO56496;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #21.
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;
KW single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
XX
OS Homo sapiens.
XX
PN WO2004044164-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035879.
XX
PR 06-NOV-2002; 2002US-0424475P.
PR 23-JUL-2003; 2003US-0489703P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM;
XX
DR WPI; 2004-411721/38.
XX
PT Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.
XX
PS Example 5; Page 84; 295pp; English.
XX
CC The invention relates to a method of identifying a subject at risk of
CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
XX
SQ Sequence 18 BP; 3 A; 7 C; 1 G; 6 T; 0 U; 1 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1529 CTCTTCTAGGCCCATT 1544
||||||| |||||||
Db 1 CTCTTCTAAGCCCATT 16

RESULT 1425
AAA47676
ID AAA47676 standard; cDNA; 15 BP.
XX
AC AAA47676;
XX
DT 08-NOV-2000 (first entry)
XX
DE Oligo d(T) primer for human DDAH1.
XX
KW Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
KW arginine deaminase; hyperlipidemia; renal failure; hypertension;
KW restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;
KW ischemia reperfusion injury; septic shock; multi organ failure;
KW arthritis; skin disorders; inflammatory cardiac disease; migraine;
KW infection; ss.
XX
OS Homo sapiens.
XX
PN WO200044888-A2.
XX
PD 03-AUG-2000.
XX
PF 26-JAN-2000; 2000WO-GB000226.
XX
PR 26-JAN-1999; 99GB-00001705.
PR 04-JUN-1999; 99GB-00013066.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Vallance PJT, Leiper JM, Whitley GSJ, Charles IG;
XX
DR WPI; 2000-543392/49.
XX
PT Novel methylarginase polypeptides and polynucleotides, used to identify
PT modulators of them, which are used in the treatment of e.g. cancer,
PT hypertension, and bacterial infections.
XX
PS Example 1; Page 33; 68pp; English.
XX
CC Nucleotides encoding methylarginase polypeptides, vectors comprising
CC these mucleotides and the polypeptides themselves can be used in
CC medicaments for the treatment of hyperlipidemia, renal failure,
CC hypertension, restenosis after angioplasty, atherosclerosis,
CC complications of heart failure, schizophrenia, multiple sclerosis or
CC cancer. Modulators of the enzyme can be used in medicaments for the
CC treatment of ischemia-reperfusion injury of the brain or heart, cancer,
CC lethal hypertension in severe inflammatory conditions such as septic
CC shock or multi-organ failure, or local and systemic inflammatory

```
CC   disorders including arthritis, skin disorders, inflammatory cardiac
CC   disease, migraine, or microbial or bacterial infection. The sequence of
CC   human DDAH1 was obtained by data base searching. The EST's used in the
CC   process are given in GENESEQ records AAA47661-A47677
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 9.9e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 15


RESULT 1426
AAD44150/c
ID   AAD44150 standard; DNA; 15 BP.
XX
AC   AAD44150;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-AT PCR primer #1 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1D; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo AT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 9.9e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||:|
Db         15 TTTTTTTTTTTTTBT 1


RESULT 1427
AAX18387
ID   AAX18387 standard; DNA; 16 BP.
XX
AC   AAX18387;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 28.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 15


RESULT 1428
AAF82119
ID   AAF82119 standard; DNA; 16 BP.
XX
AC   AAF82119;
XX
DT   27-JUN-2001  (first entry)
XX
DE   Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
KW   Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
KW   diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001025389-A.
XX
PD   30-JAN-2001.
XX
```

```
PF   15-JUL-1999;   99JP-00201279.
XX
PR   15-JUL-1999;   99JP-00201279.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-303742/32.
XX
PT   TSA7005 gene, encoding a polypeptide useful for the diagnosis and
PT   treatment of diseases associated with its expression.
XX
PS   Example 1; Page 24; 25pp; Japanese.
XX
CC   The present sequence represents a PCR primer which is used in an example
CC   from the present invention for the isolation of human TSA7005 gene. The
CC   human TSA7005 protein shares 32% homology with human and mouse Reg
CC   proteins, and 34% homology with the rat Reg protein. TSA7005 has
CC   pancreatic beta cell growth activity and hypoglycaemic activity. The
CC   TSA7005 protein can be used for the diagnosis and treatment of diseases
CC   associated with the gene and its expression product
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTH 15


RESULT 1429
AAH27758
ID   AAH27758 standard; DNA; 16 BP.
XX
AC   AAH27758;
XX
DT   15-AUG-2001  (first entry)
XX
DE   Primer used in human LUNX cDNA isolation.
XX
KW   LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001078772-A.
XX
PD   27-MAR-2001.
XX
PF   07-SEP-1999;   99JP-00253186.
XX
PR   07-SEP-1999;   99JP-00253186.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-313367/33.
XX
PT   Polynucleotide encoding LUNX gene product useful for the detection of
PT   cancer especially micrometastatic cancer.
XX
PS   Example 1; Page 27; 30pp; Japanese.
XX
CC   This invention relates to the human LUNX protein and the polynucleotide
CC   sequence encoding it. The invention includes a vector containing a LUNX
CC   polynucleotide, a host cell transformed with the vector, and an antibody
CC   that binds to LUNX. The gene can be used for cancer diagnosis and
CC   diagnosis of micrometastatic cancer and for the production of the LUNX
CC   gene product. The present sequence represents a primer used in the
CC   isolation of cDNA encoding human LUNX
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 15


RESULT 1430
AAD44145
ID   AAD44145 standard; DNA; 16 BP.
XX
AC   AAD44145;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #5 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              :|||||||||||||||
Db          2 VTTTTTTTTTTTTTT 16


RESULT 1431
AAD44143
ID   AAD44143 standard; DNA; 16 BP.
XX
AC   AAD44143;
XX
DT   13-DEC-2002  (first entry)
XX
```

```
DE   Oligo-dT PCR primer #3 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              :|||||||||||||||
Db          2 VTTTTTTTTTTTTTT 16


RESULT 1432
ADH70642/c
ID   ADH70642 standard; DNA; 19 BP.
XX
AC   ADH70642;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #432.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 836; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2392 AAATATATATACATATATA 2410
              | ||||||||  |||||||
Db         19 ATATATATATTTATATATA 1


RESULT 1433
ABL51521
ID   ABL51521 standard; DNA; 19 BP.
XX
AC   ABL51521;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Tailing reaction related exemplary primer dA18U SEQ ID NO:2.
XX
KW   Tailing reaction; tailed primer; primer; probe; identification;
KW   detection; linear amplification scheme; chain extending enzyme;
KW   telomerase; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        19
```

FT /*tag= a
XX
PN US2002031776-A1.
XX
PD 14-MAR-2002.
XX
PF 26-JUL-2001; 2001US-00917138.
XX
PR 28-MAY-1999; 99US-0136545P.
PR 25-MAY-2000; 2000US-00580358.
XX
PA (TULL/) TULLIS R H.
PA (STRE/) STREIFEL J A.
XX
PI Tullis RH, Streifel JA;
XX
DR WPI; 2002-361176/39.
XX
PT Identifying and detecting nucleic acids, particularly DNA hybridization
PT probes, involves employing chain extending enzymes (e.g. telomerase) to
PT elongate probes to render them readily detectable.
XX
PS Example 1; Page 5; 10pp; English.
XX
CC The present invention describes a method for detecting a nucleic acid
CC probe, which comprises using chain extending enzymes to elongate probes.
CC The method comprises: (a) treating the sample with a chain terminating
CC reagent to prevent polynucleotide chain growth from the nucleic acid in
CC the sample; (b) contacting the sample with the probe containing a
CC terminus capable of elongation by a chain extending enzyme, where the
CC probe hybridises to the nucleic acid in the sample; (c) contacting the
CC sample with a chain extending enzyme and its substrates, which elongates
CC the probe; and (d) detecting the elongated hybridised probe. Also
CC described is a method comprising: (a) treating nucleic acid molecules or
CC modified nucleic acids in a sample with a reagent or reagents that render
CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC (b) hybridising the treated molecules with a nucleic acid probe that
CC includes an extendable terminus, under conditions where hybrids form; and
CC (c) treating any hybrids formed with a non-template dependent chain
CC elongating enzyme and its substrates, where any hybridised probe is
CC extended. The method is useful for identifying and detecting nucleic
CC acids, particularly DNA hybridisation probes. The present sequence
CC represents a tailing reaction exemplary primer, which is used in an
CC example from the present invention
XX
SQ Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAAT 3623
||||||| ||||| | ||:
Db 1 AAAAAAAAAAAAAAAAAAU 19

RESULT 1434
ABZ85669/c
ID ABZ85669 standard; DNA; 20 BP.
XX
AC ABZ85669;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 911; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
|||||||| ||||| | ||
Db 19 GAAAAAAAGAAAAAAAAAA 1

RESULT 1435
ABD21899/c
ID ABD21899 standard; DNA; 20 BP.
XX
AC ABD21899;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stanniocalcin-derived oligo SEQ ID 911.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 911; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              |||||||| ||||| | ||
Db         19 GAAAAAAAGAAAAAAAAAA 1
```

RESULT 1436
ABL57565/c
ID ABL57565 standard; DNA; 20 BP.
XX
AC ABL57565;
XX
DT 26-JUL-2002 (first entry)
XX
DE Nucleic acid probe u.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; probe; ss.
XX
OS Unidentified.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a nucleic acid probe of the
CC invention that was used for investigating the effects or the numbers of
CC G(s) in each target nucleic acid, and the number of G(s) in its
CC corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 15 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

```
  Query Match             0.3%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db         19 ATATATATATTTTTTTTTT 1
```

RESULT 1437
ABL95912
ID ABL95912 standard; DNA; 20 BP.
XX
AC ABL95912;
XX

DT 19-JUN-2002 (first entry)
XX
DE Probe poly u for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 13; Page 62; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 20 BP; 5 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       4492 ATTTATAAGTTTTTTTTTT 4510
              || ||||  ||||||||||
Db          2 ATATATATATTTTTTTTTT 20
```

RESULT 1438
ABL57553
ID ABL57553 standard; DNA; 20 BP.
XX
AC ABL57553;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly t.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       4493 TTTATAAGTTTTTTTTTT 4511
              | ||||  ||||||||||
Db          1 TATATATATTTTTTTTTT 19
```

RESULT 1439
ABL57548
ID ABL57548 standard; DNA; 20 BP.
XX
AC ABL57548;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly o.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.

XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4493 TTTATAAGTTTTTTTTTTT 4511
| |||| ||||||||||
Db 1 TATATATATTTTTTTTTTT 19

RESULT 1440
ABA97638
ID ABA97638 standard; DNA; 20 BP.
XX
AC ABA97638;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly t nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 4 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4493 TTTATAAGTTTTTTTTTTT 4511
| |||| ||||||||||
Db 1 TATATATATTTTTTTTTTT 19

RESULT 1441
ABZ89719/c
ID ABZ89719 standard; DNA; 20 BP.
XX
AC ABZ89719;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX

PS Disclosure; SEQ ID NO 4961; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3606 AAAAAACAAAAACAGAATT 3624
||||||||||||| | ||||
Db 19 AAAAAAAAAAAAAAAAATT 1

RESULT 1442
ABD25949/c
ID ABD25949 standard; DNA; 20 BP.
XX
AC ABD25949;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA906703-derived oligonucleotide SEQ ID 4961.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4961; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3606 AAAAAACAAAAACAGAATT 3624
||||||||||||| | ||||
Db 19 AAAAAAAAAAAAAAAAATT 1

RESULT 1443
ADK01328/c
ID ADK01328 standard; DNA; 21 BP.
XX
AC ADK01328;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #48.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX

```
DR   WPI; 2003-714082/68.
XX
PT   Sorting single-stranded nucleic acid, useful for analyzing expression
PT   patterns and screening active agents, uses capture agent with variable
PT   and constant regions.
XX
PS   Example; Page 5; 8pp; German.
XX
CC   This invention describes a novel method for sorting single-stranded
CC   nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC   reading out, where the nucleic acids are selectively bound using capture
CC   agents that are (a) immobilised on the surface of a solid matrix and (b)
CC   comprise variable and non-variable regions. The capture oligonucleotides
CC   have a 5'-invariable anchor region, the complement of which is present at
CC   least once in each nucleic acid and a 3'-variable, discriminatory region
CC   that comprises all possible combinations of up to 10 nucleotides to allow
CC   binding of particular sorts of single stranded nucleic acids. The capture
CC   agents are particularly locked nucleic acids (LNA) and the anchor region
CC   comprises a sequence of 10-50, particularly 15-25, T residues. The
CC   capture oligonucleotides are biotinylated and immobilised on a surface by
CC   interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC   metal, resin, gel, crystalline material and/or membrane, having semi-
CC   conducting properties and especially in the form of a chip. Its surface
CC   is particularly a layer of (bio)molecular filaments and binding of single
CC   stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC   physical, stimulated by an electrical field or through a molecular sieve.
CC   The method is used (i) for analysis of patterns, especially in mucosal,
CC   hair root, blood, nerve or germ cells and (ii) for determining the
CC   activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC   additives or supplements, especially minerals, trace elements, organic
CC   acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC   mixtures. The method provides rapid, inexpensive and reproducible
CC   representation of differences in pools of nucleic acids from cells. It
CC   allows imaging of the complete pattern of all nucleic acid in a cell, and
CC   can detect very small differences in the nucleic acid pool. Since the
CC   method is based on comparison of nucleic acid pools, not individual
CC   genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC   capture probes used in the method of the invention.
XX
SQ   Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 1444
AAX69803
ID   AAX69803 standard; RNA; 17 BP.
XX
AC   AAX69803;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.3%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.2e+03;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTT 4514
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 14


RESULT 1445
AAX69802/c
ID   AAX69802 standard; RNA; 17 BP.
XX
AC   AAX69802;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
```

PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACA 3619
||||||||| ||||| |
Db 17 GGAAAAAAAAAAAAAAA 1

RESULT 1446
ABX79793/c
ID ABX79793 standard; cDNA; 17 BP.
XX
AC ABX79793;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #118.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX
DR WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 483; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACA 3619
||||||||| ||||| |
Db 17 GGAAAAAAAAAAAAAAA 1

RESULT 1447
ADB04270/c
ID ADB04270 standard; DNA; 17 BP.
XX
AC ADB04270;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5256.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5256; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The

```
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| |||
Db         17 AAAAAAAAAAAAAAAGA 1


RESULT 1448
ADP71260/c
ID   ADP71260 standard; DNA; 17 BP.
XX
AC   ADP71260;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Oligo #12 for gaseous sample sensor array detection method.
XX
KW   ss; sensor array system; gaseous sample; vapor sample; chemical hazard;
KW   air quality; medical condition; explosive detection; mining;
KW   hazardous chemical; odor; smell.
XX
OS   Synthetic.
XX
PN   WO2004048937-A2.
XX
PD   10-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US038186.
XX
PR   25-NOV-2002; 2002US-00303548.
PR   25-NOV-2002; 2002US-0428869P.
XX
PA   (TUFT ) UNIV TUFTS.
XX
PI   White JE,  Kauer JS;
XX
DR   WPI; 2004-487426/46.
XX
PT   Sensor array system for remote characterizing gaseous or vapor sample,
PT   has sensors having nucleic acid/fluorophore combination, measuring
PT   apparatus, transmitting device and computer having algorithm for
PT   characterizing analyte.
XX
PS   Disclosure; SEQ ID NO 10; 91pp; English.
XX
CC   The invention relates to a sensor array system for remote characterizing
CC   gaseous or vapor sample, has several sensors providing detectable signal
CC   on contacting analyte and each sensor has nucleic acid/fluorophore
CC   combination, measuring apparatus measures detectable signal, transmitting
CC   device transmits information with respect to detectable signal to remote
CC   location through internet, and computer having residential algorithm for
CC   characterizing analyte. (I) is useful in monitoring chemical hazards, air
CC   quality, and medical conditions, and detecting explosives, mines, and
CC   hazardous chemicals. (I) or (II) is useful in transmitting identified
CC   information on various odors or smells, e.g., vapor or gaseous analytes
CC   through internet. This sequence represents an oligonucleotide used in the
CC   method of the invention.
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         17 GGAAAAAAAAAAAAAAA 1


RESULT 1449
ADP86184/c
ID   ADP86184 standard; DNA; 17 BP.
XX
AC   ADP86184;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #55 (DNA-RNA hybrid).
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   misc_RNA         3
FT                    /*tag=  b
FT                    /label= RNA
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 55; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide (DNA-RNA hrbrid).
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 15 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

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Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| |||
Db         17 AAAAAAAAAAAAAAAGA 1
```

RESULT 1450
AAV54175/c
ID AAV54175 standard; cDNA; 18 BP.
XX
AC AAV54175;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 12.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 51; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match   0.3%; Score 13.8; DB 1; Length 18;
  Best Local Similarity   88.2%; Pred. No. 1.3e+03;
  Matches   15; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

```
Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         18 GGAAAAAAAAAAAAAAA 2
```

RESULT 1451
AAZ90651/c
ID AAZ90651 standard; DNA; 18 BP.
XX
AC AAZ90651;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #12.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match   0.3%; Score 13.8; DB 1; Length 18;
  Best Local Similarity   88.2%; Pred. No. 1.3e+03;
  Matches   15; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db         18 GGAAAAAAAAAAAAAAA 2
```

RESULT 1452
ABL57540/c
ID ABL57540 standard; DNA; 18 BP.
XX
AC ABL57540;
XX
DT 26-JUL-2002 (first entry)
XX
DE Nucleic acid probe d.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; probe; ss.
XX
OS Unidentified.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a

```
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a nucleic acid probe of the
CC   invention that was used for investigating the base selectivity of a
CC   target nucleic acid
XX
SQ   Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4495 TATAAGTTTTTTTTTT 4511
              ||||  ||||||||||
Db         17 TATATATTTTTTTTTT 1


RESULT 1453
AAA58385
ID   AAA58385 standard; DNA; 18 BP.
XX
AC   AAA58385;
XX
DT   01-NOV-2000  (first entry)
XX
DE   Polynucleotide # 1 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999;   99WO-US026612.
XX
PR   10-NOV-1998;   98US-0107828P.
PR   09-NOV-1999;   99US-00437076.
XX
PA   (BIOC-) BIOCRYSTAL LTD.
XX
PI   Barbera-Guillem E,  Nelson MB,  Castro S;
XX
DR   WPI; 2000-376593/32.
XX
PT   Functionalized nanocrystal carrying polynucleotide, used for detecting
PT   target analyte, forms dendrimers with complementary nanocrystals to
PT   amplify the fluorescent signal.
XX
PS   Example 3; Page 68; 72pp; English.
XX
CC   The present invention relates to functionalised nanocrystals for use in
CC   nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC   proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC   attached to their surfaces with one end of the polynucleotide extending
CC   outwardly from the nanocrystal. The present sequence is one such
CC   polynucleotide. These nanocrystals are used with a second series of
CC   nanocrystals, which have polynucleotides complementary to the first
CC   polynucleotides, so that the respective complementary strands hybridise
CC   to each other and form a dendrimer. This dendrimer produces a signal
CC   which can then be detected e.g. fluorescence. The present sequence is
CC   composed mainly of Adenine bases. This sequence may therefore be used
CC   with a polynucleotide composed mainly of Thymine bases (AAA58386)
XX
SQ   Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db          2 GGAAAAAAAAAAAAAAA 18


RESULT 1454
ADH70777
ID   ADH70777 standard; DNA; 18 BP.
XX
AC   ADH70777;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #567.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 971; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
```

```
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| || ||||
Db          1 ATATATATATATGTATA 17


RESULT 1455
ABZ77072
ID   ABZ77072 standard; DNA; 20 BP.
XX
AC   ABZ77072;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:27.
XX
KW   Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW   2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW   antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW   abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW   atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO2003012031-A2.
XX
PD   13-FEB-2003.
XX
PF   16-JUL-2002; 2002WO-US022676.
XX
PR   30-JUL-2001; 2001US-00918187.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248160/24.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding human
PT   stearoyl-CoA desaturase, useful for treating diseases associated with the
PT   desaturase, e.g. atherosclerosis, and in diagnostic and research
PT   applications.
XX
PS   Example 15; Page 94; 117pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC   desaturase, and which specifically hybridises with and inhibits the
CC   expression of human stearoyl-CoA desaturase, or which specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on a
CC   nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC   stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC   cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC   activities, and can be used in antisense therapy. The antisense compounds
CC   (I) can be used for modulating the expression of human stearoyl-CoA
CC   desaturase and for treating diseases or conditions associated with
CC   expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC   cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC   antisense compounds (I) can also be used for diagnostics, therapeutics
CC   and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumour formation, as research reagents and kits, and in distinguishing
CC   between functions of various members of a biological pathway. The present
CC   sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC   phosphorothioate antisense oligonucleotide, which is given in an example
CC   from the present invention
XX
SQ   Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2213 AAACAGCAGCTCATGGA 2229
              ||  ||||||||||||||
Db          4 AATGAGCAGCTCATGGA 20


RESULT 1456
AAD35095/c
ID   AAD35095 standard; DNA; 20 BP.
XX
AC   AAD35095;
XX
DT   25-JUL-2002  (first entry)
XX
DE   HT15-C downstream PCR primer used for identification of genes.
XX
KW   Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
KW   sex discrimination; infertility treatment; chromosomal manipulation;
KW   sperm separation; gene therapy; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   EP1195382-A2.
XX
PD   10-APR-2002.
XX
PF   02-OCT-2001; 2001EP-00123259.
XX
PR   03-OCT-2000; 2000JP-00303994.
XX
PA   (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
PA   (UYGU-) UNIV GUNMA.
XX
PI   Aizawa A,  Kawakami A,  Kondo T;
XX
DR   WPI; 2002-354153/39.
XX
PT   New X-chromosome gene expressed in haploid cells of the testis, useful
PT   for gene diagnosis, discrimination of sex, separation of sperm,
PT   infertility treatment and chromosomal manipulation.
XX
```

PS Example 1; Page 4; 28pp; English.
XX
CC The present invention relates to genes located on the X-chromosome of
CC mammals. These genes are specifically expressed in haploid cells of the
CC testis and encode amino acid sequences having homology with the amino
CC acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences
CC of the invention are used for gene diagnosis, discrimination of sex,
CC separation of sperm, infertility treatment and chromosomal manipulation,
CC especially in livestock. They are also used in gene therapy. The present
CC DNA sequence is a PCR primer which is used for the identification of
CC genes by differential display method
XX
SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAG 3620
||||||||| ||||| ||
Db 20 GAAAAAAAAAAAAAAAG 4

RESULT 1457
ABT07496
ID ABT07496 standard; DNA; 20 BP.
XX
AC ABT07496;
XX
DT 14-NOV-2002 (first entry)
XX
DE Rat protein phosphatase 2 oligo inhibitor SEQ ID No 110.
XX
KW Cytostatic; antidiabetic; antisense therapy; aberrant insulin regulation;
KW protein phosphatase 2 catalytic beta subunit; antisense compound; cancer;
KW hyperproliferative disorder; diabetes; inflammation; tumour; rat; ds.
XX
OS Rattus norvegicus.
XX
PN WO200264737-A2.
XX
PD 22-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-US002805.
XX
PR 09-FEB-2001; 2001US-00780045.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-657588/70.
XX
PT New antisense oligonucleotides targeted to nucleic acid encoding Protein
PT Phosphatase 2 catalytic subunit beta, useful for treating diseases
PT related to Protein Phosphatase 2 catalytic subunit beta expression, such
PT as cancer.
XX
PS Example 16; Page 98; 137pp; English.
XX
CC The invention relates to a novel compound 8-50 nucleotides in length
CC targeted to a nucleic acid molecule encoding a protein phosphatase 2
CC catalytic beta subunit, where the compound specifically hybridises with
CC and inhibits the expression of protein phosphatase 2 catalytic beta
CC subunits, or specifically hybridises with at least an 8-nucleotide
CC portion of an active site on a nucleic acid molecule encoding a protein
CC phosphatase 2 catalytic beta subunit. The antisense compounds are useful
CC for modulating the expression of protein phosphatase 2 catalytic beta
CC subunits and for treating diseases or conditions associated with
CC expression of protein phosphatase 2 catalytic beta subunits, e.g.
CC aberrant insulin regulation or diabetes or a hyperproliferative disorder,
CC particularly cancer. The antisense compounds are also useful for
CC diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay
CC infection, inflammation or tumour formation, as research reagents and
CC kits, and in distinguishing between functions of various members of a
CC biological pathway. This polynucleotide sequence represents an
CC oligonucleotide inhibitor of rat protein phosphatase 2 catalytic beta
CC subunit mRNA levels of the invention. NOTE: This oligonucleotide contains
CC phosphorothioate residues and has 2'- MOE wings with a deoxy gap
XX
SQ Sequence 20 BP; 7 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATACATT 2414
||||||| ||||||| ||
Db 1 TATATATGTATATATATTTT 20

RESULT 1458
AAZ09195
ID AAZ09195 standard; DNA; 20 BP.
XX
AC AAZ09195;
XX
DT 19-OCT-1999 (first entry)
XX
DE Oligonucleotide 7 for DNA analysis.
XX
KW Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS Synthetic.
XX
PN JP11196874-A.
XX
PD 27-JUL-1999.
XX
PF 14-JAN-1998; 98JP-00005399.
XX
PR 14-JAN-1998; 98JP-00005399.
XX
PA (HITA) HITACHI LTD.
XX
DR WPI; 1999-496652/42.
XX
PT Analysis of DNA fragment - comprises addition of known common
PT oligonucleotide, amplification of resultant DNA fragment and analysis and
PT labelling of amplified DNA.
XX
PS Example 1; Page 12; 17pp; Japanese.
XX
CC This invention descibes a novel method for the analysis of a DNA fragment
CC which comprises: (i) addition of a known common oligonucleotide sequence
CC to at least one terminal of each DNA fragment, (ii) amplification of the
CC resultant DNA fragment as a primer using a first common primer containing
CC a complementary nucleotide sequence to the above mentioned known common
CC oligonucleotide sequence, a second common primer containing a
CC complementary nucleotide sequence to the prepared known common
CC oligonucleotide sequence optionally having been introduced with
CC complementary nucleotide sequence at a terminal, and a specific primer
CC capable of hybridisation with a DNA fragment containing whole or part of
CC the gene having known sequence, to give amplified DNA, (iii) analysis of
CC the amplified DNA to find the information of the DNA fragment, in which
CC the specific primer is designed to prepare fragments of the common first
CC and second primers and to give short fragment of amplified DNA and (iv)
CC labelling them to make their differentiation. Differentiation of
CC informations of known and unknown genes readily provides information of
CC unknown gene and simultaneous monitoring of signals derived from minor
CC genes. Furthermore, labelling of DNAs according to functions of known
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC used to illustrate the method of the invention
XX
SQ Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3600 TCTGGAAAAAAACAAAAACA 3619
              |||  ||||||| ||||| |
Db          1 TCTCCAAAAAAAAAAAAAAA 20
```

RESULT 1459
ABZ89872
ID ABZ89872 standard; DNA; 20 BP.
XX
AC ABZ89872;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5114; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

```
  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAACAG 3620
              ||  ||||||| ||||| ||
Db          1 CTCAAAAAAAAAAAAAAAAG 20
```

RESULT 1460
ABD26102
ID ABD26102 standard; DNA; 20 BP.
XX
AC ABD26102;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA463249-derived oligonucleotide SEQ ID 5114.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 5114; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,

```
CC   inflammation, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC   transplantation rejection, pulmonary infections, bronchitis or cancer.
CC   The reduced adenosine content of the anti-sense oligos corresponding to
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAACAG 3620
              ||  ||||||| ||||| ||
Db          1 CTCAAAAAAAAAAAAAAAAG 20


RESULT 1461
AAQ75574/c
ID   AAQ75574 standard; DNA; 20 BP.
XX
AC   AAQ75574;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACAGAA 3622
              || |||||| ||||| | ||
Db         20 GGCAAAAAAAAAAAAAAAAA 1


RESULT 1462
AAQ75572/c
ID   AAQ75572 standard; DNA; 20 BP.
XX
AC   AAQ75572;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACAGA 3621
              || ||||||| ||||| | |
Db         20 TGCAAAAAAAAAAAAAAAAA 1


RESULT 1463
AAF83959/c
ID   AAF83959 standard; DNA; 20 BP.
XX
AC   AAF83959;
XX
DT   06-AUG-2001  (first entry)
XX
DE   BAP28 gene fragment amplifying primer BAP28polyTcourt.
XX
KW   BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100669-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-IB001183.
XX
```

PR 25-JUN-1999; 99US-0141323P.
PR 18-JAN-2000; 2000US-0176880P.
XX
PA (GEST) GENSET.
XX
PI Barry C, Bougueleret L, Chumakov I, Cohen-Akenine A;
XX
DR WPI; 2001-367032/38.
XX
PT New BAP28 polynucleotides and polypeptides overexpressed in prostate
PT cancer cells for diagnosing prostate tumors, e.g. by hybridization or
PT polymerase chain reaction assays.
XX
PS Example; Page 347; 349pp; English.
XX
CC The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
CC sequences and regulatory region located at the 3' and 5' ends of the
CC BAP28 coding region. The BAP28 polypeptides can be expressed by standard
CC recombinant methodology. BAP28 polynucleotides and polypeptides have been
CC found to be over expressed in prostate tumour cells, therefore levels of
CC BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
CC reaction (PCR)) to diagnose patient suffering from or susceptible to
CC prostate cancer. Antibodies specific for the BAP28 polypeptides are
CC useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
CC useful in genetic analysis. Sequences AAF83934-963 represent primers for
CC the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on
CC the opposite of the coding strand of BAP28)
XX
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3963 TATATAAACAATAAAAACAA 3982
|||| ||| || ||||| ||
Db 20 TATACAAAAAAAAAAAAAAA 1

RESULT 1464
ADK73725/c
ID ADK73725 standard; DNA; 20 BP.
XX
AC ADK73725;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1059.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1059; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2381 GGTCAAAAATAAAATATATA 2400
|||||||| |||| | | |
Db 20 GGTCAAAAAAAAAAAAAAAA 1

RESULT 1465
ADM14751/c
ID ADM14751 standard; DNA; 20 BP.
XX
AC ADM14751;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:938.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methocyethyls"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX

PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 938; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3600 TCTGGAAAAAAACAAAAACA 3619
|||| |||||| ||||| |
Db 20 TCTGCCAAAAAAAAAAAAAA 1

RESULT 1466
ABS98543
ID ABS98543 standard; DNA; 21 BP.
XX
AC ABS98543;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human acetyl choline muscarinic receptor 3 polymorphic sequence #9.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 28; Page 159; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 21 BP; 9 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.6; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2394 ATATATATACATATATACAT 2413
|||||||| |||||| ||
Db 1 ATATATATGTGTATATATAT 20

RESULT 1467

```
ABL57076/c
ID   ABL57076 standard; DNA; 16 BP.
XX
AC   ABL57076;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence (single mismatch).
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    9
FT                   /*tag=  a
FT                   /note= "mismatch site"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is that of a single mismatch target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Experiments with the present
CC   sequence and a perfectly-matched target (see ABL57071) showed that
CC   hybridisation was very specific to the matched target. The invention
CC   relates generally to the use of metal surface quenchers such as particles
CC   or films for high sensitivity applications in, for example, detection and
CC   diagnostic systems
XX
SQ   Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||| |||||||
Db         16 TTTTTTTGTTTTTTT 2


RESULT 1468
AAD57846/c
ID   AAD57846 standard; DNA; 16 BP.
XX
AC   AAD57846;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #3 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20-B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||| |||||||
Db         16 TTTTTTTGTTTTTTT 2


RESULT 1469
ADF23332/c
ID   ADF23332 standard; DNA; 16 BP.
XX
AC   ADF23332;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Binding partner sceening method molecular beacon analogue #3.
XX
KW   binding partner screening; light beam; nonlinear optical light beam; ss;
KW   molecular beacon analogue.
XX
OS   Synthetic.
XX
PN   US2003148391-A1.
XX
PD   07-AUG-2003.
XX
PF   06-JUN-2002; 2002US-00164915.
XX
PR   24-JAN-2002; 2002US-0351879P.
PR   06-FEB-2002; 2002US-0354668P.
PR   06-FEB-2002; 2002US-0354679P.
```

PR 05-MAR-2002; 2002US-0362003P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-897567/82.
XX
PT Screening of candidate binding partners for binding to test molecule
PT comprises illuminating sample with light beams and measuring physical
PT properties of nonlinear optical light beam emanating from sample.
XX
PS Disclosure; SEQ ID NO 3; 58pp; English.
XX
CC The invention describes screening a candidate binding partner by
CC illuminating the sample with light beams at fundamental frequencies to
CC binding partners, and measuring physical properties of a nonlinear
CC optical light beam emanating from sample. On binding to the test molecule
CC the properties change relative to that in absence of exposure of the test
CC molecule. The invention is used in the screening of candidate binding
CC partners for binding to test molecule. This sequence represents a
CC molecular beacon analogue, an exemplary test molecule of the invention.
XX
SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||| |||||||
Db 16 TTTTTTTGTTTTTTT 2

RESULT 1470
ADS15827/c
ID ADS15827 standard; DNA; 16 BP.
XX
AC ADS15827;
XX
DT 02-DEC-2004 (first entry)
XX
DE Control probe targeted to labelled/bound oligo in binding analysis.
XX
KW binding; sequence detection; reaction kinetics; ss; probe.
XX
OS Synthetic.
XX
PN DE10307801-A1.
XX
PD 09-SEP-2004.
XX
PF 24-FEB-2003; 2003DE-01007801.
XX
PR 24-FEB-2003; 2003DE-01007801.
XX
PA (ADVA-) ADVALYTIX AG.
XX
PI Kirchner R, Gauer C;
XX
DR WPI; 2004-654186/64.
XX
PT Analyzing binding between macromolecules, useful for detecting nucleic
PT acids by hybridization, where a labeled detector molecule is immobilized
PT and becomes fluorescent only after specific binding.
XX
PS Example; Page 6; 11pp; German.
XX
CC The invention relates to a novel analytical method for examining binding
CC events between first and second macromolecules. The method comprises
CC preparing a surface on which a fluorescently-labelled first macromolecule
CC is bound and which is at least partly fitted with a fluorescence-
CC suppressing layer. A sample liquid containing the second macromolecule is
CC applied and fluorescence is measured. The first macromolecule has a
CC secondary structure such that its fluorescence is suppressed by the
CC suppressing layer when it is not specifically bound to the second
CC macromolecule, but fluorescence is not suppressed when the two
CC macromolecules are specifically bound. The method of the invention may be
CC used to detect hybridisation of RNA or, particularly DNA, especially for
CC detecting the presence of particular sequences in samples, but also for
CC studying reaction kinetics. The method allows the use of molecular
CC beacons that are simple to prepare or synthesise, particularly because
CC they do not require incorporation of a quencher. The current sequence is
CC that of the control probe of the invention which is targeted to the
CC fluorescent-labelled and bound DNA oligonucleotide in the binding
CC analysis method.
XX
SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||| |||||||
Db 16 TTTTTTTGTTTTTTT 2

RESULT 1471
ADP86146/c
ID ADP86146 standard; DNA; 17 BP.
XX
AC ADP86146;
XX
DT 09-SEP-2004 (first entry)
XX
DE CpG immunostimulatory oligonucleotide #17.
XX
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1. .17
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN WO2004053104-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039775.
XX
PR 11-DEC-2002; 2002US-0432409P.
PR 25-SEP-2003; 2003US-0506108P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX
DR WPI; 2004-487902/46.
XX
PT New oligonucleotides, useful for treating allergy or asthma, viral and
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.
XX
PS Example; SEQ ID NO 17; 104pp; English.
XX
CC The invention relates to a class of CpG immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and

```
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| |||||||
Db         16 AAAAAAAAAAAAACA 2


RESULT 1472
ADP86185/c
ID   ADP86185 standard; DNA; 17 BP.
XX
AC   ADP86185;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #56 (DNA-RNA hybrid).
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   misc_RNA         2
FT                    /*tag=  b
FT                    /label= RNA
FT
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 56; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide (DNA-RNA hrbrid).
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 15 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
             ||||||| |||||||
Db         16 AAAAAAAAAAAAACA 2


RESULT 1473
AAQ38707/c
ID   AAQ38707 standard; RNA; 18 BP.
XX
AC   AAQ38707;
XX
DT   25-MAR-2003  (revised)
DT   15-JUL-1993  (first entry)
XX
DE   First chimeric primer for adding poly A tails.
XX
KW   oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;
KW   treatment; diagnosis; testing; assay; Candida; papillomavirus;
KW   cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;
KW   liver disease; human immunodeficiency virus; herpes simplex virus; HSV;
KW   human immunodeficiency virus; HIV; AIDS; influenza virus;
KW   genetic disease; genetic abnormalities.
XX
OS   Synthetic.
XX
PN   WO9305182-A1.
XX
PD   18-MAR-1993.
XX
PF   04-SEP-1992;   92WO-US007489.
XX
PR   05-SEP-1991;   91US-00755485.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bruice TW;
XX
DR   WPI; 1993-101001/12.
XX
PT   Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule
PT   - for use in therapeutics, diagnostics and research reagents.
XX
PS   Disclosure; Page 27; 61pp; English.
XX
CC   This sequence was used as a PCR primer in order to add a polyA tail to
CC   the 3'end of the highest specific activity selected oligonucleotide in
CC   order to form a first strand. The primer is comprised of a 5'known
CC   sequence and a 3' polynucleotide portion corresp. to the polynucleotide
CC   tail of the first strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;
```

```
  Query Match             0.3%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         18 AAAAAAAAAAAAACA 4


RESULT 1474
AAT96107/c
ID   AAT96107 standard; DNA; 18 BP.
XX
AC   AAT96107;
XX
DT   31-MAR-1998  (first entry)
XX
DE   First chimeric primer.
XX
KW   Determination; oligonucleotide; specific activity; therapy;
KW   target biomolecule; randomised oligonucleotide; diagnosis; research; PCR;
KW   chimeric; primer; ss.
XX
OS   Synthetic.
XX
PN   US5686242-A.
XX
PD   11-NOV-1997.
XX
PF   27-OCT-1994;   94US-00330000.
XX
PR   05-SEP-1991;   91US-00755485.
PR   04-SEP-1992;   92WO-US007489.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Lima WF,  Bruice TW;
XX
DR   WPI; 1997-558135/51.
XX
PT   Determination of oligo-nucleotide with specific activity for target bio-
PT   molecule - using set of randomised oligo-nucleotide(s).
XX
PS   Disclosure; Col 27-28; 22pp; English.
XX
CC   The present sequence was used in the development of a method of
CC   determining an oligonucleotide having specific activity for a target
CC   biomolecule. The method comprises assaying a set of randomised
CC   oligonucleotides for activity against a target biomolecule, separating
CC   active from inactive oligonucleotides and recovering, amplifying and
CC   determining the nucleic acid sequence of the active oligonucleotides. The
CC   oligonucleotides can be used for therapeutic, diagnostic and research
CC   purposes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         18 AAAAAAAAAAAAACA 4


RESULT 1475
AAZ88678/c
ID   AAZ88678 standard; DNA; 18 BP.
XX
AC   AAZ88678;
XX
DT   11-MAY-2000  (first entry)
XX
DE   Chimeric primer #1.
XX
KW   Primer; detection; diagnosis; ss.
XX
OS   Unidentified.
XX
PN   US6022691-A.
XX
PD   08-FEB-2000.
XX
PF   07-NOV-1997;   97US-00965908.
XX
PR   05-SEP-1991;   91US-00755485.
PR   04-SEP-1992;   92WO-US007489.
PR   27-OCT-1994;   94US-00330000.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Lima WF,  Bruice TW;
XX
DR   WPI; 2000-170669/15.
XX
PT   Assay for a chemical or drug in a sample comprises detecting binding of
PT   an oligonucleotide selected from a set of randomized oligonucleotides.
XX
PS   Disclosure; Col 27-28; 20pp; English.
XX
CC   This invention describes a novel method (I) for specifically detecting a
CC   chemical or drug in a sample comprises contacting the sample with an
CC   oligonucleotide having specific activity for a target biomolecule and
CC   detecting the presence or absence of binding where the presence of
CC   binding indicates the presence of the chemical or drug in the sample. The
CC   oligonucleotide is identified by: (a) assaying a prepared set of
CC   randomized oligonucleotides for activity against a target biomolecule;
CC   (b) separating active from inactive oligonucleotides; (c) recovering the
CC   active oligonucleotides; and (d) characterizing the recovered
CC   oligonucleotides by microanalytical structure determination. The method
CC   can be used for diagnostic or research purposes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACA 3619
              ||||||| |||||||
Db         18 AAAAAAAAAAAAACA 4


RESULT 1476
AAZ99489/c
ID   AAZ99489 standard; DNA; 19 BP.
XX
AC   AAZ99489;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX
KW   Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW   2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW   seed germination; seedling growth; gibberellin biosynthetic pathway;
KW   transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
XX
OS   Cucurbita maxima.
XX
PN   WO200009722-A2.
XX
PD   24-FEB-2000.
XX
PF   10-AUG-1999;   99WO-US018066.
XX
```

PR 10-AUG-1998; 98US-0096111P.
PR 07-JUN-1999; 99US-0137977P.
XX
PA (MONS) MONSANTO CO.
XX
PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
PI Piller KJ, Rao S, Ream JE;
XX
DR WPI; 2000-224351/19.
XX
PT Obtaining transgenic plant useful for controlling seed germination and
PT seedling growth comprises transgene comprising a sequence expressing
PT altered levels of an essential hormone.
XX
PS Example 17; Page 262; 267pp; English.
XX
CC The present primer was used to reverse transcribe cDNA encoding a C-20
CC oxidase. The amplifie fragment is used in the method of the invention.
CC The specification describes methods for the inhibition and control of
CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
CC controlled by use of a chimeric expression construct expressing a RNA or
CC protein which suppresses the gibberellin biosynthetic pathway sequence,
CC diverts substrate from the pathway, or degrades pathway substrates or
CC products. The methods uses copalyl diphosphate synthase, 3beta-
CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
CC used to control seed germination and seedling growth especially to
CC regulate gene products of gibberellin biosynthetic pathway and
CC restoration of normal seed germination, in transgenic plants. The plants
CC produced are gibberellin deficient, and have shortened hypocotyl and/or
CC epicotyl phenotypes compared to normal plants
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1477
AAD15201/c
ID AAD15201 standard; DNA; 19 BP.
XX
AC AAD15201;
XX
DT 01-NOV-2001 (first entry)
XX
DE 3' sequencing primer #1 to identify and characterise polynucleotides.
XX
KW Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW nervous system disorder; Parkinson's disease; immune system disorder;
KW ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW coagulation disorder; blood platelet disorder; autoimmune disorder;
KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
KW cardiovascular; antiviral; primer; ss.
XX
OS Unidentified.
XX
PN WO200154651-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002439.
XX
PR 25-JAN-2000; 2000US-0177963P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
XX
DR WPI; 2001-514526/56.
XX
PT New polynucleotides regulated by fatty lesion development and their
PT encoded polypeptides, useful for preventing, treating or ameliorating
PT atherosclerosis, as well as for immune or hyperproliferative disorders.
XX
PS Example 1; Page 79; 188pp; English.
XX
CC The present invention relates to an isolated nucleic acid regulated by
CC fatty lesion development, which comprises any of 55 polynucleotide
CC sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
CC antibody is useful for preventing, treating, modulating or ameliorating a
CC medical condition, particularly atherosclerosis. The invention is used as
CC a marker or detector of nervous system disorder or disease (e.g.
CC Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
CC invention may also be useful for treating deficiencies or disorders of
CC the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
CC syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
CC (e.g.Gaucher's disease), infectious disease (e.g. herpes simplex),
CC coagulation disorders, blood platelet disorders and autoimmune disorders
CC (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
CC The polynucleotide sequence is also used in gene therapy. The present
CC sequence is a 3' sequencing primer used in the identification and
CC characterisation of polynucleotides up-regulated by fatty lesion
CC development
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1478
AAH21968/c
ID AAH21968 standard; DNA; 19 BP.
XX
AC AAH21968;
XX
DT 16-AUG-2001 (first entry)
XX
DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
XX
KW Mouse; human; total gene expression analysis; TOGA; DST; EST;
KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
KW central nervous system; antidepressant; gene therapy; diagnosis;
KW neuropsychiatric disorder; schizophrenia; bipolar disorder;
KW addiction-related behaviour; chromosome identification; immune response;
KW PCR primer; probe; ss.
XX
OS Mus musculus.
XX
PN WO200130972-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029690.
XX
PR 26-OCT-1999; 99US-0161379P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW;
XX
DR WPI; 2001-300499/31.
XX

```
PT   New neuroleptic-regulated polynucleotides expressed in the central
PT   nervous system for diagnosing and treating neuropsychiatric disorders
PT   such as schizophrenia, bipolar disorder and addiction-related behavior.
XX
PS   Example 1; Page 87; 210pp; English.
XX
CC   The present invention describes isolated neuroleptic-regulated nucleic
CC   acid molecules. (I) have neuroleptic, antimanic and antidepressant
CC   activities, and can be used in gene therapy. (I), polypeptides (II)
CC   encoded by (I), or a host cell (III) comprising (I), are useful for
CC   preventing, treating, modulating or ameliorating a medical condition such
CC   as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
CC   diagnosing a pathological condition or susceptibility to a pathological
CC   condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
CC   disorder or addiction-related behaviour. (I) are useful for detecting the
CC   presence of a nucleic acid encoding a protein in a mammalian tissue
CC   sample. (I) can be used as probes and primers, for chromosome
CC   identification, to control gene expression through triple helix formation
CC   or antisense DNA or RNA, in gene therapy to treat the above mentioned
CC   disorders, identifying individuals from minute biological samples, as an
CC   alternative to restriction fragment length polymorphism (RFLP) and as
CC   polymorphic markers for forensic purposes. (I) is also useful as
CC   molecular weight markers on Southern gels, diagnostic probes for the
CC   presence of specific mRNA in a particular cell type, as a probe to
CC   subtract-out known sequences in the process of discovering novel
CC   polynucleotides, for selecting and making oligomers for attachment to a
CC   gene chip or other support, to raise anti-DNA antibodies using DNA
CC   immunisation technique, and as an antigen to elicit an immune response.
CC   AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1479
AAS06525/c
ID   AAS06525 standard; DNA; 19 BP.
XX
AC   AAS06525;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Mouse microglia and macrophage regulatory gene primer #60.
XX
KW   Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
KW   PCR-based total gene expression analysis; TOGA; infectious disorder;
KW   neuroinflammatory pathology; neurodegenerative disease; gene therapy;
KW   hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
KW   ss.
XX
OS   Mus musculus.
XX
PN   WO200134770-A2.
XX
PD   17-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-US030585.
XX
PR   12-NOV-1999;   99WO-US026824.
PR   03-MAR-2000; 2000US-0186770P.
PR   19-JUN-2000; 2000US-0212465P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Carson MJ,  Sutcliffe JG,  Almazan MT,  Tobal GM;
XX
DR   WPI; 2001-308782/32.
XX
PT   New regulated genes of microglia and macrophages, useful for diagnosing,
PT   preventing or treating neuroinflammatory pathology and neurodegenerative
PT   disease.
XX
PS   Example 1; Page 88; 244pp; English.
XX
CC   The present sequence represents a primer used to isolate novel mouse
CC   microglia and macrophage regulatory gene DST (digital sequence tag)
CC   sequences. AAS06401-AAS06590 represent these novel sequences and the
CC   primer sequences used to isolate them. The PCR-based total gene
CC   expression analysis (TOGA) system is used to examine the expression
CC   pattern of molecules corresponding to genes that are regulated in
CC   unstimulated microglia, activated microglia, unstimulated macrophage and
CC   activated macrophage. The polynucleotides of the invention, the
CC   polypeptides encoded by them and antibodies that bind to these
CC   polypeptides are useful are useful for the diagnosis, prevention,
CC   treatment or amelioration of a medical condition, preferably a
CC   neuroinflammatory pathology or a neurodegenerative disease such as
CC   Alzheimer's disease, senile dementia, Parkinson's disease, obsessive
CC   compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,
CC   depression and bipolar manic-depressive disorder. The sequences and
CC   methods of the invention can also be used for detecting or treating
CC   infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g.
CC   cancer), immune disorders (e.g. severe combined immunodeficiency, SCID)
CC   autoimmune diseases (e.g. insulin dependent diabetes mellitus),
CC   inflammatory disorders (e.g. arthritis). The polynucleotides can be used
CC   for gene therapy
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1480
ABK71509/c
ID   ABK71509 standard; DNA; 19 BP.
XX
AC   ABK71509;
XX
DT   30-JUL-2002  (first entry)
XX
DE   CNS related 3' sequencing primer.
XX
KW   Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
KW   neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
KW   Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
KW   Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
KW   addiction; multiple sclerosis; depression; manic-depressive disorder;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO200226936-A2.
XX
PD   04-APR-2002.
XX
PF   01-OCT-2001; 2001WO-US030695.
XX
PR   29-SEP-2000; 2000US-0236790P.
PR   18-JAN-2001; 2001US-0263084P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Thomas EA,  Sutcliffe JG,  Pribyl TM,  Hilbush BS,  Hasel KW;
```

XX
DR WPI; 2002-383271/41.
XX
PT New polynucleotide useful in gene therapy for preventing, treating
PT modulating or ameliorating a medical condition such as psychoses or a
PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
PT mammal.
XX
PS Example 1; Page 40; 254pp; English.
XX
CC This invention relates to the cDNA sequences of novel isolated
CC polynucleotides associated with psychoses or other neuropsychiatric
CC disorders. The sequences of the invention may act as blockers of D_2
CC receptors in the meso-limbic dopamine system. The nucleotide sequences of
CC the invention and the polypeptides encoded by them are useful in the
CC manufacture of a medicament useful for preventing, treating, modulating
CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An
CC antibody that binds the proteins of the invention is useful for
CC preventing, treating, modulating or ameliorating neurological disorders
CC such as psychoses or other neuropsychiatric disorders in a subject. The
CC sequences are also useful for diagnosing neurological disorders or a
CC susceptibility to a neurological disorder such as psychoses and other
CC neuro psychiatric disorders in a subject by determining the presence or
CC absence of mutation in the nucleotide sequence of apolipoprotein D or by
CC determining the alteration (increase or decrease) in the expression of
CC apolipoprotein D. The sequences of the invention are useful in treating
CC deficiencies or disorders of the central nervous system or peripheral
CC nervous system by activating or inhibiting the proliferation,
CC differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells
CC or glial cells. The sequences are useful as a marker or detector of a
CC particular nervous system disease or disorder such as Alzheimer's
CC disease, Pick's disease, Binswanger's disease, other senile dementia,
CC Parkinson's disease, obsessive compulsive disorders, epilepsy,
CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and
CC manic-depressive disorder. The present sequence represents an
CC oligonucleotide primer used in the identification of the cDNA sequences
CC of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1481
ABQ73231/c
ID ABQ73231 standard; DNA; 19 BP.
XX
AC ABQ73231;
XX
DT 27-SEP-2002 (first entry)
XX
DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
XX
KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
KW TOGA primer; ss.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200242420-A2.
XX
PD 30-MAY-2002.
XX
PF 21-NOV-2001; 2001WO-US044072.
XX
PR 21-NOV-2000; 2000US-0252216P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Leonardi A, Sartani A, Glass JR, Hasel KW;
XX
DR WPI; 2002-575233/61.
XX
PT New polynucleotides related to regulated genes characteristic of
PT atherosclerosis, useful for diagnosing, preventing, treating, modulating
PT or ameliorating atherosclerosis in a mammalian subject.
XX
PS Disclosure; Page 28; 130pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) and its
CC complements, and degenerate variants, comprising a sequence selected from
CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
CC (DST) corresponding to mRNAs whose expression is regulated by
CC proliferative lesion development caused by mechanically induced intimal
CC hyperplasia, or by lercanidipine treatment, or by proliferative lesions
CC and reversed by lercanidipine treatment. (I) has antiatherosclerotic
CC activity and can be used in gene therapy. (I) can be used for diagnosing
CC a medical condition (e.g. atherosclerosis) in a subject which involves
CC determining the presence or absence of a mutation in (I) and diagnosing
CC the medical condition based on the presence or absence of the mutation.
CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility
CC to atherosclerosis in a subject which involves detecting an alteration
CC (an increase or decrease) in amount of expression of (I). (I) is also
CC useful for diagnosing or monitoring the effects of treating a subject
CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
CC be used for preventing, treating, modulating, or ameliorating a medical
CC condition such as atherosclerosis in a mammalian subject. The present
CC sequence represents a TOGA primer which is used in the exemplification of
CC the present invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1482
AAD34663/c
ID AAD34663 standard; DNA; 19 BP.
XX
AC AAD34663;
XX
DT 16-JUL-2002 (first entry)
XX
DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
XX
KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
KW TOGA; TOtal Gene expression Analysis; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200222783-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US029123.
XX
PR 15-SEP-2000; 2000US-0233176P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;
XX
DR WPI; 2002-339865/37.

```
XX
PT   Preventing and treating hepatitis viral infection in a mammal, comprises
PT   administering nucleic acid molecules that up- or down-regulate in
PT   hepatitis B virus infection or polypeptides encoded by the nucleic acid
PT   molecules.
XX
PS   Disclosure; Page 28; 125pp; English.
XX
CC   The present invention relates to a method for preventing, treating,
CC   modulating or ameliorating a medical condition. The method involves
CC   administering one or more nucleic acid molecules up- or down-regulated in
CC   hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
CC   acid molecules or antibodies that bind to the polypeptide. The method is
CC   useful for preventing, treating, modulating or ameliorating a medical
CC   condition. It is also useful for determining the presence or absence of a
CC   mutation in the nucleic acid molecules or detecting an alteration in
CC   expression of the polypeptide which is useful for the diagnosis of
CC   hepatitis viral infection. The method is useful for assessing the stage
CC   of hepatitis viral infection (e.g., acute hepatitis versus chronic
CC   hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
CC   for hepatitis viral infection and a gene expression profile is useful for
CC   identifying polypeptides and polynucleotides which are associated with
CC   hepatitis viral infection. Sequences of the invention are used in gene
CC   therapy and as vaccines. Nucleic acid sequences are useful as a
CC   diagnostic markers for HBV infection and for treating infectious
CC   diseases. The present DNA sequence is a PCR primer which is used for
CC   direct sequencing of TOGA (TOtal Gene expression Analysis) generated PCR
CC   products
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1483
AAD40279/c
ID   AAD40279 standard; DNA; 19 BP.
XX
AC   AAD40279;
XX
DT   22-OCT-2002  (first entry)
XX
DE   HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX
KW   Gibberellin; transgenic plant; seed germination; seedling growth; GA;
KW   transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
XX
OS   Cucurbita pepo.
XX
PN   US2002053095-A1.
XX
PD   02-MAY-2002.
XX
PF   10-AUG-1999;   99US-00371307.
XX
PR   10-AUG-1999;   99US-00371307.
XX
PA   (BROW/) BROWN S M.
XX
PI   Brown SM,  Elich TD,  Heck GR,  Kishore GM,  Logusch EW,  Logusch SJ;
PI   Piller KJ,  Rao S,  Ream JE;
XX
DR   WPI; 2002-489107/52.
XX
PT   Control of gibberellin levels in plants useful to avoid unfavorable
PT   conditions in crops to increase yields, using transgenic plants having
PT   reduced seed germination and early seedling growth then treatment to
PT   restore these properties.
XX
PS   Example 19; Page 104; 155pp; English.
XX
CC   The invention relates to control of gibberellin (GA) levels in plants.
CC   The method involves producing transgenic plants having a phenotype of
CC   reduced seed germination and reduced early seedling growth, then
CC   restoring seed germination and early seedling growth by treating plants
CC   with an appropriate compound when conditions are favourable. The method
CC   is useful to control seed germination and/or early seedling growth in
CC   agricultural production so that unfavorable environmental conditions
CC   normally reducing agronomic output can be avoided and yields increased.
CC   Plants also demonstrate increased uniformity of germination, emergence
CC   and seedling vigor, so increasing yields at harvest. The method is
CC   especially useful in crop plants such as e.g. canola, soybean, cotton,
CC   etc., and is also useful in storage and transport of seeds to reduce
CC   premature germination which may affect agronomic or food quality of the
CC   seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta
CC   -3beta hydroxylase cDNA. This primer is used in the exemplification of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1484
ABZ68389/c
ID   ABZ68389 standard; DNA; 19 BP.
XX
AC   ABZ68389;
XX
DT   22-APR-2003  (first entry)
XX
DE   Reverse transcription primer used to produce yeast cDNA.
XX
KW   Histone acetyltransferase; histone deacetylase; gene expression profile;
KW   chromatin-associated protein; gene expression; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003000715-A1.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US019750.
XX
PR   22-JUN-2001; 2001US-0300135P.
XX
PA   (CERE-) CERES INC.
XX
PI   Dang V,  Okamuro J;
XX
DR   WPI; 2003-175280/17.
XX
PT   New chimeric polypeptide comprising a histone acetyltransferase
PT   polypeptide segment and a segment comprising a histone deacetylase
PT   chromatin-associated protein complex subunit, useful for modulating gene
PT   expression in cells.
XX
PS   Example 10; Page 54; 85pp; English.
XX
CC   The specification describes chimeric histone acetyltransferase
CC   polypeptides. The chimeric polypeptides comprise a polypeptide segment
CC   that exhibits histone acetyltransferase activity, and a polypeptide
CC   segment having 40% or greater sequence identity to a subunit of a histone
CC   deacetylase chromatin-associated protein complex. The chimeric
```

CC polypeptides are useful for determining gene expression profiles in
CC specific cells, for modulating gene expression in specific cells, and for
CC making genetically modified eukaryotes. The present sequence represents a
CC reverse transcription primer used in the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1485
ACC79402/c
ID ACC79402 standard; DNA; 19 BP.
XX
AC ACC79402;
XX
DT 04-AUG-2003 (first entry)
XX
DE M13 sequencing primer 3' primer SEQ ID NO:84.
XX
KW Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
KW cytostatic; vaccine; gene therapy; PCR primer; ss.
XX
OS Enterobacteria phage M13.
OS Synthetic.
XX
PN WO2003033668-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033311.
XX
PR 17-OCT-2001; 2001US-0330206P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;
PI Warren AJ;
XX
DR WPI; 2003-393520/37.
XX
PT Preventing or treating a pathological condition e.g., ataxia
PT telangiectasia (AT), AT tumors or other cancers comprises administering
PT polynucleotides.
XX
PS Example 1; Page 76; 184pp; English.
XX
CC The present invention describes a method for preventing or treating a
CC pathological condition (comprising ataxia telangiectasia (AT), AT tumours
CC or other cancers), which comprises administering to a mammalian subject
CC at least one of: (a) a first polynucleotide comprising a sequence having
CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
CC second polynucleotide at least 95% identical to the first polynucleotide;
CC (b) a third polynucleotide comprising at least 10-bp sequence that is
CC hybridisable to the first polynucleotide under stringent conditions; or
CC (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
CC identical to the gene. (I) have cytostatic activities, and can be used in
CC vaccines and in gene therapy. The method is useful for preventing or
CC treating e.g., ataxia telangiectasia (AT), AT tumours or other cancers.
CC ACC79393 to ACC79423 represent primers used in the exemplification of the
CC present invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1486
AAD49149/c
ID AAD49149 standard; DNA; 19 BP.
XX
AC AAD49149;
XX
DT 07-MAR-2003 (first entry)
XX
DE 3' sequencing primer #1 used in the invention.
XX
KW Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;
KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
KW food additive; food preservative; primer; ss.
XX
OS Unidentified.
XX
PN WO200281726-A2.
XX
PD 17-OCT-2002.
XX
PF 15-NOV-2001; 2001WO-US043741.
XX
PR 15-NOV-2000; 2000US-0248892P.
PR 28-NOV-2000; 2000US-0253623P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;
XX
DR WPI; 2003-058561/05.
XX
PT New polypeptide associated with atherosclerosis, useful for treating
PT atherosclerosis, nervous system disorders, immune disorders,
PT hyperproliferative disorders and infectious diseases.
XX
PS Disclosure; Page 139; 146pp; English.
XX
CC The invention relates to polynucleotides and polypeptides associated with
CC atherosclerosis. Polynucleotides of the invention are useful for delivery
CC of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
CC macromolecules. Sequences of the invention are useful for treating
CC nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
CC disorders such as rheumatoid arthritis, Addison's disease, haemolytic
CC anaemia, graft-versus-host disease, inflammation), hyperproliferative
CC disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
CC bacterial, fungal or parasite infection). They are used for regeneration
CC of tissues, to repair, replace or protect damage tissues, for increasing
CC chemotaxis activity of cells, for increasing or decreasing the
CC differentiation or proliferation of embryonic stem cells from a lineage,
CC for modulating mammalian characteristics, (such as body weight or
CC height), for modulating mammalian metabolism affecting catabolism,
CC anabolism, processing utilisation and storage of energy, to change a
CC mammal's mental or physical state, or as a food additive or preservative.
CC The invention is useful in gene therapy. The present sequence is a
CC sequencing primer used in the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622

```
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1487
AAD50267/c
ID   AAD50267 standard; DNA; 19 BP.
XX
AC   AAD50267;
XX
DT   24-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used to illustrate the method of the invention.
XX
KW   Gene expression; drug interaction mechanism; drug screening; primer;
KW   genomic mapping; ss.
XX
OS   Unidentified.
XX
PN   WO200261045-A2.
XX
PD   08-AUG-2002.
XX
PF   01-FEB-2002; 2002WO-US002666.
XX
PR   01-FEB-2001; 2001US-00775217.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA   (QUAN/) QUAN J.
XX
PI   Quan J,  Hilbush BS,  Hasel KWPD,  Sutcliffe GJ,  Chang HW;
PI   Callahan MA;
XX
DR   WPI; 2003-092784/08.
XX
PT   Simplified TOGA method for simultaneous sequence-specific identification
PT   of multiple mRNA molecules in mRNA population, useful for determining
PT   tissue-specific patterns of gene expression or mechanisms of drug
PT   interaction.
XX
PS   Disclosure; Page 39; 93pp; English.
XX
CC   The present invention relates to a novel simplified TOGA (RTM) method for
CC   simultaneous sequence-specific identification of multiple mRNA molecules
CC   in a RNA population. The method involves characterising each of the
CC   sequence-specific polymerase chain reaction (PCR) products by partial
CC   sequence and length. The method is useful for determining tissue-specific
CC   patterns of gene expression or mechanisms of drug interaction. It is also
CC   useful for drug screening, studying physiological processes, genomic
CC   mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
CC   The present sequence is a primer used to illustrate the method of the
CC   invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1488
ADC21495/c
ID   ADC21495 standard; DNA; 19 BP.
XX
AC   ADC21495;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human PRDI-BF1 RT-PCR primer.
XX
KW   tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
KW   multiple myeloma cell; human; PRDI-BF1;
KW   positive regulatory domain I-binding factor-1; MHC;
KW   major histocompatibility complex Class I; cytostatic; vaccine; ss;
KW   primer; PCR.
XX
OS   Homo sapiens.
XX
PN   WO2003029282-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-EP010701.
XX
PR   29-SEP-2001; 2001DE-01048236.
XX
PA   (IMMU-) IMMUGENICS AG.
XX
PI   Theobald M,  Lotz C;
XX
DR   WPI; 2003-354724/33.
XX
PT   New tumor-associated oligopeptide, useful particularly for treating
PT   multiple myeloma, is recognized by CD8 cytotoxic T cells, also
PT   derivatives and related nucleic acid.
XX
PS   Disclosure; Page 22; 64pp; German.
XX
CC   This invention describes a novel tumor-associated oligopeptide that is
CC   recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
CC   CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
CC   myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
CC   regulatory domain I-binding factor-1) which is able to induce an MHC
CC   (major histocompatibility complex) Class I allele variant A2-restricted
CC   immune response of CD8+ CTL against tumor cells. The products of the
CC   invention have cytostatic activity and can be used in a vaccine. The
CC   peptide of the invention, also related retro-inverse and pseudopeptides,
CC   fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
CC   and T cell receptors specific for PRDI-BFI peptides are useful for
CC   treating diseases associated with PRDI-BF1, particularly tumors. The
CC   products of the invention are also useful as diagnostic, therapeutic and
CC   prophylactic agents for detecting, modifying, generating, expanding
CC   and/or regulating activation and functional status of T cells, and for
CC   preparation of poly- or mono-clonal or recombinant A2-restricted T cell
CC   receptors and their functional equivalents. This sequence represents an
CC   RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
CC   invention.
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGAA 3622
              :||||||| ||||| | ||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 1489
ADF74670
ID   ADF74670 standard; DNA; 19 BP.
XX
AC   ADF74670;
XX
DT   26-FEB-2004  (first entry)
XX
DE   DNA oligo (30) used in preparing a library of same length signatures.
XX
KW   ss; tag-DNA signature; adapter-signature-adapter; parallel sequencing;
KW   genomic mapping; genetic identification; medical diagnostic.
XX
```

OS Unidentified.
XX
PN WO2003091416-A2.
XX
PD 06-NOV-2003.
XX
PF 25-APR-2003; 2003WO-US013076.
XX
PR 26-APR-2002; 2002US-0375782P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Fischer A, Hiemisch H, Williams S, Brenner S, Walker R;
PI Vermaas E, Fu R;
XX
DR WPI; 2003-865585/80.
XX
PT Preparing a library of same-length signature sequences from a source
PT nucleic acid population by ligating to the cleaved ends, a second adapter
PT containing a recognition and cleavage site for a second restriction
PT endonuclease.
XX
PS Disclosure; Fig 2a; 54pp; English.
XX
CC This invention relates to a novel method for preparing a library of same-
CC length signature sequences from a source nucleic acid population.
CC Specifically, it comprises producing solid phase cloned libraries of
CC oligonucleotide tag-DNA signature sequence constructs, which are useful
CC for sequencing many polynucleotides simultaneously. The present invention
CC describes a kit for the construction of adapter-signature-adapter
CC constructs using 'first' and 'second' adapters each containing a specific
CC restriction endonuclease recognition site, and which flanks the same
CC length signature sequence. As such, using the method described herein it
CC is possible to do parallel sequencing of large populations of
CC polynucleotides for genomic mapping, genetic identification and medical
CC diagnostics. This oligonucleotide sequence is a DNA oligo involved in the
CC step wise process of preparing a library of same length signature
CC sequences from restriction fragments in an exemplification of the
CC invention.
XX
SQ Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 1 BAAAAAAAAAAAAAAAAAA 19

RESULT 1490
ADL24850/c
ID ADL24850 standard; DNA; 19 BP.
XX
AC ADL24850;
XX
DT 20-MAY-2004 (first entry)
XX
DE Intestinal epithelium/peyer's patch M cell-related primer #15.
XX
KW intestinal epithelium cell development; peyer's patch M cell development;
KW inflammatory bowel disease; glutenenteropathy; infectious disease;
KW autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
KW immune system disorder; hypersensitivity; anaphylaxis;
KW blood group incompatibility; ss; PCR; primer.
XX
OS Unidentified.
XX
PN WO200280852-A2.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US010873.
XX
PR 04-APR-2001; 2001US-0281416P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
XX
DR WPI; 2003-075470/07.
XX
PT Novel isolated or purified polypeptide encoded by genes associated with
PT intestinal epithelium or M cell development, differentiation or function,
PT useful for treating autoimmune diseases and infectious diseases.
XX
PS Disclosure; SEQ ID NO 360; 152pp; English.
XX
CC The invention comprises DNA sequences which are associated with
CC intestinal epithelium and peyer's patch M cells. The DNA sequences of the
CC invention are useful for assessing, modifying, modulating or regulating
CC intestinal epithelium or M cell development. The DNA sequences of the
CC invention are also useful in the treatment of: inflammatory bowel
CC disease, glutenenteropathy, infectious diseases, autoimmune diseases
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
CC diseases or disorders of the immune system, hypersensitivity,
CC anaphylaxis, and blood group incompatibility. The present DNA sequence
CC represents a primer that was used in the exemplification of the
CC invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGAA 3622
:||||||| ||||| | ||
Db 19 BAAAAAAAAAAAAAAAAAA 1

RESULT 1491
ADM16445/c
ID ADM16445 standard; RNA; 19 BP.
XX
AC ADM16445;
XX
DT 17-JUN-2004 (first entry)
XX
DE RNA intron poly-pyrimidine tract, seq id 2.
XX
KW Cytostatic; antimicrobial; virucide; gene therapy; RNA intron; cancer;
KW viral; microbial; infection; poly-pyrimidine tract; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 2. .4
FT /*tag= a
FT /note= "optionally between 1-3 bases at this position"
FT misc_feature 5
FT /*tag= b
FT /note= "optionally absent base"
FT misc_feature 6. .17
FT /*tag= c
FT /note= "optionally between 7-12 bases at this position"
FT misc_feature 19
FT /*tag= d
FT /note= "optionally absent base"
XX
PN WO2004024940-A2.
XX
PD 25-MAR-2004.

XX
PF 16-SEP-2003; 2003WO-US029274.
XX
PR 16-SEP-2002; 2002US-0411062P.
PR 12-OCT-2002; 2002US-0418405P.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Lin S, Ying S;
XX
DR WPI; 2004-270056/25.
XX
PT New isolated RNAs comprising an intron RNA that is released in a cell,
PT thus modulating the function of a target gene, useful for treating and
PT preventing diseases such as cancer and viral/microbial infections.
XX
PS Claim 2; SEQ ID NO 2; 54pp; English.
XX
CC The invention relates to isolated RNAs comprising an intron RNA that is
CC released in a cell, thus modulating the function of a target gene. Also
CC disclosed is a DNA template for the isolated RNA, an expression vector
CC comprising the DNA, and a composition comprising one or more agents that
CC induce RNA-mediated modulation of the functions of two or more target
CC genes in a cell, such as a mammalian cell. The isolated RNAs and
CC compositions are useful for modulating the function of a target gene in a
CC cell, e.g. to inhibit a cancer-related gene, potential viral gene, and
CC microbe-related gene, and thus useful for treating and preventing
CC diseases such as cancer and viral/microbial infections. The current
CC sequence represents a potential poly-pyrimidine tract of the artificial
CC RNA intron.
XX
SQ Sequence 19 BP; 0 A; 3 C; 0 G; 0 T; 13 U; 3 Other;

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 1.5e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACAGA 3621
|||||||||| |||| ::|
Db 19 GGAAAAAAAAAAAAGRRRA 1

RESULT 1492
AAV54170/c
ID AAV54170 standard; cDNA; 18 BP.
XX
AC AAV54170;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 7.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 49; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3601 CTGGAAAAAAACAAAAAC 3618
|| ||||||| ||||||
Db 18 CTAAAAAAAAAAAAAAAC 1

RESULT 1493
AAZ90640/c
ID AAZ90640 standard; DNA; 18 BP.
XX
AC AAZ90640;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #1.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3601 CTGGAAAAAAACAAAAAC 3618
|| ||||||| ||||||
Db 18 CTAAAAAAAAAAAAAAAC 1

RESULT 1494
ADL95317

```
ID   ADL95317 standard; DNA; 18 BP.
XX
AC   ADL95317;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Anti-proliferative oligonucleotide #8.
XX
KW   ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
KW   cancer; malignant tumour.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   8
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally 32-P labelled"
XX
PN   US2004067197-A1.
XX
PD   08-APR-2004.
XX
PF   02-FEB-2001; 2001US-00775479.
XX
PR   26-NOV-1997;   97WO-CA000892.
PR   24-MAY-1999;   99US-00318106.
XX
PA   (LECL/) LECLERC G.
PA   (MART/) MARTEL R.
XX
PI   Leclerc G,  Martel R;
XX
DR   WPI; 2004-314974/29.
XX
PT   New anti-proliferative substance comprising a radiolabeled DNA carrier,
PT   useful for preventing or treating uncontrolled cellular proliferation
PT   e.g. restenosis, cancer or malignant tumors.
XX
PS   Claim 13; SEQ ID NO 8; 28pp; English.
XX
CC   The invention relates to an anti-proliferative substance for preventing
CC   uncontrolled cellular proliferation comprising a radiolabelled DNA
CC   carrier, where a radioisotope is located internally within the DNA
CC   sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier
CC   penetrates the cell membrane and is retained intracellularly for a time
CC   sufficient for the radio-isotope to effect a dose therapy. The carrier in
CC   the anti-proliferative substance is an oligonucleotide, which is linear
CC   or a plasmid, which is circular. The plasmid is of viral or bacterial
CC   origin. The oligonucleotide is a double- or a single-stranded DNA
CC   sequence, which is conjugated with an antibody for cell-specific
CC   delivery. The oligonucleotide is also conjugated to a stent surface,
CC   cholesterol, oleic acid, linoleic acid, TGFalpha, antibody, TGFbeta,
CC   cytokines or growth factors. The anti-proliferative substance is useful
CC   for preventing or treating uncontrolled cellular proliferation. The
CC   uncontrolled cell proliferation is a restenosis following angioplasty, or
CC   cancer or a malignant tumour. The present sequence represents an
CC   oligonucleotide carrier used in the invention.
XX
SQ   Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3608 AAAACAAAAACAGAATTT 3625
              |||| ||||| | |||||
Db          1 AAAAAAAAAAAAAAATTT 18


RESULT 1495
AAV54167/c
ID   AAV54167 standard; cDNA; 18 BP.
XX
AC   AAV54167;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 4.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAAC 3983
              ||||| || ||||| |||
Db         18 ATAAAAAAAAAAAAAAAC 1


RESULT 1496
AAZ90643/c
ID   AAZ90643 standard; DNA; 18 BP.
XX
AC   AAZ90643;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #4.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
```

```
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3966 ATAAACAATAAAAACAAC 3983
              ||||| || ||||| |||
Db         18 ATAAAAAAAAAAAAAAAC 1


RESULT 1497
AAV07750
ID   AAV07750 standard; DNA; 18 BP.
XX
AC   AAV07750;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Phosphorothioate oligodeoxynucleotide.
XX
KW   phosphorothioate; electrospray ionisation-Fourier transform;
KW   mass spectrometry; off-resonance excitation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .18
FT                   /*tag=  a
FT                   /note= "phosphorothioate internucleotide linkages"
XX
PN   WO9840520-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998;   98WO-US004919.
XX
PR   14-MAR-1997;   97US-0040717P.
XX
PA   (HYBR-) HYBRIDON INC.
XX
PI   Wang BH;
XX
DR   WPI; 1998-520830/44.
XX
PT   Determining the nucleotide sequence of a nucleic acid analyte - using
PT   electro-spray ionisation.
XX
PS   Example 1; Fig 3A; 25pp; English.
XX
CC   The invention relates to an analytical method for determining the
CC   nucleotide sequence of nucleic acid analytes, including chemically
CC   modified oligonucleotides. This new method utilises electrospray
CC   ionisation-Fourier transform mass spectrometry. The ions are excited by
CC   sustained off-resonance excitation with single shot excitation, and the
CC   target fragmented by collisionally activated dissociation by a neutral
CC   gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
CC   can be nozzle skimmer dissociation. The method is used in molecular
CC   biology and biomedical applications. The method, utilising electrospray
CC   ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
CC   is extremely rapid and acts directly on the oligonucleotide. The method
CC   is effective for a variety of nucleic acid analytes, particularly
CC   chemically modified oligonucleotides which have not previously been
CC   successfully sequenced. The present sequence represents a
CC   phosphorothioate oligodeoxynucleotide
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3606 AAAAAACAAAAACAGAAT 3623
              |||||| ||||| | |||
Db          1 AAAAAAAAAAAAAAAAAT 18


RESULT 1498
AAQ34110
ID   AAQ34110 standard; DNA; 18 BP.
XX
AC   AAQ34110;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of a microsatellite from clone TGLA60B.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A1.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US000340.
XX
PR   15-JAN-1991;   91US-00642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification, gene
PT   mapping, and selective breeding.
XX
PS   Table 7; Page 375; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between 250 and 500
CC   bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC   clones cross-hybridised. Assuming independent distribution of
CC   microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC   in the bovine genome is estimated at >100, 000. The sequence information
CC   for ca. 230 such bovine microsatellites is summarised in the
CC   specification and indexed herein (see below). The sequences upstream and
CC   downstream of the microsatellite sequence were used to generate the
CC   required PCR primers for in vitro amplification of the corresp.
CC   microsatellite (using the program OPTIPRIM). The microsatellites may be
CC   used to identify individuals, for parentage testing, and in the genetic
CC   mapping of economic trait loci, or genes involved the determinism of
CC   economically important traits esp. in cattle, to allow selective
CC   breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
```

```
  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1499
AAQ75025/c
ID   AAQ75025 standard; RNA; 18 BP.
XX
AC   AAQ75025;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   PCR primer.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 12; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC   oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC   contain HEV Abs were immobilised on plastic tubes or wells, then
CC   incubated for 30-60 mins with the peptide-oligo proruct. The vessels were
CC   washed; bound oligo was released with 0.2M glycine and amplified in a
CC   separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC   The amplification product - AAQ75031 - was treated with uracil DNA
CC   glycoslase to remove the U18 fragment, and the product captured by
CC   immoblised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1500
AAT94668/c
ID   AAT94668 standard; DNA; 18 BP.
XX
AC   AAT94668;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchC.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1501
AAV37712
ID   AAV37712 standard; cDNA; 18 BP.
XX
AC   AAV37712;
XX
DT   25-MAR-2003  (revised)
DT   07-SEP-1998  (first entry)
XX
DE   Human protein AQ2_1i 3'-portion and polyA tail.
XX
KW   Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
KW   bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i;
KW   AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
XX
OS   Homo sapiens.
XX
```

PN WO9820130-A2.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US019857.
XX
PR 01-NOV-1996; 96US-00742973.
PR 29-OCT-1997; 97US-00960024.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-286946/25.
XX
PT New secreted proteins and associated polynucleotides - obtained from
PT murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT and murine adult thymus.
XX
PS Disclosure; Page 58; 75pp; English.
XX
CC The present invention describes novel proteins isolated from cDNA clones:
CC AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; or
CC L256_1i, deposited as ATCC 98237. The present sequence represents the 3'-
CC portion of AQ2_1i isolated from a human ovary cDNA library. The proteins
CC from the present invention may be administered in a composition to
CC prevent, treat or ameliorate a medical condition. The proteins may
CC exhibit biological activities such as nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating or
CC suppressing activity, haematopoiesis regulating activity, tissue growth
CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC inflammatory activity, cadherin/tumour invasion suppressor activity,
CC tumour inhibition activity and other activities. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGA 3621
||||||| ||||| | |
Db 1 GAAAAAAAAAAAAAAAAA 18

RESULT 1502
AAV21970/c
ID AAV21970 standard; DNA; 18 BP.
XX
AC AAV21970;
XX
DT 14-JUL-1998 (first entry)
XX
DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX
KW Nuclease resistant; bacterial infection; antibiotic; target;
KW veterinary medicine; treatment; human; industrial process;
KW bacterial control; ss.
XX
OS Synthetic.
XX
PN WO9803533-A1.
XX
PD 29-JAN-1998.
XX
PF 23-JUL-1997; 97WO-US012961.
XX
PR 24-JUL-1996; 96US-00685575.
XX
PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI Arrow A, Dale RMK, Thompson TL;
XX
DR WPI; 1998-120687/11.
XX
PT Treating bacterial infections in humans or animals with
PT oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT with antibiotics.
XX
PS Claim 49; Page 87; 163pp; English.
XX
CC This antisense oligonucleotide is nuclease resistant and can be used in
CC the treatment of animals, including humans, having a bacterial infection.
CC The treatment comprises administration of such nuclease resistant
CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC and formulated with a carrier. A compound comprising this nuclease
CC resistant oligonucleotide can be covalently linked to an antibiotic. The
CC method is used to treat infections by a wide variety of Gram-positive and
CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC The methods are particularly used in immuno-compromised individuals (e.g.
CC patients with acquired immunodeficiency syndrome or those receiving
CC chemotherapy or radiation therapy), optionally in combination with, or
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC therapeutic use, the oligonucleotides can be used to control bacteria in
CC laboratory cultures, foods, beverages and industrial processes. The
CC oligonucleotides are specific for bacteria, without affecting metabolism
CC in mammalian cells. They may also activate RNase H and have a general,
CC non-specific immune-stimulating effect. The oligonucleotides can be
CC administered orally, intranasally, rectally, topically or by injection,
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC enhances cellular uptake
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1503
AAX19943/c
ID AAX19943 standard; DNA; 18 BP.
XX
AC AAX19943;
XX
DT 14-JUN-1999 (first entry)
XX
DE Primer SEQ ID NO:3 from JP11075880.
XX
KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS Synthetic.
XX
PN JP11075880-A.
XX
PD 23-MAR-1999.
XX
PF 10-JUL-1998; 98JP-00195719.
XX
PR 14-JUL-1997; 97JP-00205378.
XX
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI; 1999-257710/22.
XX
PT Labelling of an oligonucleotide - useful for detecting genes.
XX
PS Example 1; Page 7; 10pp; Japanese.

```
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1504
AAX19942
ID   AAX19942 standard; DNA; 18 BP.
XX
AC   AAX19942;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:2 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1505
AAA40563
ID   AAA40563 standard; cDNA; 18 BP.
XX
AC   AAA40563;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human adult ovary cDNA fragment AQ2_1i #2.
XX
KW   Secreted protein; cytostatic; immunostimulatory; antimicrobial;
KW   antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;
KW   cell proliferation; differentiation; regulator; treatment; tumor;
KW   autoimmune disease; inflammatory disorder; wound; microbial infection;
KW   viral disease; graft versus host reaction suppression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200037630-A1.
XX
PD   29-JUN-2000.
XX
PF   22-DEC-1999;   99WO-US031005.
XX
PR   23-DEC-1998;   98US-00220876.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M,  Bowman MR;
XX
DR   WPI; 2000-442661/38.
DR   P-PSDB; AAB10274.
XX
PT   Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors,
PT   autoimmune diseases, inflammatory disorders, wounds, microbial infections
PT   and viral diseases.
XX
PS   Disclosure; Page 269; 293pp; English.
XX
CC   This invention describes novel secreted human proteins (I) which have
CC   cytostatic, immunostimulatory, antimicrobial, antiviral,
CC   immunosuppressive, antiinflammatory and vulnerary activity and which act
CC   as cytokine, cell proliferation or differentiation regulators. (I) is
CC   useful for treating tumors, autoimmune diseases, inflammatory disorders,
CC   wounds, microbial infections and viral diseases. (I) is also useful for
CC   suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
CC   fragments that encode the secreted proteins AAB10226-B10288 described in
CC   the method of the invention
XX
SQ   Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| | |
Db          1 GAAAAAAAAAAAAAAAAA 18


RESULT 1506
AAZ87161
ID   AAZ87161 standard; RNA; 18 BP.
XX
AC   AAZ87161;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Oligoarabinonucleotide SEQ ID NO:2.
XX
```

```
KW   Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW   reverse transcription; viral replication; RNase H cleavage;
KW   triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 1; Page 29; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1507
AAZ87162/c
ID   AAZ87162 standard; RNA; 18 BP.
XX
AC   AAZ87162;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Oligoarabinonucleotide SEQ ID NO:3.
XX
KW   Beta-D-arabinose; antisense; inhibition; transcription; expression;
KW   reverse transcription; viral replication; RNase H cleavage;
KW   triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 1; Page 29; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87160-Z87164 represent
CC   oligoarabinonucleotides containing beta-D-arabinose used in an
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1508
AAZ87166/c
ID   AAZ87166 standard; DNA; 18 BP.
XX
AC   AAZ87166;
XX
DT   08-MAY-2000  (first entry)
XX
```

```
DE   Deoxyarabinonucleotide SEQ ID NO:7.
XX
KW   2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW   transcription; expression; reverse transcription; viral replication;
KW   RNase H cleavage; triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT                   fluoro-beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 2; Page 31; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87165-Z87169 represent
CC   oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC   arabinose used in an exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1509
AAZ87167
ID   AAZ87167 standard; DNA; 18 BP.
XX
AC   AAZ87167;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Deoxyarabinonucleotide SEQ ID NO:8.
XX
KW   2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
KW   transcription; expression; reverse transcription; viral replication;
KW   RNase H cleavage; triple helix formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT                   fluoro-beta-D-arabinose"
XX
PN   WO9967378-A1.
XX
PD   29-DEC-1999.
XX
PF   17-JUN-1999;   99WO-CA000571.
XX
PR   19-JUN-1998;   98CA-02241361.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA,  Noronha AM,  Wilds C,  Borkow G,  Arion D;
XX
DR   WPI; 2000-160584/14.
XX
PT   Therapeutic composition containing antisense oligonucleotides that
PT   include arabinose sugars, particularly for inhibiting viral replication.
XX
PS   Example 2; Page 31; 91pp; English.
XX
CC   The invention relates to a new composition for selective, sequence-
CC   specific inhibition of gene transcription and expression in a host. The
CC   composition comprises oligonucleotides containing arabinose sugars that
CC   can hybridise to either a a single-stranded (ss) RNA to induce RNase H
CC   cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC   helix, thereby inhibiting DNA replication and/or transcription. The
CC   oligoarabinonucleotides are used for antisense inhibition of gene
CC   expression or to prevent DNA replication, or reverse transcription of RNA
CC   by retroviruses. The compositions are therefore particularly used to
CC   inhibit retroviral replication. The oligoarabinonucleotides can also be
CC   used, in combination with RNase H, as reagents for sequence-specific
CC   cleavage or RNA mapping, and additionally for the study and control of
CC   gene expression in cells. The oligoarabinonucleotides have excellent
CC   affinity for RNA, increased resistance to nucleases and show little if
CC   any non-specific binding to cellular or serum proteins. They target ss
CC   RNA, but not complementary ss DNA, so may be useful for targetting
CC   retroviral genomic RNA to inhibit the early stages of viral replication.
CC   Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC   with significantly higher thermal stability than those produced by normal
CC   oligonucleotides. Sequences AAZ87165-Z87169 represent
CC   oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-
CC   arabinose used in an exemplification of the present invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1510
AAD03565/c
ID   AAD03565 standard; DNA; 18 BP.
XX
```

```
AC   AAD03565;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX
KW   Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
KW   antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
KW   antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
KW   antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
KW   nootropic; neuroprotective; congestive heart failure; myocarditis;
KW   hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
KW   kidney disease; acute renal failure; renal glucosuria; renal infarction;
KW   polycystic kidney disease; hereditary nephritis; inflammatory disease;
KW   tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
KW   stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
KW   ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX
OS   Rattus norvegicus.
XX
PN   WO200123564-A1.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026544.
XX
PR   27-SEP-1999;   99US-0156280P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW,  Kapoun AM;
XX
DR   WPI; 2001-266159/27.
XX
PT   Novel secreted factor encoded by clone P00188D12 which is differentially
PT   expressed in certain disease states, useful in diagnosing and treating
PT   cardiac, renal or inflammatory diseases.
XX
PS   Example 1; Page 42; 71pp; English.
XX
CC   The patent discloses novel secreted factor protein encoded by clone
CC   P00188_D12. The secreted factor is differentially expressed in certain
CC   disease states. Secreted protein, its antibodies, antagonists or
CC   compositions comprising them are useful in the diagnosis and treatment of
CC   cardiac diseases such as congestive heart failure, myocarditis,
CC   hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
CC   cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
CC   failure, renal glucosuria, renal infarction, nephrogenic diabetes
CC   insipidus, polycystic kidney disease, hereditary nephritis and
CC   inflammatory diseases such as asthma, autoimmune diabetes, tumour
CC   angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
CC   asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
CC   Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
CC   protein DNA is useful in antisense-mediated gene inhibition and in gene
CC   therapy. An array comprising one or more oligonucleotides complementary
CC   to reference RNA or DNA encoding the secreted factor is useful for
CC   detecting cardiac, kidney and inflammatory disease. The present DNA
CC   sequence is an oligonucleotide which is used in the preparation of a
CC   normalised cDNA library containing secreted factor DNAs. The normalised
CC   cDNA libraries are used in the identification of differentially expressed
CC   rat secreted factor P00188_D12 gene
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

```
RESULT 1511
AAD17014
ID   AAD17014 standard; DNA; 18 BP.
XX
AC   AAD17014;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Oligonucleotide A18-2PEG linker.
XX
KW   Scaffold protein; antibody mimic; fibronectin type III domain;
KW   randomised loop; randomised beta-sheet; diagnostic purpose;
KW   protein designing; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    18
FT                   /*tag=  a
FT                   /note= "Linked to (PEG)2CCPuromycin"
XX
PN   WO200164942-A1.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006414.
XX
PR   29-FEB-2000; 2000US-00515260.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lipovsek D,  Wagner RW,  Kuimelis RG;
XX
DR   WPI; 2001-557782/62.
XX
PT   Fibronectin scaffold protein array for obtaining a protein/compound which
PT   binds to a compound/protein, comprises a fibronectin type III domain
PT   having a randomized loop, a randomized beta-sheet or their combination.
XX
PS   Disclosure; Page 25; 67pp; English.
XX
CC   The present invention relates to an array of proteins (antibody mimics)
CC   comprising a fibronectin type III domain having a randomised loop, a
CC   randomised beta-sheet, or their combination, and has the capacity to bind
CC   to a compound that is not bound by a corresponding naturally- occurring
CC   fibronectin, immobilised onto a solid support. The antibody mimics is
CC   useful for detecting a compound preferably a protein, in a biological
CC   sample. It is also useful to detect one or more different analytes
CC   simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC   is also useful for the purpose of designing proteins capable of binding
CC   to virtually any compound of interest. The present sequence is an
CC   oligonucleotide A18-2PEG linker used in an exemplification of the
CC   invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         1 AAAAAAAAAAAAAAAAAA 18


RESULT 1512
AAF75598/c
ID   AAF75598 standard; DNA; 18 BP.
XX
AC   AAF75598;
XX
DT   10-MAY-2001  (first entry)
XX
```

DE Binary encoded sequence tag method anchored primer #3.
XX
KW Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200112855-A2.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022164.
XX
PR 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX
PA (UYYA) UNIV YALE.
XX
PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX
DR WPI; 2001-202878/20.
XX
PT Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX
PS Disclosure; Page 101; 101pp; English.
XX
CC The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3602 TGGAAAAAAACAAAAACA 3619
|| ||||||| ||||| |
Db 18 TGAAAAAAAAAAAAAAAA 1

RESULT 1513
AAF99708/c
ID AAF99708 standard; DNA; 18 BP.
XX
AC AAF99708;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1514
AAF99734/c
ID AAF99734 standard; DNA; 18 BP.
XX
AC AAF99734;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #850.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.

XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1515
AAF82472/c
ID AAF82472 standard; DNA; 18 BP.
XX
AC AAF82472;
XX
DT 29-JUN-2001 (first entry)
XX
DE Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX
KW Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;
KW renal disease; inflammatory disease; polylinker; ss.
XX
OS Synthetic.
XX
PN WO200123419-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026582.
XX
PR 27-SEP-1999; 99US-0156277P.
XX
PA (SCIO-) SCIOS INC.
XX
PI Stanton LW, Kapoun AM;
XX
DR WPI; 2001-328177/34.
XX
PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
PT treating and/or preventing various cardiac, renal and inflammatory
PT diseases.
XX
PS Example 1; Page 41; 69pp; English.
XX
CC The present sequence corresponds to polylinker DNA of the phagemid vector
CC pCR2.1. It was used in the construction of a normalised rat cDNA library,
CC which was used in an example demonstrating differential expression of a
CC rat gene referred to as clone P00210D09. The invention relates to a
CC polypeptide comprising a sequence of at least 80% identity to residues 22
CC -122 of the present sequence, or a sequence encoded by a nucleic acid
CC hybridising under stringent conditions to the complement of the coding
CC region comprising 1031 nucleotides, and having at least one biological
CC activity of the polypeptide encoded by clone P00210D09. The polypeptides
CC and polynucleotides of the invention are useful for the treatment of
CC cardiac, renal and inflammatory diseases. The polynucleotides are useful
CC in antisense mediated gene inhibition and in gene therapy. The
CC polypeptides are useful in assays for identifying lead compounds that may
CC be used as therapeutic agents in the treatment of cardiac, kidney or
CC inflammatory diseases
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1516
AAS94743/c
ID AAS94743 standard; DNA; 18 BP.
XX
AC AAS94743;
XX
DT 12-MAR-2002 (first entry)
XX
DE Rat secreted factor DNA oligonucleotide probe #6.
XX
KW Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
KW renal infarction; hereditary nephritis; polycystic kidney disease;
KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;
KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
KW Alzheimer's disease; gene therapy.
XX
OS Synthetic.
XX
PN WO200174901-A2.
XX
PD 11-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-US009555.
XX
PR 31-MAR-2000; 2000US-0193548P.
PR 14-MAR-2001; 2001US-00809545.
XX
PA (SCIO-) SCIOS INC.
XX
PI Stanton LW, White RT;
XX
DR WPI; 2002-010779/01.
XX
PT Novel secreted factor polypeptide useful for treating cardiac diseases
PT such as arteriosclerosis, myocardial infarction, inflammatory diseases
PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.
XX
PS Example 1; Page 51; 189pp; English.
XX
CC The invention relates to rat secreted factor polypeptides and the
CC polynucleotides encoding them. The sequences are useful for treating
CC cardiac, renal or inflammatory diseases. These include cardiac diseases
CC such as congestive heart failure, myocarditis, dilated congestive
CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac
CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic

CC syndrome, renal infarction, hereditary nephritis, polycystic kidney
CC disease, chronic renal failure, renal vein thrombosis and medullary
CC sponge kidney and inflammatory diseases such as asthma, rheumatoid
CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode
CC the secreted factor polypeptides of the invention, and oligonucleotide
CC probes and PCR primers
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1517
ABS78455/c
ID ABS78455 standard; DNA; 18 BP.
XX
AC ABS78455;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #939.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1518
ABS78429/c
ID ABS78429 standard; DNA; 18 BP.
XX
AC ABS78429;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #913.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 35; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 1519
ABL39401/c
ID ABL39401 standard; DNA; 18 BP.
XX
AC ABL39401;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 837.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 308; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

```
  Query Match              0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 1520
AAD41497/c
ID AAD41497 standard; DNA; 18 BP.
XX
AC AAD41497;
XX
DT 30-OCT-2002 (first entry)
XX
DE Oligonucleotide used for amplifying sea hare cyplasin L DNA.
XX
KW Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;
KW heart disease; stroke; vascular disease; nootropic; neuroprotective;
KW cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.
XX
OS Unidentified.
XX
PN WO200231144-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-EP011837.
XX
PR 13-OCT-2000; 2000EP-00122466.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Butzke D, Machuy N, Rudel T, Meyer TF;
XX
DR WPI; 2002-537205/57.
XX
PT Novel polypeptide having cytotoxic activity obtainable from Aplysia,
PT useful for destroying tumors, for identifying novel targets for the
PT development of anti-tumor agents, and as specific ion channel modulators.
XX
PS Example 5; Page 37; 87pp; English.
XX
CC The present invention relates to novel polypeptides having cytotoxic
CC activity obtainable from sea hare Aplysia. Sequences of the invention are
CC useful for the manufacture of cytotoxic agents against apoptosis-
CC resistant cells, where the agents are useful for diagnosis, prevention,
CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
CC protein, factors for generating or detoxifying reactive oxygen species
CC (ROS) and factors for blocking and/or by-passing of caspases. They are
CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
CC for destroying tumours and/or selectively killing cells in tissues, for
CC identifying novel targets for the development of pharmaceutical agents,
CC preferably anti-tumour agents and as specific ion channel modulators,
CC e.g., blockers or openers for therapy, diagnostic or research. They are
CC useful for the diagnosis and therapy of hyperproliferative diseases,
CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
CC They are also useful for development of drugs for the treatment of
CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
CC present sequence is an oligonucleotide which is used for amplifying sea
CC hare cyplasin L DNA. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

```
  Query Match              0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 1521
ABS53437/c

```
ID   ABS53437 standard; DNA; 18 BP.
XX
AC   ABS53437;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Poly d(T) primer.
XX
KW   Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
KW   poly d(T).
XX
OS   Synthetic.
XX
PN   WO200265093-A2.
XX
PD   22-AUG-2002.
XX
PF   14-FEB-2002; 2002WO-US005713.
XX
PR   14-FEB-2001; 2001US-0268645P.
PR   14-FEB-2001; 2001US-0268664P.
PR   18-JUL-2001; 2001US-0306216P.
PR   07-NOV-2001; 2001US-0344557P.
PR   07-NOV-2001; 2001US-0348242P.
PR   09-NOV-2001; 2001US-0350176P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (REME-) RES FOUND MENTAL HYGIENE INC.
XX
PI   Ginsberg SD,  Che S;
XX
DR   WPI; 2002-567050/60.
XX
PT   Increasing efficiency of second strand cDNA synthesis using terminal
PT   continuation model before performing further RNA amplification by RNA
PT   transcription.
XX
PS   Example 7; Page 80; 128pp; English.
XX
CC   This invention relates to a novel method for increasing the efficiency of
CC   second strand cDNA synthesis through a mechanism of terminal
CC   continuation. In the method an RNA molecule is obtained and a first
CC   primer is added that comprises a region that hybridises to a
CC   complementary region of the molecule before a second primer is added
CC   comprising at least one riboguanine at the 3' end of the primer. A first
CC   complementary nucleic acid molecule is synthesised, the RNA molecule and
CC   second primer are removed and a second complementary nucleic acid
CC   molecule is synthesised to form a second hybrid with an extension product
CC   of the third primer bound to the first complementary molecule. The method
CC   of the invention is useful for increasing the efficiency of second strand
CC   cDNA synthesis and may be used for linear amplification of genetic
CC   signals from histologically stained tissue. The present sequence
CC   represents a poly d(T) PCR primer used in the method of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1522
ABA93239/c
ID   ABA93239 standard; DNA; 18 BP.
XX
AC   ABA93239;
XX
DT   18-APR-2002  (first entry)
XX
DE   Adaptor oligonucleotide SEQ ID NO:2.
XX
KW   Detection; comparative detection; adaptor; ss.
XX
OS   Synthetic.
XX
PN   JP2001333800-A.
XX
PD   04-DEC-2001.
XX
PF   30-MAY-2000; 2000JP-00160324.
XX
PR   30-MAY-2000; 2000JP-00160324.
XX
PA   (UNIT-) UNITECH CO LTD.
XX
DR   WPI; 2002-135950/18.
XX
PT   Comparative detection of the amounts of RNA and DNA.
XX
PS   Disclosure; Page 9; 9pp; Japanese.
XX
CC   The present invention describes a method for the comparative detection of
CC   the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC   transcribing respectively from at least two tissue RNAs are respectively
CC   fragmented by using a same restriction enzyme; (b) each different adaptor
CC   and a common adaptor are added to each of the cDNA fragments derived from
CC   the same or different tissues by the step (a); (c) the resultant adaptor-
CC   added cDNAs are mixed together; (d) an adaptor primer having the common
CC   sequence to said different adaptor and a gene-specific adaptor are used
CC   to amplify said adaptor-added cDNAs containing no region derived from
CC   polyadenylic acid of the mRNA before the addition of the adaptor among
CC   the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC   cDNA amounts are measured between the tissues; (f) the RNA is detected
CC   from the measured result; (g) each different adaptor and a common adaptor
CC   are added to each of the genomic DNA fragments derived from a same or
CC   different individuals; (h) the resultant adaptor-added genomic DNAs are
CC   mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC   an adaptor primer having the common sequence to the different adaptor and
CC   a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC   of the genomic DNAs are measured between the individuals. The method is
CC   used for the detection of the amounts of RNA and DNA. The present
CC   sequence represents an oligonucleotide which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1523
AAD56466
ID   AAD56466 standard; RNA; 18 BP.
XX
AC   AAD56466;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Target RNA #1 used in the exemplification of the invention.
XX
KW   Acyclic linker; gene expression; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
```

```
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is a target RNA, used in the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
                ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1524
AAD56440/c
ID   AAD56440 standard; DNA; 18 BP.
XX
AC   AAD56440;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 9; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
                ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1525
AAD56446/c
ID   AAD56446 standard; DNA; 18 BP.
XX
AC   AAD56446;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
```

CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1526
ACH03247/c
ID ACH03247 standard; DNA; 18 BP.
XX
AC ACH03247;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #882.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 33; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1527
AAD57871/c
ID AAD57871 standard; DNA; 18 BP.
XX
AC AAD57871;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense oligo #1 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
XX
OS Unidentified.
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CA000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA;
XX
DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense oligonucleotide used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1528
AAD57878/c
ID AAD57878 standard; DNA; 18 BP.
XX
AC AAD57878;
XX
DT 20-NOV-2003 (first entry)

```
XX
DE   Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .3
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7. .9
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .15
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1529
AAD57879/c
ID   AAD57879 standard; DNA; 18 BP.
XX
AC   AAD57879;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .6
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13. .18
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1530
AAD57877/c
ID   AAD57877 standard; DNA; 18 BP.
XX
AC   AAD57877;
```

```
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW   ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1
FT                   /*tag=  a
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        3
FT                   /*tag=  b
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        5
FT                   /*tag=  c
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        7
FT                   /*tag=  d
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        9
FT                   /*tag=  e
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        11
FT                   /*tag=  f
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        13
FT                   /*tag=  g
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        15
FT                   /*tag=  h
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
FT   misc_RNA        17
FT                   /*tag=  i
FT                   /label= RNA
FT                   /note= "2'-O-methyl-D-uridine"
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 2; Page 35; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1531
AAD57890
ID   AAD57890 standard; RNA; 18 BP.
XX
AC   AAD57890;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target RNA #1 used in RNase H assay.
XX
KW   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW   hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS   Unidentified.
XX
PN   WO2003064441-A2.
XX
PD   07-AUG-2003.
XX
PF   31-JAN-2003; 2003WO-CA000129.
XX
PR   01-FEB-2002; 2002US-0352873P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Parniak MA;
XX
DR   WPI; 2003-689523/65.
XX
PT   New oligonucleotide, useful for preventing or treating a disease related
PT   to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS   Example 4; Page 38; 73pp; English.
XX
CC   The present invention relates to a new oligonucleoside which comprises
CC   alternating first and second segments. The first segment comprises at
CC   least one sugar modified nucleoside. The second segment comprises at
CC   least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC   each of the first and second segments, so that it comprises at least 4
CC   alternating segments. The oligonucleotide is useful for preparing a
CC   composition for inducing RNase H-mediated cleavage of a target RNA in a
CC   system, preventing or decreasing translation, transcription or
CC   replication of a target RNA in a system, detecting the presence of a
CC   target RNA in a system, validating a gene target corresponding to a
CC   target RNA in a system or preventing or treating a disease related to a
CC   target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC   or hepatitis B. The invention is useful in gene therapy. The present
CC   sequence is a target RNA used in RNase H assay. This sequence is used in
CC   the exemplification of the invention
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
```

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18
```

RESULT 1532
ADB37210/c
ID ADB37210 standard; DNA; 18 BP.
XX
AC ADB37210;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 1533
ADB37236/c
ID ADB37236 standard; DNA; 18 BP.
XX
AC ADB37236;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #850.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 1534
ADE77617
ID ADE77617 standard; DNA; 18 BP.
XX
AC ADE77617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW multiplexed elongation assay; enzymatic recognition;
KW cystic fibrosis conductance transmembrane regulator.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003034029-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033012.
XX
PR 15-OCT-2001; 2001US-0329427P.
PR 15-OCT-2001; 2001US-0329428P.
PR 15-OCT-2001; 2001US-0329619P.
PR 15-OCT-2001; 2001US-0329620P.

PR 14-MAR-2002; 2002US-0364416P.
XX
PA (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI Li AX, Hashmi G, Seul M;
XX
DR WPI; 2003-393553/37.
XX
PT Concurrent interrogation of a number of polymorphic sites, useful for
PT genetic testing, carrier screening, genetic profiling, and identity
PT testing, comprises conducting a multiplexed elongation assay using
PT probes.
XX
PS Example 9; Page 46; 143pp; English.
XX
CC This invention relates to a novel method for the concurrent interrogation
CC of a number of polymorphic sites in the presence of, and without
CC interference from, non-designated polymorphic sites. Specifically, it
CC comprises conducting a multiplexed elongation assay by applying one or
CC more temperature cycles to achieve linear amplification of the target or
CC a combination of annealing and elongation steps under temperature-
CC controlled conditions. Furthermore, this detection method uses probe
CC extension or elongation and relies on enzymatic recognition, a superior
CC technique that no longer depends on differential hybridisation. The
CC present invention describes probes and methods useful for identifying or
CC detecting polymorphisms at one or more designated sites, such that they
CC can identify mutations within the cystic fibrosis conductance
CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC genes. In addition, concurrent interrogation of a multiplicity of
CC polymorphic sites is useful for genetic testing, carrier screening,
CC genotyping or genetic profiling, and identity testing. This
CC oligonucleotide is the negative control probe used for the elongation
CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC invention.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1535
ADI34489/c
ID ADI34489 standard; DNA; 18 BP.
XX
AC ADI34489;
XX
DT 22-APR-2004 (first entry)
XX
DE Nucleotide sequence of an oligo dT18.
XX
KW Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
OS Synthetic.
XX
PN WO2003102243-A1.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-US017103.
XX
PR 31-MAY-2002; 2002US-0384454P.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Kamme FC, Zhu JY;
XX
DR WPI; 2004-035466/03.
XX
PT Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT RNA transcription from a polynucleotide template, comprises eliminating
PT single-stranded oligonucleotide from the transcription sample.
XX
PS Example 1; SEQ ID NO 8; 26pp; English.
XX
CC The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction.
CC Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
CC transcription reaction.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1536
ADH78590
ID ADH78590 standard; DNA; 18 BP.
XX
AC ADH78590;
XX
DT 22-APR-2004 (first entry)
XX
DE Test element oligonucleotide #2.
XX
KW Fluid functional property; fluid flow pattern;
KW fluid reagent distribution; time dependent fluid reactivity; ss.
XX
OS Synthetic.
XX
PN US2003232343-A1.
XX
PD 18-DEC-2003.
XX
PF 14-JUN-2002; 2002US-00172675.
XX
PR 14-JUN-2002; 2002US-00172675.
XX
PA (LEPR/) LEPROUST E M.
PA (AMOR/) AMORESE D A.
PA (PECK/) PECK B J.
XX
PI Leproust EM, Amorese DA, Peck BJ;
XX
DR WPI; 2004-061269/06.
XX
PT Determining a functional property of fluid in chamber by introducing a
PT support comprising test elements having reaction and detection domains,
PT introducing a test fluid, and detecting locations not reactive with the
PT fluid.
XX
PS Example 2; SEQ ID NO 2; 22pp; English.
XX
CC The invention relates to a method of determining a functional property of
CC a fluid in a chamber comprising introducing into the chamber a support to

```
CC   which is bound several test elements, each of the test elements
CC   comprising a reaction domain and a detection domain, introducing into the
CC   chamber a fluid that is interactive with the reaction domains, removing
CC   the fluid from the chamber, determining by means of the detection domains
CC   the locations at which the fluid has not interacted with the reaction
CC   domains, and relating the locations to the functional property of the
CC   fluid. The reaction domains involves nucleotides. The detection domain
CC   comprises a member of a specific binding pair. The determining of the
CC   step involves treating the test elements to modify only those reaction
CC   domains that have interacted with the fluid. The functional property is
CC   chosen from the flow pattern of the fluid, reagent distribution within
CC   the fluid and time dependent reactivity of the fluid. The method is
CC   useful for determining a functional property of a fluid in a chamber and
CC   for synthesising arrays of biopolymers e.g., arrays of polynucleotides.
CC   The method provides for the characterisation of a new fluid in a known
CC   flow cell, a known fluid in a new flow cell or a new fluid/flow cell
CC   combination. This sequence represents a test element used in the method
CC   of the invention.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1537
ADO28710
ID   ADO28710 standard; DNA; 18 BP.
XX
AC   ADO28710;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Single stranded cDNA production poly-A-tail seqid 6.
XX
KW   single stranded cDNA; adaptor-mediated process; cDNA synthesis;
KW   poly-A-tail; ss.
XX
OS   Synthetic.
XX
PN   US6706476-B1.
XX
PD   16-MAR-2004.
XX
PF   09-MAR-2001; 2001US-00803263.
XX
PR   22-AUG-2000; 2000US-0226954P.
XX
PA   (AZIG-) AZIGN BIOSCIENCE AS.
XX
PI   Thirstrup K,  Warthoe P,  Pettersson NB;
XX
DR   WPI; 2004-326403/30.
XX
PT   Synthesizing single stranded cDNA, involves annealing cDNA synthesis
PT   primer to RNA and synthesizing first cDNA strand, ligating adaptor to
PT   single stranded cDNA using DNA ligase, and amplifying ligated single
PT   stranded cDNA fragment.
XX
PS   Example 1; SEQ ID NO 6; 22pp; English.
XX
CC   The invention describes a method of synthesising single stranded cDNA by
CC   a 5'-ligated adaptor-mediated process involving: annealing a cDNA
CC   synthesis primer to RNA, separating the cDNA strand from the RNA,
CC   purifying the cDNA, contacting the cDNA with an adaptor, ligating the
CC   adaptor through 5'-phosphate on strand (II) of the adaptor to single
CC   stranded using DNA ligase, and amplifying the obtained ligated single
CC   stranded fragment in an molecular amplification procedure. The method is
CC   useful for: synthesising a single stranded cDNA by a 5'-ligated adaptor-
CC   mediated process, where the source of nucleic acid is chosen from blood,
CC   serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and
CC   saliva. The tissue sample comprises a cell population which may be single
CC   cell, 100-1000000 cells or more as desired; making a cDNA library from a
CC   collection of mRNA molecules in a sample, where the method is applied to
CC   amplify the cDNAs corresponding to the mRNAs by annealing one or more
CC   cDNA synthesis primers to several mRNAs in the sample; producing a
CC   subtractive hybridisation probe which involves synthesising a double-
CC   stranded cDNA collection from a first mRNA population by the method,
CC   where primer 1 is modified by biotin in the 5' end, isolating the biotin-
CC   containing single stranded cDNA (sense) by use of streptavidin coated
CC   magnetic beads, synthesising a double-stranded cDNA collection from a
CC   second mRNA population according to the method, isolating the non-biotin-
CC   containing single stranded cDNA (anti-sense) by use of streptavidin
CC   coated magnetic beads, hybridising the sense to the anti-sense cDNA,
CC   where an unhybridised sub-population of the anti-sense cDNA is found,
CC   isolating the unhybridised sub-population of the antisense cDNA by use of
CC   streptavidin coated cDNA, and generating a second double-stranded cDNA
CC   collection from the unhybridised sub-population by PCR using primer 1 and
CC   primer 2; and detecting expression of a gene in a pre-selected cell
CC   population. The method is an improved method for producing amplified
CC   heterogeneous populations of cDNA from limited quantities of RNA or other
CC   nucleic acid. This sequence represents a poly-A-tail used to in the
CC   production single stranded cDNA.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1538
ADO28711/c
ID   ADO28711 standard; DNA; 18 BP.
XX
AC   ADO28711;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Single stranded cDNA production poly-A-tail complement seqid 7.
XX
KW   single stranded cDNA; adaptor-mediated process; cDNA synthesis;
KW   poly-A-tail; ss.
XX
OS   Synthetic.
XX
PN   US6706476-B1.
XX
PD   16-MAR-2004.
XX
PF   09-MAR-2001; 2001US-00803263.
XX
PR   22-AUG-2000; 2000US-0226954P.
XX
PA   (AZIG-) AZIGN BIOSCIENCE AS.
XX
PI   Thirstrup K,  Warthoe P,  Pettersson NB;
XX
DR   WPI; 2004-326403/30.
XX
PT   Synthesizing single stranded cDNA, involves annealing cDNA synthesis
PT   primer to RNA and synthesizing first cDNA strand, ligating adaptor to
PT   single stranded cDNA using DNA ligase, and amplifying ligated single
PT   stranded cDNA fragment.
XX
PS   Example 1; SEQ ID NO 7; 22pp; English.
XX
```

CC The invention describes a method of synthesising single stranded cDNA by
CC a 5'-ligated adaptor-mediated process involving: annealing a cDNA
CC synthesis primer to RNA, separating the cDNA strand from the RNA,
CC purifying the cDNA, contacting the cDNA with an adaptor, ligating the
CC adaptor through 5'-phosphate on strand (II) of the adaptor to single
CC stranded using DNA ligase, and amplifying the obtained ligated single
CC stranded fragment in an molecular amplification procedure. The method is
CC useful for: synthesising a single stranded cDNA by a 5'-ligated adaptor-
CC mediated process, where the source of nucleic acid is chosen from blood,
CC serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and
CC saliva. The tissue sample comprises a cell population which may be single
CC cell, 100-1000000 cells or more as desired; making a cDNA library from a
CC collection of mRNA molecules in a sample, where the method is applied to
CC amplify the cDNAs corresponding to the mRNAs by annealing one or more
CC cDNA synthesis primers to several mRNAs in the sample; producing a
CC subtractive hybridisation probe which involves synthesising a double-
CC stranded cDNA collection from a first mRNA population by the method,
CC where primer 1 is modified by biotin in the 5' end, isolating the biotin-
CC containing single stranded cDNA (sense) by use of streptavidin coated
CC magnetic beads, synthesising a double-stranded cDNA collection from a
CC second mRNA population according to the method, isolating the non-biotin-
CC containing single stranded cDNA (anti-sense) by use of streptavidin
CC coated magnetic beads, hybridising the sense to the anti-sense cDNA,
CC where an unhybridised sub-population of the anti-sense cDNA is found,
CC isolating the unhybridised sub-population of the antisense cDNA by use of
CC streptavidin coated cDNA, and generating a second double-stranded cDNA
CC collection from the unhybridised sub-population by PCR using primer 1 and
CC primer 2; and detecting expression of a gene in a pre-selected cell
CC population. The method is an improved method for producing amplified
CC heterogeneous populations of cDNA from limited quantities of RNA or other
CC nucleic acid. This sequence represents the complement of a poly-A-tail
CC used to in the production single stranded cDNA.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1539
ADO26684/c
ID ADO26684 standard; DNA; 18 BP.
XX
AC ADO26684;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:77.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
DR WPI; 2004-411519/38.
DR P-PSDB; ADO26685.
XX
PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 77; 86pp; English.
XX
CC The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1540
ADO26682
ID ADO26682 standard; DNA; 18 BP.
XX
AC ADO26682;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:75.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX

```
PD   21-MAY-2004.
XX
PF   10-NOV-2003; 2003WO-AU001487.
XX
PR   08-NOV-2002; 2002US-0425163P.
XX
PA   (UYQU ) UNIV QUEENSLAND.
XX
PI   Frazer IH;
XX
DR   WPI; 2004-411519/38.
DR   P-PSDB; ADO26683.
XX
PT   Constructing synthetic polynucleotide for modulating the quality of a
PT   selected phenotype displayed by an organism comprises replacing a first
PT   codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS   Example 1; SEQ ID NO 75; 86pp; English.
XX
CC   The present invention describes a method for constructing a synthetic
CC   polynucleotide from which a polypeptide is producible to confer a
CC   selected phenotype to an organism of interest or part in a different
CC   quality than that conferred by a parent polynucleotide that encodes the
CC   same polypeptide. The method comprises: (a) selecting a first codon of
CC   the parent polynucleotide for replacement with a synonymous codon, where
CC   the synonymous codon is selected on the basis that it exhibits a
CC   different phenotypic preference than the first codon in a comparison of
CC   phenotypic preferences in test organisms or parts, where the test
CC   organism are selected from organisms of the same species as the organism
CC   of interest and organisms that are related to the organisms of interest;
CC   and (b) replacing the first codon with the synonymous codon to construct
CC   the synthetic polynucleotide. Also described: (1) a method for
CC   determining the phenotypic preference of a first codon in an organism of
CC   interest or its parts; (2) a synthetic polynucleotide constructed from
CC   the method above; (3) an organism or interest or part containing a
CC   synthetic polynucleotide constructed from the method above; (4) an
CC   organism or interest or part containing a synthetic construct that
CC   comprises a regulatory polynucleotide operably linked to a tandem repeat
CC   of a first codon fused in frame with a reporter polynucleotide that
CC   encodes a reporter protein, which produces, or is predicted to produce a
CC   selected phenotype or a phenotype of the same class as the selected
CC   phenotype in the organism or part; (5) a method of modulating the quality
CC   of a selected phenotype that is displayed by an organism of interest or
CC   part and that results from the expression of a parent polynucleotide that
CC   encodes the polypeptide; (6) a method of enhancing the quality of a
CC   selected phenotype that is displayed by an organism of interest or part
CC   and that results from the expression of a parent polynucleotide that
CC   encodes the polypeptide; and (7) a method of reducing the quality of a
CC   selected phenotype that is displayed by an organism of interest or part
CC   and that results from the expression of a parent polynucleotide that
CC   encodes the polypeptide. The method is useful for constructing a
CC   synthetic polynucleotide from which a polypeptide is producible to confer
CC   a selected phenotype to an organism of interest or part in a different
CC   quality than that conferred by a parent polynucleotide that encodes the
CC   same polypeptide. It is useful for modulating the quality of a selected
CC   phenotype displayed by an organism or part. The present sequence encodes
CC   a synthetic leader sequence, which is used in an example from the present
CC   invention.
XX
SQ   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1541
ADP86130/c
ID   ADP86130 standard; DNA; 18 BP.
XX
AC   ADP86130;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #1.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 1; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1542
ADR32355/c
ID   ADR32355 standard; DNA; 18 BP.
XX
```

AC ADR32355;
XX
DT 04-NOV-2004 (first entry)
XX
DE Rat KDR cytosolic domain cloning RT-PCR primer.
XX
KW Rat; receptor tyrosine kinase; KDR; therapy; cancer;
KW ischaemic ocular disease; proliferative retinopathy; inflammation;
KW reverse transcription; RT; PCR; primer; ss.
XX
OS Rattus norvegicus.
XX
PN WO2004070004-A2.
XX
PD 19-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001928.
XX
PR 29-JAN-2003; 2003US-0443335P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Thomas RA, Pan B, Mcgaughey GB;
XX
DR WPI; 2004-604429/58.
XX
PT New nucleic acid molecules encoding rat KDR protein, useful for
PT identifying inhibitors of KDR activity for treating cancer, ischemic
PT ocular diseases, and inflammation.
XX
PS Example 2; Page 30; 77pp; English.
XX
CC The invention relates to rat receptor tyrosine kinase (KDR) and its
CC corresponding nucleic acid sequence. The nucleic acid molecules of the
CC invention are useful for identifying compounds that modulate wild-type
CC rat KDR activity to evaluate the safety and efficacy of specific
CC inhibitors of KDR in rats. KDR inhibitors are useful for treating cancer,
CC ischaemic ocular diseases such as proliferative retinopathy and
CC inflammation. The present sequence is a reverse transcription (RT) PCR
CC primer used for cloning rat KDR cytosolic domain. This sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1543
ADR57967/c
ID ADR57967 standard; DNA; 18 BP.
XX
AC ADR57967;
XX
DT 18-NOV-2004 (first entry)
XX
DE Nucleotide #4 for signal amplification method.
XX
KW ss; signal amplification method; gene expression; reverse transcription;
KW self-assembly reaction; DNA chip.
XX
OS Unidentified.
XX
PN WO2004072302-A1.
XX
PD 26-AUG-2004.
XX
PF 13-FEB-2004; 2004WO-JP001588.
XX
PR 14-FEB-2003; 2003JP-00037212.
XX
PA (PALM-) PALMA BEEZ RES INST CO LTD.
XX
PI Usui M, Fujikawa T;
XX
DR WPI; 2004-642306/62.
XX
PT Signal amplification method for detecting expressed gene, by using
PT reverse transcription reaction and self-assembly reaction of
PT oligonucleotide probes.
XX
PS Disclosure; SEQ ID NO 4; 27pp; Japanese.
XX
CC The invention relates to a signal amplification method (M1) for detecting
CC expressed gene using reverse transcription reaction and a self-assembly
CC reaction of forming a self assembly of oligonucleotide probes, thus
CC improving detection sensitivity of the expressed gene in a DNA chip. (M1)
CC is useful for signal amplification method (M1) for detecting expressed
CC gene (claimed). (M1) improves detection sensitivity of the expressed gene
CC in a DNA chip (claimed). (M1) does not require use of expensive enzymes
CC and enables detection corresponding to the original RNA length or
CC expression amount because of using neither linear amplification nor PCR.
CC This sequence corresponds to a nucleotide used in the method of the
CC invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1544
ADE27190/c
ID ADE27190 standard; RNA; 19 BP.
XX
AC ADE27190;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:134.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX

```
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 134; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 1 G; 0 T; 8 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATATA 2410
              ||| ||||||  ||||||
Db         18 AATGTATATATGTATATA 1


RESULT 1545
ADE27480
ID   ADE27480 standard; RNA; 19 BP.
XX
AC   ADE27480;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:424.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 424; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 1 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   44.4%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2393 AATATATATACATATATA 2410
              ||: :|:|:|  :|:|:|
Db          2 AAUGUAUAUAUGUAUAUA 19


RESULT 1546
ACA98771
ID   ACA98771 standard; DNA; 19 BP.
XX
AC   ACA98771;
XX
DT   28-JUL-2003  (first entry)
XX
DE   Human CYP2C8 SNP detection PCR primer #211.
XX
KW   Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
KW   cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
KW   single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200299099-A2.
XX
PD   12-DEC-2002.
XX
PF   31-MAY-2002; 2002WO-EP006000.
XX
PR   01-JUN-2001; 2001EP-00112899.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Penger A,  Sprenger R,  Brinkmann U;
XX
DR   WPI; 2003-167344/16.
XX
PT   New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT   2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT   arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
PS   Example 2; Page 52; 178pp; English.
XX
CC   The invention describes a new polynucleotide comprises a polynucleotide:
```

```
CC   (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC   in the specification; (b) encoding any of seven polypeptides having 7
CC   amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC   hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC   encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC   polynucleotide, gene, vector, polypeptide or antibody is useful for
CC   diagnosing or treating a disease, for preparing a diagnostic composition
CC   for diagnosing a disease, or for preparing a pharmaceutical composition
CC   for treating a disease. This disease includes arachidonic acid
CC   metabolism, cancer or cardiovascular diseases. This sequence represents a
CC   primer used to isolate regions of the human cytochrome P450 polypetide
CC   2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
CC   (SNP) in that region of different individuals useful in disease diagnosis
XX
SQ   Sequence 19 BP; 10 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATA 2408
              ||||| ||||||  ||||
Db          1 AAAATGTATATATGTATA 18


RESULT 1547
ACA98774/c
ID   ACA98774 standard; DNA; 19 BP.
XX
AC   ACA98774;
XX
DT   28-JUL-2003  (first entry)
XX
DE   Human CYP2C8 SNP detection PCR primer #214.
XX
KW   Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
KW   cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
KW   single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200299099-A2.
XX
PD   12-DEC-2002.
XX
PF   31-MAY-2002; 2002WO-EP006000.
XX
PR   01-JUN-2001; 2001EP-00112899.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Penger A,  Sprenger R,  Brinkmann U;
XX
DR   WPI; 2003-167344/16.
XX
PT   New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT   2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT   arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
PS   Example 2; Page 52; 178pp; English.
XX
CC   The invention describes a new polynucleotide comprises a polynucleotide:
CC   (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC   in the specification; (b) encoding any of seven polypeptides having 7
CC   amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC   hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC   encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC   polynucleotide, gene, vector, polypeptide or antibody is useful for
CC   diagnosing or treating a disease, for preparing a diagnostic composition
CC   for diagnosing a disease, or for preparing a pharmaceutical composition
CC   for treating a disease. This disease includes arachidonic acid
CC   metabolism, cancer or cardiovascular diseases. This sequence represents a
CC   primer used to isolate regions of the human cytochrome P450 polypetide
CC   2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
CC   (SNP) in that region of different individuals useful in disease diagnosis
XX
SQ   Sequence 19 BP; 7 A; 2 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATA 2408
              ||||| ||||||  ||||
Db         19 AAAATGTATATATGTATA 2


RESULT 1548
AAQ75557/c
ID   AAQ75557 standard; DNA; 19 BP.
XX
AC   AAQ75557;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              |||||||| ||||| | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1549
AAQ75555/c
ID   AAQ75555 standard; DNA; 19 BP.
XX
AC   AAQ75555;
XX
DT   04-AUG-1995  (first entry)
```

XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGA 3621
||||||||| ||||| | |
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1550
ABL57547
ID ABL57547 standard; DNA; 20 BP.
XX
AC ABL57547;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly n.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4493 TTTATAAGTTTTTTTTTT 4510
| |||| ||||||||||
Db 1 TATATATATTTTTTTTTT 18

RESULT 1551
ABA97632
ID ABA97632 standard; DNA; 20 BP.
XX
AC ABA97632;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly n nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX

```
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4493 TTTATAAGTTTTTTTTTT 4510
              | ||||  ||||||||||
Db          1 TATATATATTTTTTTTTT 18


RESULT 1552
ADH70655
ID   ADH70655 standard; DNA; 20 BP.
XX
AC   ADH70655;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #445.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 849; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              || |||| ||||| ||||
Db          3 AAGAAAAAAAAAAAAGAA 20


RESULT 1553
AAT04917/c
ID   AAT04917 standard; cDNA; 20 BP.
XX
AC   AAT04917;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1996  (first entry)
XX
DE   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KW   Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW   thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW   transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS   Synthetic.
XX
PN   EP676470-A1.
XX
PD   11-OCT-1995.
XX
PF   04-OCT-1990;   95EP-00105391.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 1995-346090/45.
XX
PT   New stem cell factor polypeptide(s) - for stimulating the growth of
PT   primitive progenitor cells, esp. for treating disorders involving blood
PT   cells.
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
```

CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC naturally occuring SCF and C-terminally truncated polypeptides, having
CC amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC stimulate growth of primitive progenitors such as haematopoietic
CC progenitor cells, neural stem cells and primordial germ stem cells. The
CC peptides can be used in a composition for treating leucopenia, anaemia or
CC thrombocytopenia, for enhancing engraftment of bone marrow during
CC transplantation or for bone marrow recovery after chemotherapy or
CC radiation-induced bone marrow aplasia or myelosuppression. They can also
CC be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC damage or myeloproliferative disorders. Antibodies may be raised against
CC the peptides for use in detection or neutralisation of SCF in serum. SCF
CC may be useful for the treatment of AIDS and severe combined
CC immunodeficiency (SCID) states alone or in combination with other factors
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1554
AAA13752/c
ID AAA13752 standard; DNA; 20 BP.
XX
AC AAA13752;
XX
DT 27-JUL-2000 (first entry)
XX
DE Stem cell factor universal oligonucleotide 220-3.
XX
KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW primitive progenitor cell; haematopoietic disorder; syngeneic;
KW allogeneic; autologous bone marrow transplant; gene therapy;
KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW cancer; ss.
XX
OS Synthetic.
XX
PN EP992579-A1.
XX
PD 12-APR-2000.
XX
PF 04-OCT-1990; 99EP-00122861.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
PR 04-OCT-1990; 90EP-00310899.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX
DR WPI; 2000-259135/23.
XX
PT Production of hematopoietic cells suitable for administration to a
PT subject using progenitor cells and expanding the cells using stem cell
PT factor.
XX
PS Example 3; Fig 12C; 123pp; English.
XX
CC A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural
CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early haematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is useful
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC or autologous bone marrow transplant. SCF is useful for enhancing the
CC efficiency of gene therapy based on transfecting haematopoietic stem
CC cells. SCF is also useful for combating the myelosuppressive effects of
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC after acute blood loss and as a boost to the immune system for fighting
CC neoplasia (cancer). The present sequence represents a universal
CC oligonucleotide which is used in an example from the present invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1555
AAH41331/c
ID AAH41331 standard; DNA; 20 BP.
XX
AC AAH41331;
XX
DT 21-AUG-2001 (first entry)
XX
DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
XX
KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS Synthetic.
XX
PN US6207454-B1.
XX
PD 27-MAR-2001.
XX
PF 31-DEC-1998; 98US-00224681.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449653.
PR 12-JAN-1998; 98US-00005893.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-366062/38.
XX
PT Enhancing efficiency of transfer of polynucleotide into a target
PT mammalian cell in vitro, involves exposing cell that expresses a stem
PT cell factor receptor to stem cell factor, and introducing polynucleotide
PT into cell in vitro.
XX
PS Example 3; Fig 12C; 210pp; English.
XX
CC The present invention describes a method for enhancing (E) the efficiency

CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC receptor to a biologically active SCF, its analogue or fragment, which
CC induces cell proliferation, and introducing (I) to (II) in vitro.
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC The method is useful for enhancing the efficiency of the transfer of a
CC polynucleotide into a target mammalian cell in vitro. The method is
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC AAB98390 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1556
AAS04111/c
ID AAS04111 standard; DNA; 20 BP.
XX
AC AAS04111;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6207417-B1.
XX
PD 27-MAR-2001.
XX
PF 07-JUN-1995; 95US-00482918.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-298941/31.
XX
PT Novel nucleic acids encoding stem cell factor useful for treating
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT disease, Kala azar, anemia and septicemia.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1557
AAF89091/c
ID AAF89091 standard; DNA; 20 BP.
XX
AC AAF89091;
XX
DT 13-JUL-2001 (first entry)
XX
DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.
XX
KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency; PCR primer; ss.
XX
OS Mammalia.
XX
PN US6207802-B1.
XX
PD 27-MAR-2001.
XX
PF 09-NOV-1994; 94US-00336728.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-353108/37.
XX
PT Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early hematopoietic progenitor cells, useful for
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention
XX

```
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1558
AAH23889/c
ID   AAH23889 standard; DNA; 20 BP.
XX
AC   AAH23889;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1559
AAS04212/c
ID   AAS04212 standard; DNA; 20 BP.
XX
AC   AAS04212;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
PS   Example 3; Fig 12C; 167pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC   and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC   cells including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC   (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
```

```
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1560
AAS10447/c
ID   AAS10447 standard; DNA; 20 BP.
XX
AC   AAS10447;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW   blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW   hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6248319-B1.
XX
PD   19-JUN-2001.
XX
PF   24-MAY-1995;   95US-00449653.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-407312/43.
XX
PT   Increasing the number of early hematopoietic progenitor cells in the
PT   peripheral blood useful for the treatment of blood disorders including
PT   Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
CC   primers (AAS10435-AAS10453) used to amplify various portions of the human
CC   SCF cDNA sequence. The sequence is described in an invention relating to
CC   novel stem cell factors, the polynucleotides encoding them and methods
CC   for producing the stem cell factors. The methods involve increasing the
CC   number of early haematopoietic progenitor cells in human peripheral blood
CC   by administering a haematopoietically effective human stem cell factor
CC   polypeptide. The methods are useful for the treatment of blood disorders,
CC   including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC   carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC   lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC   disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1
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RESULT 1561
AAD35464/c
ID   AAD35464 standard; DNA; 20 BP.
XX
AC   AAD35464;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Rat SCF 5' cDNA amplifying PCR primer, 220-3.
XX
KW   Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW   anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW   infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW   metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW   Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW   Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW   Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
KW   disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW   acquired immune deficiency syndrome; malaria; military tuberculosis;
KW   pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW   Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW   primer; ss.
XX
OS   Rattus sp.
XX
PN   US2002018763-A1.
XX
PD   14-FEB-2002.
XX
PF   12-JAN-1998;   98US-00005243.
XX
PR   24-MAY-1995;   95US-00449653.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2002-350789/38.
XX
PT   Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT   treating leucopenia, thrombocytopenia, anemia and for enhancing
PT   engraftment of bone marrow during transplantation in a mammal.
XX
PS   Example 3; Fig 12C; 217pp; English.
XX
CC   The present invention relates to novel non-naturally-occurring stem cell
CC   factor (SCF) polypeptides having an amino acid sequence sufficiently
CC   duplicative of that of naturally-occurring SCF to allow possession of
CC   haematopoietic biological activity of naturally occurring SCF. Sequences
CC   of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC   anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC   engraftment of bone marrow during transplantation in mammals and chemical
CC   or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC   are also useful for treating acquired immune deficiency in a human, nerve
CC   damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC   damage in a mammal. SCF sequences are useful for preparing biologically
CC   active polymer polypeptide adduct, for enhancing transfection of early
CC   haematopoietic progenitor cells with a gene, and transfer of a gene into
CC   a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC   osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC   Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC   Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC   syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC   splenic pancytopaenia, disseminated fungus disease, malaria, military
CC   tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC   and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC   disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC   and vitiligo. The present sequence is a PCR primer which is used for
CC   amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC   exemplification of the invention
```

```
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1562
ABS73848/c
ID   ABS73848 standard; DNA; 20 BP.
XX
AC   ABS73848;
XX
DT   05-DEC-2002  (first entry)
XX
DE   SCF universal oligonucleotide 220-3.
XX
KW   Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW   haematopoietic system; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW   refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW   disseminated fungus disease; haematopoietic; tuberculostatic;
KW   antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS   Synthetic.
XX
PN   EP1241258-A2.
XX
PD   18-SEP-2002.
XX
PF   04-OCT-1990; 2002EP-00008587.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
PR   04-OCT-1990;   95EP-00105391.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 2002-684093/74.
XX
PT   Production of a human stem cell factor (SCF) polypeptide for treating
PT   disorders involving blood cells, such as leukemia, comprises culturing
PT   mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT   encoding the human SCF.
XX
PS   Example 3; Fig 12C; 120pp; English.
XX
CC   The present invention relates to novel stem cell factors (SCFs),
CC   polynucleotide sequences encoding the SCFs, and methods of producing
CC   them. SCFs are involved in the blood-forming (haematopoietic) system in
CC   mammals, particularly humans. The method of the invention is useful for
CC   the production of human SCF. The stem cell factors are useful to treat
CC   disorders involving blood cells e.g. metastatic carcinoma, acute
CC   leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC   erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC   disease, malaria, and vitiligo. The present sequence representing a
CC   universal oligonucleotide for SCF DNA is used in the examples of the
CC   present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1563
ADE52460/c
ID   ADE52460 standard; DNA; 20 BP.
XX
AC   ADE52460;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stem cell factor (SCF) related DNA #31.
XX
KW   Stem cell factor; SCF; haematopoietic activity; infertility;
KW   intestinal damage; myeloproliferative disorder; leucopenia;
KW   thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW   neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW   miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS   Synthetic.
XX
PN   US2002031491-A1.
XX
PD   14-MAR-2002.
XX
PF   31-DEC-1998;   98US-00224683.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2003-851459/79.
XX
PT   New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT   immune deficiency, also related nucleic acid and antibodies.
XX
PS   Disclosure; SEQ ID NO 32; 217pp; English.
XX
CC   The invention relates to stem cell factor (SCF) polypeptides with
CC   haematopoietic activity and the polynucleotides encoding them. The
CC   polypeptides are used for treating infertility, intestinal damage,
CC   myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC   for improving engraftment of bone marrow transplants, for enhancing bone
CC   marrow recovery after radiotherapy or chemotherapy and in treatment of
CC   immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC   carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC   also used to expand haematopoietic progenitor cells for transplantation
CC   and to prepare such cells for transfection with a gene. The SCF
CC   polynucleotides can be used for recombinant expression of the
CC   polypeptides and also as probes for mapping of the SCF gene, for
CC   identifying SCF-related diseases and as a marker for neighbouring genes.
CC   Antibodies raised against the polypeptides are useful in diagnosis and to
CC   remove SCF from blood. This sequence represents SCF related DNA of the
CC   invention.
XX
```

```
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1564
ADL59742
ID   ADL59742 standard; DNA; 20 BP.
XX
AC   ADL59742;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1991.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1991; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| || |
Db          3 AAAAAAAAAAAAAAAGCA 20


RESULT 1565
ADM14467/c
ID   ADM14467 standard; DNA; 20 BP.
XX
AC   ADM14467;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:654.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages and all cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methocyethyls"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 654; 132pp; English.
```

```
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1566
ADP99302/c
ID   ADP99302 standard; DNA; 20 BP.
XX
AC   ADP99302;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Stem cell factor, SCF, universal PCR primer #2.
XX
KW   SCF; stem cell factor; gene therapy; haematopoietic progenitor cell;
KW   aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;
KW   myelosclerosis; osteopetrosis; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;
KW   Niemann-Pick disease; Letterer-Siwe disease;
KW   refractory erythroblastic anaemia; Di Guglielmo syndrome;
KW   congestive splenomegaly; Kala awar; sarcoidosis;
KW   primary splenic pancytopaenia; miliary tuberculosis;
KW   disseminated fungus disease; Fulminating septicaemia; malaria;
KW   vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;
KW   Diamond Blackfan anaemia; hypopigmentation disorder; piebaldism;
KW   vitiligo; neurological damage; infertility; intestinal damage;
KW   irradiation; chemotherapy; AIDS; haematopoietic recovery;
KW   acute blood loss; neoplasm; cancer; ss; PCR; primer.
XX
OS   Mammalia.
XX
PN   US6759215-B1.
XX
PD   06-JUL-2004.
XX
PF   07-AUG-2000; 2000US-00635251.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449182.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2004-497128/47.
XX
PT   Preparing a human stem cell factor (SCF) polypeptide, useful for treating
PT   hematopoietic disorders, e.g., aplastic anemia, comprises growing host
PT   cells transformed or transfected with DNA encoding a human SCF.
XX
PS   Example 3; SEQ ID NO 32; 210pp; English.
XX
CC   The invention relates to preparing a (vertebrate) human stem cell factor
CC   (SCF) polypeptide comprising growing host cells transformed or
CC   transfected with DNA encoding a human SCF that stimulates growth of
CC   haematopoietic progenitor cells under nutrient conditions, the DNA being
CC   operatively linked to an expression control sequence, and isolating the
CC   polypeptide produced. Also included is a recombinant host cell
CC   transformed or transfected with an expression construct comprising a
CC   vertebrate SCF polypeptide-encoding DNA operatively linked to a
CC   heterologous expression regulatory sequence, permitting the expression of
CC   the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat
CC   and human nucleic acids encoding SCF, SCF proteins from a number of other
CC   mammals and recombinantly expressed SCF protein fragments. The DNA
CC   sequences are useful for effecting the large scale synthesis of SCF by a
CC   variety of recombinant techniques or for generating new and useful viral
CC   and circular plasmid DNA vectors, new and useful transformed and
CC   transfected prokaryotic and eukaryotic host cells, and new and useful
CC   methods for cultured growth of such host cells capable of expression of
CC   SCF and its related products. The DNA sequences are also useful as
CC   labelled probes in isolating human genomic DNA encoding SCF, in methods
CC   of protein synthesis, in genetic therapy in humans and other mammals, and
CC   in developing transgenic mammalian species which may serve as eukaryotic
CC   hosts for production of SCF and SCF products in quantity. The SCF is
CC   useful for treating haematopoietic disorders, e.g., aplastic anaemia,
CC   paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelosclerosis,
CC   osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC   Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC   Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC   syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary
CC   splenic pancytopaenia, miliary tuberculosis, disseminated fungus disease,
CC   Fulminating septicaemia, malaria, vitamin B 12 and folic acid deficiency,
CC   pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation
CC   disorders such as piebaldism and vitiligo. The SCF are also useful for
CC   treating neurological damage, infertility states, intestinal damage
CC   resulting from irradiation or chemotherapy, and AIDS. SCF is also useful
CC   for enhancing haematopoietic recovery after acute blood loss and as a
CC   boost to the immune system for fighting neoplasia (cancer). The present
CC   sequence is a universal SCF PCR primer used in the isolation of SCF DNA.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1567
AAQ75601/c
ID   AAQ75601 standard; DNA; 20 BP.
XX
AC   AAQ75601;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
```

XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3604 GAAAAAAACAAAAACAGA 3621
||||||| ||||| | |
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1568
ADP69379/c
ID ADP69379 standard; DNA; 20 BP.
XX
AC ADP69379;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #273.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 273; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3965 TATAAACAATAAAAACAA 3982
| ||||||| ||||| ||
Db 20 TTTAAACAAAAAAAAAAA 3

RESULT 1569
AAQ75591/c
ID AAQ75591 standard; DNA; 20 BP.
XX
AC AAQ75591;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;

```
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1570
ABL57552
ID   ABL57552 standard; DNA; 20 BP.
XX
AC   ABL57552;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly s.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 6; Page 23; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the effects of
CC   the number of G(s) in each target nucleic acid, and the number of G(S) in
CC   its corresponding invention nucleic acid probe
XX
SQ   Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4493 TTTATAAGTTTTTTTTTT 4510
              | ||||  ||||||||||
Db          1 TATATATATTTTTTTTTT 18


RESULT 1571
ABA97637
ID   ABA97637 standard; DNA; 20 BP.
XX
AC   ABA97637;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly s nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4493 TTTATAAGTTTTTTTTTT 4510
              | ||||  ||||||||||
Db          1 TATATATATTTTTTTTTT 18


RESULT 1572
ABZ88618
ID   ABZ88618 standard; DNA; 20 BP.
XX
AC   ABZ88618;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
```

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3860; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          2 AAAAAAAAAAAAAAAAAA 19
```

RESULT 1573
ABD24848
ID ABD24848 standard; DNA; 20 BP.
XX
AC ABD24848;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI092623-derived oligonucleotide SEQ ID 3860.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 3860; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          2 AAAAAAAAAAAAAAAAAA 19
```

RESULT 1574

```
ADH67348/c
ID   ADH67348 standard; DNA; 20 BP.
XX
AC   ADH67348;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human glucocorticoid receptor-specific antisense oligonucleotide #4182.
XX
KW   antisense oligonucleotide; glucocorticoid receptor; infection;
KW   inflammation; tumour formation; diabetes; obesity;
KW   cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW   phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS   Homo sapiens.
XX
PN   WO2003099215-A2.
XX
PD   04-DEC-2003.
XX
PF   20-MAY-2003; 2003WO-US016084.
XX
PR   20-MAY-2002; 2002US-0381857P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Crosby SD,  Nalseth AE;
XX
DR   WPI; 2004-035034/03.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT   cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS   Claim 4; SEQ ID NO 4182; 985pp; English.
XX
CC   The invention comprises an antisense oligonucleotides that are targeted
CC   to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC   antisense oligonucleotides of the invention are useful for preventing or
CC   delaying infection, inflammation or tumour formation. The antisense
CC   oligonucleotides are also useful for treating diabetes, obesity,
CC   cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC   present DNA sequence represents an antisense oligonucleotide that targets
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 1575
ADH67400/c
ID   ADH67400 standard; DNA; 20 BP.
XX
AC   ADH67400;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human glucocorticoid receptor-specific antisense oligonucleotide #4234.
XX
KW   antisense oligonucleotide; glucocorticoid receptor; infection;
KW   inflammation; tumour formation; diabetes; obesity;
KW   cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW   phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS   Homo sapiens.
XX
PN   WO2003099215-A2.
XX
PD   04-DEC-2003.
XX
PF   20-MAY-2003; 2003WO-US016084.
XX
PR   20-MAY-2002; 2002US-0381857P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Crosby SD,  Nalseth AE;
XX
DR   WPI; 2004-035034/03.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT   cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS   Claim 4; SEQ ID NO 4234; 985pp; English.
XX
CC   The invention comprises an antisense oligonucleotides that are targeted
CC   to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC   antisense oligonucleotides of the invention are useful for preventing or
CC   delaying infection, inflammation or tumour formation. The antisense
CC   oligonucleotides are also useful for treating diabetes, obesity,
CC   cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC   present DNA sequence represents an antisense oligonucleotide that targets
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1576
ADK74647/c
ID   ADK74647 standard; DNA; 20 BP.
XX
AC   ADK74647;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1981.
XX
KW   Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW   diabetic neuropathy; arthritic pain; migraine headache;
KW   infantile epilepsy; ataxia; ss.
XX
OS   Synthetic.
XX
PN   WO2004016754-A2.
XX
PD   26-FEB-2004.
XX
PF   14-AUG-2003; 2003WO-US025465.
XX
PR   14-AUG-2002; 2002US-0403416P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Roberds SL;
XX
DR   WPI; 2004-203785/19.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
```

PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1981; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1577
ADK73558/c
ID ADK73558 standard; DNA; 20 BP.
XX
AC ADK73558;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #892.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 892; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2381 GGTCAAAAATAAAATATA 2398
||||||||| |||| | |
Db 19 GGTCAAAAAAAAAAAAAA 2

RESULT 1578
ADK74442/c
ID ADK74442 standard; DNA; 20 BP.
XX
AC ADK74442;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1776.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1776; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.

```
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1579
ADL59743
ID   ADL59743 standard; DNA; 20 BP.
XX
AC   ADL59743;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1992.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1992; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| || |
Db          2 AAAAAAAAAAAAAAAAGCA 19


RESULT 1580
ADM14246/c
ID   ADM14246 standard; DNA; 20 BP.
XX
AC   ADM14246;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:433.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages and all cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methocyethyls"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
```

PS Claim 4; SEQ ID NO 433; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1581
ADK01302/c
ID ADK01302 standard; DNA; 21 BP.
XX
AC ADK01302;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #22.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1582
AAQ75777/c
ID AAQ75777 standard; DNA; 21 BP.
XX
AC AAQ75777;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of

```
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1583
AAQ75737/c
ID   AAQ75737 standard; DNA; 21 BP.
XX
AC   AAQ75737;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1584
ADK01304/c
ID   ADK01304 standard; DNA; 21 BP.
XX
AC   ADK01304;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Rat DNA microarray capture oligonucleotide #24.
XX
KW   ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW   blood; nerve; germ cell; food additive; food supplement.
XX
OS   Rattus sp.
XX
PN   DE10208794-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2002; 2002DE-01008794.
XX
PR   28-FEB-2002; 2002DE-01008794.
XX
PA   (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI   Boekenkamp D,  Dieck HT,  Hoppe H;
XX
DR   WPI; 2003-714082/68.
XX
PT   Sorting single-stranded nucleic acid, useful for analyzing expression
PT   patterns and screening active agents, uses capture agent with variable
PT   and constant regions.
XX
PS   Example; Page 5; 8pp; German.
XX
CC   This invention describes a novel method for sorting single-stranded
CC   nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC   reading out, where the nucleic acids are selectively bound using capture
CC   agents that are (a) immobilised on the surface of a solid matrix and (b)
CC   comprise variable and non-variable regions. The capture oligonucleotides
CC   have a 5'-invariable anchor region, the complement of which is present at
CC   least once in each nucleic acid and a 3'-variable, discriminatory region
CC   that comprises all possible combinations of up to 10 nucleotides to allow
CC   binding of particular sorts of single stranded nucleic acids. The capture
CC   agents are particularly locked nucleic acids (LNA) and the anchor region
CC   comprises a sequence of 10-50, particularly 15-25, T residues. The
CC   capture oligonucleotides are biotinylated and immobilised on a surface by
CC   interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC   metal, resin, gel, crystalline material and/or membrane, having semi-
CC   conducting properties and especially in the form of a chip. Its surface
CC   is particularly a layer of (bio)molecular filaments and binding of single
CC   stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC   physical, stimulated by an electrical field or through a molecular sieve.
CC   The method is used (i) for analysis of patterns, especially in mucosal,
CC   hair root, blood, nerve or germ cells and (ii) for determining the
CC   activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC   additives or supplements, especially minerals, trace elements, organic
CC   acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC   mixtures. The method provides rapid, inexpensive and reproducible
CC   representation of differences in pools of nucleic acids from cells. It
CC   allows imaging of the complete pattern of all nucleic acid in a cell, and
CC   can detect very small differences in the nucleic acid pool. Since the
CC   method is based on comparison of nucleic acid pools, not individual
CC   genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC   capture probes used in the method of the invention.
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              |||||||  |||||  | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1585
AAV35395
```

ID AAV35395 standard; DNA; 21 BP.
XX
AC AAV35395;
XX
DT 13-OCT-1998 (first entry)
XX
DE HIV-1 gag protein DNA primer #8.
XX
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX
OS Synthetic.
XX
PN WO9822596-A1.
XX
PD 28-MAY-1998.
XX
PF 19-NOV-1997; 97WO-JP004216.
XX
PR 19-NOV-1996; 96JP-00323412.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (JAPG) NIPPON ZEON KK.
XX
PI Kojima A, Kurata T, Yasuda A;
XX
DR WPI; 1998-312481/27.
XX
PT Recombinant vaccinia virus containing fusion HIB gag gene - for
PT production in host cells of gag protein for use as vaccine.
XX
PS Example 1; Page 66; 84pp; Japanese.
XX
CC AAV35388-V35414 are primers used in a method which results in a
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC region (30-300 bases in length) of a retroviral gene other than the gag
CC gene. The gag gene may be altered so as to produce a gag protein modified
CC from the natural sequence by the addition, deletion or substitution of at
CC least 1 amino acid residue. The fusion gene is inserted into a region of
CC a vaccinia virus not essential to its propagation, to give a recombinant
CC vaccinia virus vector which is used to transform a host cell (such as
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC culturing the host cell produces particulate structures containing the
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC protein particles may be used in the production of vaccines for
CC protecting against infection with retroviruses such as HIV
XX
SQ Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 3 AAAAAAAAAAAAAAAAAA 20

RESULT 1586
ADK01334/c
ID ADK01334 standard; DNA; 21 BP.
XX
AC ADK01334;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #54.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.

XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1587
ADK01303/c
ID ADK01303 standard; DNA; 21 BP.
XX
AC ADK01303;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #23.
XX

KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1588
ADK01301/c
ID ADK01301 standard; DNA; 21 BP.
XX
AC ADK01301;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #21.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3605 AAAAAAACAAAAACAGAA 3622
||||||| ||||| | ||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1589
AAQ75778/c

```
ID   AAQ75778 standard; DNA; 21 BP.
XX
AC   AAQ75778;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1590
AAQ75775/c
ID   AAQ75775 standard; DNA; 21 BP.
XX
AC   AAQ75775;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1591
AAQ75776/c
ID   AAQ75776 standard; DNA; 21 BP.
XX
AC   AAQ75776;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
```

```
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1592
AAQ75745/c
ID   AAQ75745 standard; DNA; 21 BP.
XX
AC   AAQ75745;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACAGA 3621
              ||||||||  |||||  | |
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1593
ADK01312/c
ID   ADK01312 standard; DNA; 21 BP.
XX
AC   ADK01312;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Rat DNA microarray capture oligonucleotide #32.
XX
KW   ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW   blood; nerve; germ cell; food additive; food supplement.
XX
OS   Rattus sp.
XX
PN   DE10208794-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2002; 2002DE-01008794.
XX
PR   28-FEB-2002; 2002DE-01008794.
XX
PA   (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI   Boekenkamp D,  Dieck HT,  Hoppe H;
XX
DR   WPI; 2003-714082/68.
XX
PT   Sorting single-stranded nucleic acid, useful for analyzing expression
PT   patterns and screening active agents, uses capture agent with variable
PT   and constant regions.
XX
PS   Example; Page 5; 8pp; German.
XX
CC   This invention describes a novel method for sorting single-stranded
CC   nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC   reading out, where the nucleic acids are selectively bound using capture
CC   agents that are (a) immobilised on the surface of a solid matrix and (b)
CC   comprise variable and non-variable regions. The capture oligonucleotides
CC   have a 5'-invariable anchor region, the complement of which is present at
CC   least once in each nucleic acid and a 3'-variable, discriminatory region
CC   that comprises all possible combinations of up to 10 nucleotides to allow
CC   binding of particular sorts of single stranded nucleic acids. The capture
CC   agents are particularly locked nucleic acids (LNA) and the anchor region
CC   comprises a sequence of 10-50, particularly 15-25, T residues. The
CC   capture oligonucleotides are biotinylated and immobilised on a surface by
CC   interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC   metal, resin, gel, crystalline material and/or membrane, having semi-
CC   conducting properties and especially in the form of a chip. Its surface
CC   is particularly a layer of (bio)molecular filaments and binding of single
CC   stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC   physical, stimulated by an electrical field or through a molecular sieve.
CC   The method is used (i) for analysis of patterns, especially in mucosal,
CC   hair root, blood, nerve or germ cells and (ii) for determining the
CC   activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC   additives or supplements, especially minerals, trace elements, organic
CC   acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC   mixtures. The method provides rapid, inexpensive and reproducible
CC   representation of differences in pools of nucleic acids from cells. It
CC   allows imaging of the complete pattern of all nucleic acid in a cell, and
CC   can detect very small differences in the nucleic acid pool. Since the
CC   method is based on comparison of nucleic acid pools, not individual
CC   genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC   capture probes used in the method of the invention.
XX
SQ   Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              |||||||  |||||  | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1594
AAQ75028
ID   AAQ75028 standard; DNA; 23 BP.
XX
AC   AAQ75028;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
```

```
DE   LCR oligo 2.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 23;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          6 AAAAAAAAAAAAAAAAAA 23


RESULT 1595
AAQ75029/c
ID   AAQ75029 standard; RNA; 23 BP.
XX
AC   AAQ75029;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 3.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 23;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1596
AAD44151/c
ID   AAD44151 standard; DNA; 17 BP.
XX
AC   AAD44151;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-AT PCR primer #2 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1D; 19pp; English.
XX
```

```
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo AT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGA 3621
              ||||||| ||||| |:|
Db         17 AAAAAAAAAAAAAAAABA 1


RESULT 1597
AAX69804
ID   AAX69804 standard; RNA; 17 BP.
XX
AC   AAX69804;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.3%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   13;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              :::::::::::::
Db          1 UUUUUUUUUUUUU 13


RESULT 1598
ADE27483
ID   ADE27483 standard; RNA; 19 BP.
XX
AC   ADE27483;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:427.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 427; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 0 G; 0 T; 8 U; 0 Other;

  Query Match             0.3%;  Score 13;  DB 1;  Length 19;
  Best Local Similarity   69.2%;  Pred. No. 1.7e+03;
```

```
  Matches    9;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2335 TTTCCAAACATCC 2347
              :::|||||||:||
Db          1 UUUCCAAACAUCC 13


RESULT 1599
ADE27193/c
ID   ADE27193 standard; RNA; 19 BP.
XX
AC   ADE27193;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:137.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 137; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 0 C; 7 G; 0 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 13;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2335 TTTCCAAACATCC 2347
              |||||||||||||
Db         19 TTTCCAAACATCC 7


RESULT 1600
AAQ75611/c
ID   AAQ75611 standard; DNA; 21 BP.
XX
AC   AAQ75611;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 13;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3601 CTGGAAAAAAACAAAAACAGA 3621
              ||  ||||||| ||||| | |
Db         21 CTCCAAAAAAAAAAAAAAAAA 1


RESULT 1601
AAQ75620/c
ID   AAQ75620 standard; DNA; 21 BP.
XX
AC   AAQ75620;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
```

PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3602 TGGAAAAAAACAAAAACAGAA 3622
|| |||||| ||||| | ||
Db 21 TGCCAAAAAAAAAAAAAAAAA 1

RESULT 1602
AAQ75614/c
ID AAQ75614 standard; DNA; 21 BP.
XX
AC AAQ75614;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3599 GTCTGGAAAAAAACAAAAACA 3619
||| ||||||| ||||| |
Db 21 GTCCAAAAAAAAAAAAAAAAA 1

RESULT 1603
ADH70350
ID ADH70350 standard; DNA; 16 BP.
XX
AC ADH70350;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #140.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 544; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple

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CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 16 BP; 7 A; 0 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||| |||||||
Db          1 TATATATGTATATATA 16


RESULT 1604
ABL57075
ID   ABL57075 standard; DNA; 16 BP.
XX
AC   ABL57075;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .16
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 5-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 GAAAAAAAAAAAAAAA 16


RESULT 1605
AAD57845
ID   AAD57845 standard; DNA; 16 BP.
XX
AC   AAD57845;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20-B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||| ||||| |
Db          1 GAAAAAAAAAAAAAAA 16
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RESULT 1606
ADF23331
ID   ADF23331 standard; DNA; 16 BP.
XX
AC   ADF23331;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Binding partner sceening method molecular beacon analogue #2.
XX
KW   binding partner screening; light beam; nonlinear optical light beam; ss;
KW   molecular beacon analogue.
XX
OS   Synthetic.
XX
PN   US2003148391-A1.
XX
PD   07-AUG-2003.
XX
PF   06-JUN-2002; 2002US-00164915.
XX
PR   24-JAN-2002; 2002US-0351879P.
PR   06-FEB-2002; 2002US-0354668P.
PR   06-FEB-2002; 2002US-0354679P.
PR   05-MAR-2002; 2002US-0362003P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-897567/82.
XX
PT   Screening of candidate binding partners for binding to test molecule
PT   comprises illuminating sample with light beams and measuring physical
PT   properties of nonlinear optical light beam emanating from sample.
XX
PS   Disclosure; SEQ ID NO 2; 58pp; English.
XX
CC   The invention describes screening a candidate binding partner by
CC   illuminating the sample with light beams at fundamental frequencies to
CC   binding partners, and measuring physical properties of a nonlinear
CC   optical light beam emanating from sample. On binding to the test molecule
CC   the properties change relative to that in absence of exposure of the test
CC   molecule. The invention is used in the screening of candidate binding
CC   partners for binding to test molecule. This sequence represents a
CC   molecular beacon analogue, an exemplary test molecule of the invention.
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3604 GAAAAAAACAAAAACA 3619
              |||||||| ||||| |
Db          1 GAAAAAAAAAAAAAAA 16


RESULT 1607
ADH70347/c
ID   ADH70347 standard; DNA; 16 BP.
XX
AC   ADH70347;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #137.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 541; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 16 BP; 8 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              |||||||| ||||||
Db         16 TATATATATGTATATA 1


Search completed: October 24, 2005, 15:54:45
Job time : 72 secs
```

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;             APPLICATION NUMBER: 09/486,546
;             FILING DATE: 24-MAY-1995
;             APPLICATION NUMBER: 08/172,329
;             FILING DATE: 21-DEC-1993
;             APPLICATION NUMBER: 07/982,255
;             FILING DATE: 25-NOV-1992
;             APPLICATION NUMBER: 07/684,535
;             FILING DATE: 10-APR-1991
;             APPLICATION NUMBER: 09/589,701
;             FILING DATE: 10-OCT-1991
;             APPLICATION NUMBER: 07/573,616
;             FILING DATE: 24-AUG-1990
;             APPLICATION NUMBER: 07/537,198
;             FILING DATE: 11-JUN-1990
;             APPLICATION NUMBER: 07/422,383
;             FILING DATE: 16-OCT-1989
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Clough, David W.
;             REGISTRATION NUMBER: 36,107
;             REFERENCE/DOCKET NUMBER: 01017/35199
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 32:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-620-642-32

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 887
US-10-728-399-273/c
; Sequence 273, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-273

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3965 TATAAACAATAAAAACAA 3982
              | ||||||| ||||| ||
Db         20 TTTAAACAAAAAAAAAAA 3


RESULT 888
US-10-671-395-433/c
; Sequence 433, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Gierse, James K
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: 1179/1/US
;  CURRENT APPLICATION NUMBER: US/10/671,395
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: 60/413,549
;  PRIOR FILING DATE: 2002-09-25
;  NUMBER OF SEQ ID NOS: 1809
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 433
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-433

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 889
US-10-728-078-14
; Sequence 14, Application US/10728078
; Publication No. US20050038229A1
; GENERAL INFORMATION:
;  APPLICANT: Lipovsek, Dasa
;  APPLICANT:  Wagner, Richard W
;  APPLICANT:  Kuimelis, Robert G
;  TITLE OF INVENTION: PROTEIN SCAFFOLDS FOR ANTIBODY MIMICS
;  TITLE OF INVENTION:  AND OTHER BINDING PROTEINS
;  FILE REFERENCE: 50036/021004
;  CURRENT APPLICATION NUMBER: US/10/728,078
;  CURRENT FILING DATE:  2003-12-03
;  PRIOR APPLICATION NUMBER: US/09/688,566
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: US 60/111,737
;  PRIOR FILING DATE: 1998-12-10
;  PRIOR APPLICATION NUMBER: US 09/456,693
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: US 09/515,260
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 202
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Puromycin linker oligonucleotide
US-10-728-078-14

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db          1 AAAAAAAAAAAAAAAAAA 18
```

```
RESULT 890
US-10-831-901A-29730/c
; Sequence 29730, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29730
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-29730

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 891
US-10-831-901A-29731/c
; Sequence 29731, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29731
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-29731

  Query Match             0.3%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 9e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3605 AAAAAAACAAAAACAGAA 3622
              ||||||| ||||| | ||
Db         19 AAAAAAAAAAAAAAAAAA 2


RESULT 892
US-10-683-990-97/c
; Sequence 97, Application US/10683990
; Publication No. US20040198682A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Usman, Nassim
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
;  TITLE OF INVENTION:  Gene Expression Using SHort Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/134 (02-742-H)
;  CURRENT APPLICATION NUMBER: US/10/683,990
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US 60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US 60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 256
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense re
US-10-683-990-97
```

```
  Query Match             0.3%;  Score 13;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              |||||||||||||
Db         19 TTTTTTTTTTTTT 7


RESULT 893
US-10-683-990-194
; Sequence 194, Application US/10683990
; Publication No. US20040198682A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Usman, Nassim
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
;  TITLE OF INVENTION:  Gene Expression Using SHort Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/134 (02-742-H)
;  CURRENT APPLICATION NUMBER: US/10/683,990
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US 60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US 60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US 60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 256
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-683-990-194

  Query Match             0.3%;  Score 13;  DB 1;  Length 19;
  Best Local Similarity   0.0%;  Pred. No. 9.4e+02;
  Matches    0;  Conservative   13;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTT 4513
              :::::::::::::
Db          1 UUUUUUUUUUUUU 13


RESULT 894
US-09-263-959-544
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  544:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-544

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 9.3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||| |||||||
Db          1 TATATATGTATATATA 16


RESULT 895
US-10-164-915-2
; Sequence 2, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
;  APPLICANT: Salafsky, Joshua S.
;  TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optica
;  TITLE OF INVENTION:  for Detection of Interactions Involving a Conformational Change
;  FILE REFERENCE: 11100-035-999
;  CURRENT APPLICATION NUMBER: US/10/164,915
;  CURRENT FILING DATE:  2002-06-06
;  PRIOR APPLICATION NUMBER: 60/253,862
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/260,249
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/265,775
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: 60/278,941
;  PRIOR FILING DATE: 2001-01-27
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
;    LENGTH: 16
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Aritificial Sequence: Oligonucleotide structure fo
;    OTHER INFORMATION: molecular beacon
US-10-164-915-2

  Query Match             0.3%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 9.3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       3604 GAAAAAAACAAAAACA 3619
              ||||||||| ||||| |
Db          1 GAAAAAAAAAAAAAAA 16
```

Search completed: October 24, 2005, 15:36:08
Job time : 40 secs

```
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 2 C; 5 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3909 GAAATGTCTGCTGGTATTT 3927
              ||||:|:|:||:||:|:::
Db          1 GAAAUGUCUGCUGGUAUUU 19


RESULT 175
ADE27284
ID   ADE27284 standard; RNA; 19 BP.
XX
AC   ADE27284;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:228.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 228; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 1 C; 12 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4089 CTGTGGGTGTGGGTGGGAG 4107
              |:|:|||:|:|||:|||||
Db          1 CUGUGGGUGUGGGUGGGAG 19


RESULT 176
ADE27311
ID   ADE27311 standard; RNA; 19 BP.
XX
AC   ADE27311;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:255.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 255; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
```

CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 3 C; 5 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 4575 CTTGGGTGTATTCTCTGTA 4593
||::|||:|:|::|:|:|:|
Db 1 CUUGGGUGUAUUCUCUGUA 19

RESULT 177
ADE27319
ID ADE27319 standard; RNA; 19 BP.
XX
AC ADE27319;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:263.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 263; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 4719 ACTTAACTATAAGGTGCCT 4737
||::|||:|:||||:|||:
Db 1 ACUUAACUAUAAGGUGCCU 19

RESULT 178
ADE27408/c
ID ADE27408 standard; RNA; 19 BP.
XX
AC ADE27408;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:352.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 352; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

```
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1101 CACTTGGAGCTGTGGGTGA 1119
              |||||||||||||||||||
Db         19 CACTTGGAGCTGTGGGTGA 1

RESULT 179
ADE27422/c
ID   ADE27422 standard; RNA; 19 BP.
XX
AC   ADE27422;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:366.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 366; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1353 CCAGGCAGAGGTTTTAATG 1371
              |||||||||||||||||||
Db         19 CCAGGCAGAGGTTTTAATG 1

RESULT 180
ADE27425/c
ID   ADE27425 standard; RNA; 19 BP.
XX
AC   ADE27425;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:369.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 369; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1407 GCTAAAGATGATGATGTTA 1425
||||||||||||||||||
Db 19 GCTAAAGATGATGATGTTA 1

RESULT 181
ADE27432/c
ID ADE27432 standard; RNA; 19 BP.
XX
AC ADE27432;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:376.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 376; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 3 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1533 TCTAGGCCCATTGTCCTCC 1551
||||||||||||||||||
Db 19 TCTAGGCCCATTGTCCTCC 1

RESULT 182
ADE27471/c
ID ADE27471 standard; RNA; 19 BP.
XX
AC ADE27471;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:415.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 415; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

```
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2235 GAGTATTCCATGAGCTGCT 2253
              |||||||||||||||||||
Db         19 GAGTATTCCATGAGCTGCT 1


RESULT 183
ADE27480/c
ID   ADE27480 standard; RNA; 19 BP.
XX
AC   ADE27480;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:424.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 424; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 1 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2397 TATATACATATATACATTG 2415
              |||||||||||||||||||
Db         19 TATATACATATATACATTG 1


RESULT 184
ADE27481/c
ID   ADE27481 standard; RNA; 19 BP.
XX
AC   ADE27481;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:425.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 425; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
```

XX
SQ Sequence 19 BP; 6 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2415 GCTTAGAACGTTAAACTAT 2433
||||||||||||||||||
Db 19 GCTTAGAACGTTAAACTAT 1

RESULT 185
ADE27485/c
ID ADE27485 standard; RNA; 19 BP.
XX
AC ADE27485;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:429.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 429; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX

SQ Sequence 19 BP; 5 A; 7 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2487 AGGAATTAGTTGGGATGCC 2505
||||||||||||||||||
Db 19 AGGAATTAGTTGGGATGCC 1

RESULT 186
ADE27514/c
ID ADE27514 standard; RNA; 19 BP.
XX
AC ADE27514;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:458.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 458; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 5 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3009 ACAGAATGCTCAGGGTCAC 3027
              ||||||||||||||||||
Db         19 ACAGAATGCTCAGGGTCAC 1


RESULT 187
ADE27517/c
ID   ADE27517 standard; RNA; 19 BP.
XX
AC   ADE27517;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:461.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 461; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3063 TGCCACTTTCACGTGGCCT 3081
              ||||||||||||||||||
Db         19 TGCCACTTTCACGTGGCCT 1


RESULT 188
ADE27521/c
ID   ADE27521 standard; RNA; 19 BP.
XX
AC   ADE27521;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:465.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 465; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 5 C; 6 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
```

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3135 GACAAGGCTGGCAAACCCT 3153
              ||||||||||||||||||
Db         19 GACAAGGCTGGCAAACCCT 1
```

RESULT 189
ADE27558/c
ID ADE27558 standard; RNA; 19 BP.
XX
AC ADE27558;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:502.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 502; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3801 GCCTGGACTAAAGGCATCC 3819
              |||||||||||||||||||
Db         19 GCCTGGACTAAAGGCATCC 1
```

RESULT 190
ADE27565/c
ID ADE27565 standard; RNA; 19 BP.
XX
AC ADE27565;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:509.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 509; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 2 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3927 TCTAATTCCACAGGTCATC 3945
             |||||||||||||||||||
Db         19 TCTAATTCCACAGGTCATC 1
```

```
RESULT 191
ADE27574/c
ID   ADE27574 standard; RNA; 19 BP.
XX
AC   ADE27574;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:518.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 518; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 12 C; 1 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4089 CTGTGGGTGTGGGTGGGAG 4107
             |||||||||||||||||||
Db         19 CTGTGGGTGTGGGTGGGAG 1
```

```
RESULT 192
ADE27599/c
ID   ADE27599 standard; RNA; 19 BP.
XX
AC   ADE27599;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:543.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 543; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 1 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4539 TTAAAATGGAAAATTTTCT 4557
```

```
                    ||||||||||||||||||||
Db         19 TTAAAATGGAAAATTTTCT 1
```

RESULT 193
ADE27623/c
ID ADE27623 standard; RNA; 19 BP.
XX
AC ADE27623;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:567.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 567; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 7 C; 3 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4971 GAAGCGGTGGATAACTAGC 4989
              ||||||||||||||||||||
Db         19 GAAGCGGTGGATAACTAGC 1
```

RESULT 194
ADE27624/c
ID ADE27624 standard; RNA; 19 BP.
XX
AC ADE27624;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:568.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 568; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 3 C; 3 G; 0 T; 9 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4989 CCAGACAAAATTTGAGAAT 5007
              ||||||||||||||||||||
Db         19 CCAGACAAAATTTGAGAAT 1
```

```
RESULT 195
ADE27629/c
ID   ADE27629 standard; RNA; 19 BP.
XX
AC   ADE27629;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:573.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 573; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 5 C; 0 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5079 TTTTATGTGGGATATAGTA 5097
              ||||||||||||||||||
Db         19 TTTTATGTGGGATATAGTA 1
```

```
RESULT 196
ADE27149
ID   ADE27149 standard; RNA; 19 BP.
XX
AC   ADE27149;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:93.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 93; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 4 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1659 AGCCTAAAACGAATGGTCT 1677
              ||||:||||||||:||:|:
Db          1 AGCCUAAAACGAAUGGUCU 19
```

RESULT 197
ADE27157
ID ADE27157 standard; RNA; 19 BP.
XX
AC ADE27157;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:101.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 101; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1803 ATGGAATGGAAAAGCAACT 1821
|:||||:||||||||||:
Db 1 AUGGAAUGGAAAAGCAACU 19

RESULT 198
ADE27160
ID ADE27160 standard; RNA; 19 BP.
XX
AC ADE27160;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:104.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 104; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 2 C; 9 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1857 TCGGGGGAGAGAGTTAGCA 1875
:||||||||||||::||||
Db 1 UCGGGGGAGAGAGUUAGCA 19

RESULT 199
ADE27164

```
ID   ADE27164 standard; RNA; 19 BP.
XX
AC   ADE27164;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:108.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 108; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 7 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1929 CAGACATACAGCTGCCTAC 1947
              ||||||:|||||:|||:||
Db          1 CAGACAUACAGCUGCCUAC 19


RESULT 200
ADE27171
ID   ADE27171 standard; RNA; 19 BP.
XX
AC   ADE27171;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:115.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 115; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2055 TAGTTGAGGCCGAGGATAA 2073
              :||::|||||||||||:||
Db          1 UAGUUGAGGCCGAGGAUAA 19


RESULT 201
ADE27208
ID   ADE27208 standard; RNA; 19 BP.
XX
```

AC ADE27208;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:152.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 152; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2721 AACTAGAAGGCTTCTCTCC 2739
              |||:|||||||::|:|:||
Db          1 AACUAGAAGGCUUCUCUCC 19
```

RESULT 202
ADE27221
ID ADE27221 standard; RNA; 19 BP.
XX
AC ADE27221;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:165.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 165; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 2 C; 7 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2955 TGTGTGTATTCAGAGGCAG 2973
              :|:|:|:|::||||||||||
Db          1 UGUGUGUAUUCAGAGGCAG 19
```

RESULT 203
ADE27231
ID ADE27231 standard; RNA; 19 BP.
XX
AC ADE27231;
XX

```
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:175.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 175; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3135 GACAAGGCTGGCAAACCCT 3153
              ||||||||:|||||||||:
Db          1 GACAAGGCUGGCAAACCCU 19


RESULT 204
ADE27232
ID   ADE27232 standard; RNA; 19 BP.
XX
AC   ADE27232;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:176.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 176; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3153 TCCCAGAAACATCTCTGGC 3171
              :||||||||||:|:|:|||
Db          1 UCCCAGAAACAUCUCUGGC 19


RESULT 205
ADE27245
ID   ADE27245 standard; RNA; 19 BP.
XX
AC   ADE27245;
XX
DT   29-JAN-2004  (first entry)
XX
```

DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:189.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 189; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 2 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3387 AGTAGGAGGAAACAGTTCT 3405
              ||:|||||||||||::|:
Db          1 AGUAGGAGGAAACAGUUCU 19
```

RESULT 206
ADE27255
ID ADE27255 standard; RNA; 19 BP.
XX
AC ADE27255;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:199.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 199; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3567 CCCTACAGCCTAGGGCAGA 3585
              |||:|||||:||||||||
Db          1 CCCUACAGCCUAGGGCAGA 19
```

RESULT 207
ADE27293
ID ADE27293 standard; RNA; 19 BP.
XX
AC ADE27293;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:237.
XX

```
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 237; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 1 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4251 TGCCTTACATCTTTTCTAA 4269
              :|||::|||:|::::|:||
Db          1 UGCCUUACAUCUUUUCUAA 19


RESULT 208
ADE27294
ID   ADE27294 standard; RNA; 19 BP.
XX
AC   ADE27294;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:238.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 238; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4269 ATCACAGTGTTGCATATGA 4287
              |:|||||:|::|||:|:||
Db          1 AUCACAGUGUUGCAUAUGA 19


RESULT 209
ADE27309
ID   ADE27309 standard; RNA; 19 BP.
XX
AC   ADE27309;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:253.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
```

KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 253; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 1 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4539 TTAAAATGGAAAATTTTCT 4557
              ::||||:||||||::::|:
Db          1 UUAAAAUGGAAAAUUUUCU 19
```

RESULT 210
ADE27313
ID ADE27313 standard; RNA; 19 BP.
XX
AC ADE27313;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:257.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 257; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4611 TCATCATGAAAGGTTAAAA 4629
              :||:||:||||||::||||
Db          1 UCAUCAUGAAAGGUUAAAA 19
```

RESULT 211
ADE27317
ID ADE27317 standard; RNA; 19 BP.
XX
AC ADE27317;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:261.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;

```
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 261; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 5 C; 5 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4683 TGTGCCACTGACTTGCTGT 4701
              :|:|||||:|||::||:|:
Db          1 UGUGCCACUGACUUGCUGU 19


RESULT 212
ADE27333
ID   ADE27333 standard; RNA; 19 BP.
XX
AC   ADE27333;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:277.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 277; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4971 GAAGCGGTGGATAACTAGC 4989
              |||||||:|||:|||:|||
Db          1 GAAGCGGUGGAUAACUAGC 19


RESULT 213
ADE27438/c
ID   ADE27438 standard; RNA; 19 BP.
XX
AC   ADE27438;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:382.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
```

```
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 382; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1641 CCTAGACAACCTTTCTGTA 1659
             |||||||||||||||||||
Db         19 CCTAGACAACCTTTCTGTA 1

RESULT 214
ADE27456/c
ID   ADE27456 standard; RNA; 19 BP.
XX
AC   ADE27456;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:400.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 400; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 2 C; 9 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1965 CCCCACCACATAGCATGCT 1983
             |||||||||||||||||||
Db         19 CCCCACCACATAGCATGCT 1

RESULT 215
ADE27461/c
ID   ADE27461 standard; RNA; 19 BP.
XX
AC   ADE27461;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:405.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
```

```
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 405; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2055 TAGTTGAGGCCGAGGATAA 2073
              ||||||||||||||||||
Db         19 TAGTTGAGGCCGAGGATAA 1


RESULT 216
ADE27466/c
ID   ADE27466 standard; RNA; 19 BP.
XX
AC   ADE27466;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:410.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 410; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2145 AATAACAAGGAGATTTCTT 2163
              ||||||||||||||||||
Db         19 AATAACAAGGAGATTTCTT 1


RESULT 217
ADE27482/c
ID   ADE27482 standard; RNA; 19 BP.
XX
AC   ADE27482;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:426.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
```

PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 426; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 2 C; 5 G; 0 T; 4 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2433 TTAGAGTATTTCCCTTCCA 2451
              |||||||||||||||||||
Db         19 TTAGAGTATTTCCCTTCCA 1
```

RESULT 218
ADE27512/c
ID ADE27512 standard; RNA; 19 BP.
XX
AC ADE27512;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:456.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 456; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2973 GTGATGACTTGCTGTCCAG 2991
              |||||||||||||||||||
Db         19 GTGATGACTTGCTGTCCAG 1
```

RESULT 219
ADE27519/c
ID ADE27519 standard; RNA; 19 BP.
XX
AC ADE27519;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:463.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX

```
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 463; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3099 ACACCCCTGTGCTCCCCTG 3117
              ||||||||||||||||||||
Db         19 ACACCCCTGTGCTCCCCTG 1


RESULT 220
ADE27538/c
ID   ADE27538 standard; RNA; 19 BP.
XX
AC   ADE27538;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:482.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 482; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 5 C; 7 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3441 TCACCTCGAAAGGAGGCCC 3459
              ||||||||||||||||||||
Db         19 TCACCTCGAAAGGAGGCCC 1


RESULT 221
ADE27539/c
ID   ADE27539 standard; RNA; 19 BP.
XX
AC   ADE27539;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:483.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
```

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 483; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3459 CTGTTCCCTGGAGTCAGGG 3477
||||||||||||||||||||
Db 19 CTGTTCCCTGGAGTCAGGG 1

RESULT 222
ADE27540/c
ID ADE27540 standard; RNA; 19 BP.
XX
AC ADE27540;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:484.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 484; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3477 GTGAACTGCAAAGCTTTGG 3495
||||||||||||||||||||
Db 19 GTGAACTGCAAAGCTTTGG 1

RESULT 223
ADE27562/c
ID ADE27562 standard; RNA; 19 BP.
XX
AC ADE27562;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:506.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 506; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3873 TAGTTTAGTTCTGTTGACC 3891
||||||||||||||||||||
Db 19 TAGTTTAGTTCTGTTGACC 1

RESULT 224
ADE27581/c
ID ADE27581 standard; RNA; 19 BP.
XX
AC ADE27581;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:525.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 525; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4215 CCTGCTTTGGGGGGTGTGC 4233
||||||||||||||||||||
Db 19 CCTGCTTTGGGGGGTGTGC 1

RESULT 225
ADE27596/c
ID ADE27596 standard; RNA; 19 BP.
XX
AC ADE27596;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:540.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 540; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 11 A; 3 C; 0 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4485 GTATTTGATTTATAAGTTT 4503
              |||||||||||||||||||
Db         19 GTATTTGATTTATAAGTTT 1
```

RESULT 226
ADE27603/c
ID ADE27603 standard; RNA; 19 BP.
XX
AC ADE27603;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:547.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 547; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4611 TCATCATGAAAGGTTAAAA 4629
              |||||||||||||||||||
Db         19 TCATCATGAAAGGTTAAAA 1
```

RESULT 227
ADE27609/c
ID ADE27609 standard; RNA; 19 BP.
XX
AC ADE27609;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:553.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 553; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 3 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4719 ACTTAACTATAAGGTGCCT 4737
||||||||||||||||||||
Db 19 ACTTAACTATAAGGTGCCT 1

RESULT 228
ADE27616/c
ID ADE27616 standard; RNA; 19 BP.
XX
AC ADE27616;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:560.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 560; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4845 AGGAATTCTCAAGACCTGA 4863
||||||||||||||||||||
Db 19 AGGAATTCTCAAGACCTGA 1

RESULT 229
ADE27112
ID ADE27112 standard; RNA; 19 BP.
XX
AC ADE27112;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:56.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

```
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 56; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 2 C; 6 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        993 GATATGCTGTGGTGCTTAA 1011
              ||:|:||:|:||:||::||
Db          1 GAUAUGCUGUGGUGCUUAA 19


RESULT 230
ADE27135
ID   ADE27135 standard; RNA; 19 BP.
XX
AC   ADE27135;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:79.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 79; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 1 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1407 GCTAAAGATGATGATGTTA 1425
              ||:|||||:||:||:|::|
Db          1 GCUAAAGAUGAUGAUGUUA 19


RESULT 231
ADE27151
ID   ADE27151 standard; RNA; 19 BP.
XX
AC   ADE27151;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:95.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
```

```
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 95; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 4 C; 5 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1695 CTTTCCTTGAGCTGTTGTG 1713
              |:::||::||||:|::|:|
Db          1 CUUUCCUUGAGCUGUUGUG 19


RESULT 232
ADE27170
ID   ADE27170 standard; RNA; 19 BP.
XX
AC   ADE27170;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:114.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 114; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 5 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2037 ATTCAATGCCGCAACATAT 2055
              |::|||:|||||||||:|:
Db          1 AUUCAAUGCCGCAACAUAU 19


RESULT 233
ADE27181
ID   ADE27181 standard; RNA; 19 BP.
XX
AC   ADE27181;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:125.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

```
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 125; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2235 GAGTATTCCATGAGCTGCT 2253
              |||:|::|||:||||:||:
Db          1 GAGUAUUCCAUGAGCUGCU 19


RESULT 234
ADE27201
ID   ADE27201 standard; RNA; 19 BP.
XX
AC   ADE27201;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:145.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 145; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2595 GATCTGAGAACACGTTGCC 2613
              ||:|:|||||||||::|||
Db          1 GAUCUGAGAACACGUUGCC 19


RESULT 235
ADE27212
ID   ADE27212 standard; RNA; 19 BP.
XX
AC   ADE27212;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:156.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
```

```
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 156; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 4 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2793 AACATCTAGCCTAAAGTAT 2811
              ||||:|:||||:||||:|:
Db          1 AACAUCUAGCCUAAAGUAU 19


RESULT 236
ADE27256
ID   ADE27256 standard; RNA; 19 BP.
XX
AC   ADE27256;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:200.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 200; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3585 ACAATAGTATAGAAGTCTG 3603
              ||||:||:|:|||||:|:|
Db          1 ACAAUAGUAUAGAAGUCUG 19


RESULT 237
ADE27279
ID   ADE27279 standard; RNA; 19 BP.
XX
AC   ADE27279;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:223.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
```

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 223; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3999 TTGTAATCGTGTGCCATGG 4017
              ::|:||:||:|:||||:||
Db          1 UUGUAAUCGUGUGCCAUGG 19
```

RESULT 238
ADE27327
ID ADE27327 standard; RNA; 19 BP.
XX
AC ADE27327;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:271.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 271; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 0 C; 3 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4863 AGTATTTTTTATAATAGGA 4881
              ||:|::::::|:||:||||
Db          1 AGUAUUUUUUAUAAUAGGA 19
```

RESULT 239
ADE27329
ID ADE27329 standard; RNA; 19 BP.
XX
AC ADE27329;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:273.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

XX
PS Example 3; SEQ ID NO 273; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4899 GATACGTCCGTGTGTCCCA 4917
              ||:|||:|||:|:|:||||
Db          1 GAUACGUCCGUGUGUCCCA 19
```

RESULT 240
ADE27400/c
ID ADE27400 standard; RNA; 19 BP.
XX
AC ADE27400;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:344.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 344; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        957 CTTTTCAAAACAGTGTGTT 975
              |||||||||||||||||||
Db         19 CTTTTCAAAACAGTGTGTT 1
```

RESULT 241
ADE27411/c
ID ADE27411 standard; RNA; 19 BP.
XX
AC ADE27411;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:355.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 355; 139pp; English.

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1155 ACTACTCTGCCAGTGAGTA 1173
              |||||||||||||||||||
Db         19 ACTACTCTGCCAGTGAGTA 1


RESULT 242
ADE27428/c
ID   ADE27428 standard; RNA; 19 BP.
XX
AC   ADE27428;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:372.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 372; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 4 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1461 AGTATTGAAAGCCAACAAC 1479
              |||||||||||||||||||
Db         19 AGTATTGAAAGCCAACAAC 1


RESULT 243
ADE27433/c
ID   ADE27433 standard; RNA; 19 BP.
XX
AC   ADE27433;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:377.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 377; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
```

CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 11 A; 1 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1551 CTTTTCACTTTATTGCTAT 1569
||||||||||||||||||
Db 19 CTTTTCACTTTATTGCTAT 1

RESULT 244
ADE27443/c
ID ADE27443 standard; RNA; 19 BP.
XX
AC ADE27443;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:387.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 387; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 3 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1731 CTTGAGCTAGAGATAAAAC 1749
||||||||||||||||||
Db 19 CTTGAGCTAGAGATAAAAC 1

RESULT 245
ADE27464/c
ID ADE27464 standard; RNA; 19 BP.
XX
AC ADE27464;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:408.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 408; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD

CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 8 C; 2 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 TCTGCTGGGGAAGGGTTTT 2127
||||||||||||||||||||
Db 19 TCTGCTGGGGAAGGGTTTT 1

RESULT 246
ADE27470/c
ID ADE27470 standard; RNA; 19 BP.
XX
AC ADE27470;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:414.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 414; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2217 AGCAGCTCATGGAATTTTG 2235
||||||||||||||||||||
Db 19 AGCAGCTCATGGAATTTTG 1

RESULT 247
ADE27472/c
ID ADE27472 standard; RNA; 19 BP.
XX
AC ADE27472;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:416.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 416; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or

CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 1 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2253 TCATTACAGTTCTTTCCTC 2271
||||||||||||||||||||
Db 19 TCATTACAGTTCTTTCCTC 1

RESULT 248
ADE27490/c
ID ADE27490 standard; RNA; 19 BP.
XX
AC ADE27490;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:434.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 434; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2577 GAACTTCACATAGGAAGGG 2595
||||||||||||||||||||
Db 19 GAACTTCACATAGGAAGGG 1

RESULT 249
ADE27501/c
ID ADE27501 standard; RNA; 19 BP.
XX
AC ADE27501;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:445.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 445; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and

CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 8 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2775 GAGAAGGGGGTCTCTGTTA 2793
||||||||||||||||||||
Db 19 GAGAAGGGGGTCTCTGTTA 1

RESULT 250
ADE27523/c
ID ADE27523 standard; RNA; 19 BP.
XX
AC ADE27523;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:467.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 467; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 2 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3171 CCCAGAAAGCCTCTCTCTC 3189
||||||||||||||||||||
Db 19 CCCAGAAAGCCTCTCTCTC 1

RESULT 251
ADE27575/c
ID ADE27575 standard; RNA; 19 BP.
XX
AC ADE27575;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:519.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 519; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

```
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 8 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4107 GTGTGTCTGCTGAGTAAGG 4125
              |||||||||||||||||||
Db         19 GTGTGTCTGCTGAGTAAGG 1


RESULT 252
ADE27601/c
ID   ADE27601 standard; RNA; 19 BP.
XX
AC   ADE27601;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:545.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 545; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 5 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4575 CTTGGGTGTATTCTCTGTA 4593
              |||||||||||||||||||
Db         19 CTTGGGTGTATTCTCTGTA 1


RESULT 253
ADE27620/c
ID   ADE27620 standard; RNA; 19 BP.
XX
AC   ADE27620;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:564.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 564; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 4 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4917 AGATGCTGTCATTAGTCTA 4935
||||||||||||||||||
Db 19 AGATGCTGTCATTAGTCTA 1

RESULT 254
ADE27172
ID ADE27172 standard; RNA; 19 BP.
XX
AC ADE27172;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:116.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 116; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 1 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2073 AAGAAAAGACATTTTAAGT 2091
||||||||||:::::|||:
Db 1 AAGAAAAGACAUUUUAAGU 19

RESULT 255
ADE27175
ID ADE27175 standard; RNA; 19 BP.
XX
AC ADE27175;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:119.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 119; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

```
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 3 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   21.1%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTTTA 2145
              :|::::|:::::::|:::|
Db          1 UCUUUUCUUUUUUUCUUUA 19


RESULT 256
ADE27263
ID   ADE27263 standard; RNA; 19 BP.
XX
AC   ADE27263;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:207.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 207; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 8 C; 1 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3711 TACCAAACACTCAGTCCAC 3729
              :|||||||||:|||:||||
Db          1 UACCAAACACUCAGUCCAC 19


RESULT 257
ADE27271
ID   ADE27271 standard; RNA; 19 BP.
XX
AC   ADE27271;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:215.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 215; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
```

```
XX
SQ   Sequence 19 BP; 6 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3855 TCTAAGGGAAGATCACTGT 3873
              :|:||||||||||:|||:|:
Db          1 UCUAAGGGAAGAUCACUGU 19


RESULT 258
ADE27286
ID   ADE27286 standard; RNA; 19 BP.
XX
AC   ADE27286;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:230.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 230; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 3 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4125 GAACACGATTTTCAAGATT 4143
              ||||||||::::|||||::
Db          1 GAACACGAUUUUCAAGAUU 19


RESULT 259
ADE27289
ID   ADE27289 standard; RNA; 19 BP.
XX
AC   ADE27289;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:233.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 233; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
```

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4179 CTCAGATCTGATCAAGAGT 4197
              |:||||:|:||:||||||:
Db          1 CUCAGAUCUGAUCAAGAGU 19


RESULT 260
ADE27304
ID   ADE27304 standard; RNA; 19 BP.
XX
AC   ADE27304;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:248.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 248; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4449 TGCCCACATTTGATGGAGG 4467
              :|||||||:::||:|||||
Db          1 UGCCCACAUUUGAUGGAGG 19


RESULT 261
ADE27315
ID   ADE27315 standard; RNA; 19 BP.
XX
AC   ADE27315;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:259.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 259; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 7 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
```

```
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4647 TATGCTGGTGGTTAAGGCC 4665
              :|:||:||:||::||||||
Db          1 UAUGCUGGUGGUUAAGGCC 19


RESULT 262
ADE27334
ID   ADE27334 standard; RNA; 19 BP.
XX
AC   ADE27334;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:278.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 278; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4989 CCAGACAAAATTTGAGAAT 5007
              ||||||||||:::|||||:
Db          1 CCAGACAAAAUUUGAGAAU 19


RESULT 263
ADE27335
ID   ADE27335 standard; RNA; 19 BP.
XX
AC   ADE27335;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:279.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 279; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 5 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       5007 TACATAAACAACGCATTGC 5025
              :|||:||||||||||::||
Db          1 UACAUAAACAACGCAUUGC 19
```

RESULT 264
ADE27345
ID ADE27345 standard; RNA; 19 BP.
XX
AC ADE27345;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:289.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 289; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 1 C; 4 G; 0 T; 4 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAATC 5205
              ||:|||||:||||:|||:|
Db          1 AAUAAAAGUGAAGUGAAUC 19
```

RESULT 265
ADE27491/c
ID ADE27491 standard; RNA; 19 BP.
XX
AC ADE27491;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:435.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 435; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2595 GATCTGAGAACACGTTGCC 2613
```

```
                    ||||||||||||||||||||
Db          19 GATCTGAGAACACGTTGCC 1
```

RESULT 266
ADE27493/c
ID ADE27493 standard; RNA; 19 BP.
XX
AC ADE27493;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:437.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 437; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 7 C; 1 G; 0 T; 5 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2631 ACTGAGTGAGTTATTGGGA 2649
              |||||||||||||||||||
```

```
Db          19 ACTGAGTGAGTTATTGGGA 1
```

RESULT 267
ADE27516/c
ID ADE27516 standard; RNA; 19 BP.
XX
AC ADE27516;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:460.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 460; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3045 TTTGAAAGTAGAGCTAGCT 3063
              |||||||||||||||||||
Db          19 TTTGAAAGTAGAGCTAGCT 1
```

```
RESULT 268
ADE27527/c
ID   ADE27527 standard; RNA; 19 BP.
XX
AC   ADE27527;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:471.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 471; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 0 A; 5 C; 6 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3243 GCCAGCCACAGAGCAAAAG 3261
              ||||||||||||||||||||
Db         19 GCCAGCCACAGAGCAAAAG 1
```

```
RESULT 269
ADE27534/c
ID   ADE27534 standard; RNA; 19 BP.
XX
AC   ADE27534;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:478.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 478; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3369 CAGTGCAATGCTTGTAGAA 3387
              |||||||||||||||||||
Db         19 CAGTGCAATGCTTGTAGAA 1
```

RESULT 270
ADE27536/c
ID ADE27536 standard; RNA; 19 BP.
XX
AC ADE27536;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:480.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 480; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 7 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3405 TCACTGGGAAGAAGCAAGG 3423
||||||||||||||||||||
Db 19 TCACTGGGAAGAAGCAAGG 1

RESULT 271
ADE27541/c
ID ADE27541 standard; RNA; 19 BP.
XX
AC ADE27541;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:485.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 485; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3495 GCTGAGACCTGGGATTTGA 3513
||||||||||||||||||||
Db 19 GCTGAGACCTGGGATTTGA 1

RESULT 272
ADE27577/c

```
ID   ADE27577 standard; RNA; 19 BP.
XX
AC   ADE27577;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:521.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 521; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4143 TCTAAAGCTCAATTCAAGT 4161
             |||||||||||||||||||
Db         19 TCTAAAGCTCAATTCAAGT 1


RESULT 273
ADE27588/c
ID   ADE27588 standard; RNA; 19 BP.
XX
AC   ADE27588;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:532.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 532; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 9 C; 1 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4341 TGGCTGGTAGAAAAAGGGG 4359
             |||||||||||||||||||
Db         19 TGGCTGGTAGAAAAAGGGG 1


RESULT 274
ADE27589/c
ID   ADE27589 standard; RNA; 19 BP.
XX
```

AC ADE27589;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:533.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 533; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4359 GCCTGAGTGGAGGATTATC 4377
||||||||||||||||||||
Db 19 GCCTGAGTGGAGGATTATC 1

RESULT 275
ADE27602/c
ID ADE27602 standard; RNA; 19 BP.
XX
AC ADE27602;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:546.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 546; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4593 AAGTGTAGCTCAAATAGGT 4611
||||||||||||||||||||
Db 19 AAGTGTAGCTCAAATAGGT 1

RESULT 276
ADE27611/c
ID ADE27611 standard; RNA; 19 BP.
XX
AC ADE27611;
XX

DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:555.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 555; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 1 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4755 AAATGGGGATAATAATACT 4773
||||||||||||||||||
Db 19 AAATGGGGATAATAATACT 1

RESULT 277
ADE27628/c
ID ADE27628 standard; RNA; 19 BP.
XX
AC ADE27628;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:572.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 572; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 6 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5061 GGGTGGGATTTTTTCCCTT 5079
||||||||||||||||||
Db 19 GGGTGGGATTTTTTCCCTT 1

RESULT 278
ADE27118
ID ADE27118 standard; RNA; 19 BP.
XX
AC ADE27118;
XX
DT 29-JAN-2004 (first entry)
XX

```
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:62.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 62; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 8 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1101 CACTTGGAGCTGTGGGTGA 1119
              |||::|||||:|:|||:||
Db          1 CACUUGGAGCUGUGGGUGA 19


RESULT 279
ADE27134
ID   ADE27134 standard; RNA; 19 BP.
XX
AC   ADE27134;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:78.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 78; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1389 GAATAATGCTACCAGGATG 1407
              |||:||:||:|||||||:|
Db          1 GAAUAAUGCUACCAGGAUG 19


RESULT 280
ADE27140
ID   ADE27140 standard; RNA; 19 BP.
XX
AC   ADE27140;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:84.
XX
```

```
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 84; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 2 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 AAGCTGATATTATTTCTTC 1515
              ||||:||:|::|:::|::|
Db          1 AAGCUGAUAUUAUUUCUUC 19


RESULT 281
ADE27145
ID   ADE27145 standard; RNA; 19 BP.
XX
AC   ADE27145;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:89.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 89; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1587 TTGCCTCCCAGGCAAGCAG 1605
              ::|||:|||||||||||||
Db          1 UUGCCUCCCAGGCAAGCAG 19


RESULT 282
ADE27147
ID   ADE27147 standard; RNA; 19 BP.
XX
AC   ADE27147;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:91.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
```

KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 91; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1623 AGTGTCCAGCTTCCAAAGC 1641
              ||:|:|||||::|||||||
Db          1 AGUGUCCAGCUUCCAAAGC 19
```

RESULT 283
ADE27159
ID ADE27159 standard; RNA; 19 BP.
XX
AC ADE27159;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:103.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 103; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 2 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1839 TCTAAAGCAGGTAAATTGT 1857
              :|:|||||||:|||::|:
Db          1 UCUAAAGCAGGUAAAUUGU 19
```

RESULT 284
ADE27167
ID ADE27167 standard; RNA; 19 BP.
XX
AC ADE27167;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:111.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;

```
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 111; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 0 A; 8 C; 2 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1983 TTCCTTTCTCTCCTGGCTC 2001
              ::||:::|:|:||:|||:|
Db          1 UUCCUUUCUCUCCUGGCUC 19


RESULT 285
ADE27176
ID   ADE27176 standard; RNA; 19 BP.
XX
AC   ADE27176;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:120.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 120; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2145 AATAACAAGGAGATTTCTT 2163
              ||:||||||||||:::|::
Db          1 AAUAACAAGGAGAUUUCUU 19


RESULT 286
ADE27215
ID   ADE27215 standard; RNA; 19 BP.
XX
AC   ADE27215;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:159.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
```

OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 159; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 2 G; 0 T; 8 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2847 ACTACCCTGATTCTTGATT 2865
              ||:||||:||::|::||::
Db          1 ACUACCCUGAUUCUUGAUU 19
```

RESULT 287
ADE27276
ID ADE27276 standard; RNA; 19 BP.
XX
AC ADE27276;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:220.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 220; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3945 CAGATGCCTGCTTGATAAT 3963
              ||||:|||:||::||:||:
Db          1 CAGAUGCCUGCUUGAUAAU 19
```

RESULT 288
ADE27282
ID ADE27282 standard; RNA; 19 BP.
XX
AC ADE27282;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:226.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX

PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 226; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4053 TGGCACCTCAGGCTGAGGG 4071
              :|||||:|||||:|||||
Db          1 UGGCACCUCAGGCUGAGGG 19
```

RESULT 289
ADE27296
ID ADE27296 standard; RNA; 19 BP.
XX
AC ADE27296;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:240.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 240; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4305 CTGCAGAATCCCTTTGCAC 4323
              |:||||||:|||:::||||
Db          1 CUGCAGAAUCCCUUUGCAC 19
```

RESULT 290
ADE27308
ID ADE27308 standard; RNA; 19 BP.
XX
AC ADE27308;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:252.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX

```
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 252; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 1 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4521 AAAAGATGGTTGTAGCATT 4539
              ||||||:||::|:||||::
Db          1 AAAAGAUGGUUGUAGCAUU 19


RESULT 291
ADE27314
ID   ADE27314 standard; RNA; 19 BP.
XX
AC   ADE27314;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:258.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 258; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 7 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4629 AAAGCGAGGTGGCCATGTT 4647
              |||||||||:|||||:|::
Db          1 AAAGCGAGGUGGCCAUGUU 19


RESULT 292
ADE27322
ID   ADE27322 standard; RNA; 19 BP.
XX
AC   ADE27322;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:266.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
```

```
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 266; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4773 TGACCTACCTCAAAGGGCA 4791
              :||||:|||:|||||||||
Db          1 UGACCUACCUCAAAGGGCA 19


RESULT 293
ADE27343
ID   ADE27343 standard; RNA; 19 BP.
XX
AC   ADE27343;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:287.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 287; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5151 AGCTAATTGTACTAATCTG 5169
              |||:||::|:||:||:|:|
Db          1 AGCUAAUUGUACUAAUCUG 19


RESULT 294
ADE27412/c
ID   ADE27412 standard; RNA; 19 BP.
XX
AC   ADE27412;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:356.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 356; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 3 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1173 ACCGCTGGCACATCAACTT 1191
||||||||||||||||||||
Db 19 ACCGCTGGCACATCAACTT 1

RESULT 295
ADE27413/c
ID ADE27413 standard; RNA; 19 BP.
XX
AC ADE27413;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:357.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 357; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 1 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1191 TCACCACATTCTTCATTGA 1209
||||||||||||||||||||
Db 19 TCACCACATTCTTCATTGA 1

RESULT 296
ADE27453/c
ID ADE27453 standard; RNA; 19 BP.
XX
AC ADE27453;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:397.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 397; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1911 GGAACCTCTCGCCATGATC 1929
||||||||||||||||||
Db 19 GGAACCTCTCGCCATGATC 1

RESULT 297
ADE27505/c
ID ADE27505 standard; RNA; 19 BP.
XX
AC ADE27505;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:449.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 449; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 2 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2847 ACTACCCTGATTCTTGATT 2865
||||||||||||||||||
Db 19 ACTACCCTGATTCTTGATT 1

RESULT 298
ADE27507/c
ID ADE27507 standard; RNA; 19 BP.
XX
AC ADE27507;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:451.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 451; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2883 TGTCCCTTTTCTTTGACCA 2901
||||||||||||||||||||
Db 19 TGTCCCTTTTCTTTGACCA 1

RESULT 299
ADE27529/c
ID ADE27529 standard; RNA; 19 BP.
XX
AC ADE27529;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:473.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 473; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3279 CCCTCTCTCTGGGTCAGAA 3297
||||||||||||||||||||
Db 19 CCCTCTCTCTGGGTCAGAA 1

RESULT 300
ADE27550/c
ID ADE27550 standard; RNA; 19 BP.
XX
AC ADE27550;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:494.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 494; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 4 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3657 TCAGTCATCAAAGCAGAAG 3675
||||||||||||||||||||
Db 19 TCAGTCATCAAAGCAGAAG 1

RESULT 301
ADE27563/c
ID ADE27563 standard; RNA; 19 BP.
XX
AC ADE27563;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:507.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 507; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3891 CTGTGCACCTACCCCTTGG 3909
||||||||||||||||||||
Db 19 CTGTGCACCTACCCCTTGG 1

RESULT 302
ADE27622/c
ID ADE27622 standard; RNA; 19 BP.
XX
AC ADE27622;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:566.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 566; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4953 CTGAATGAATCCATTGGAG 4971
||||||||||||||||||
Db 19 CTGAATGAATCCATTGGAG 1

RESULT 303
ADE27625/c
ID ADE27625 standard; RNA; 19 BP.
XX
AC ADE27625;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:569.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 569; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 2 C; 5 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5007 TACATAAACAACGCATTGC 5025
||||||||||||||||||
Db 19 TACATAAACAACGCATTGC 1

RESULT 304
ADE27119
ID ADE27119 standard; RNA; 19 BP.
XX
AC ADE27119;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:63.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.

```
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 63; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 7 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1119 AGGGCTTCCACAACTACCA 1137
              |||||::|||||||:||||
Db          1 AGGGCUUCCACAACUACCA 19


RESULT 305
ADE27121
ID   ADE27121 standard; RNA; 19 BP.
XX
AC   ADE27121;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:65.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 65; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1155 ACTACTCTGCCAGTGAGTA 1173
              ||:||:|:|||||:|||:|
Db          1 ACUACUCUGCCAGUGAGUA 19


RESULT 306
ADE27125
ID   ADE27125 standard; RNA; 19 BP.
XX
AC   ADE27125;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:69.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 69; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1227 GTCTGGCCTATGACCGGAA 1245
              |:|:||||:|:||||||||
Db          1 GUCUGGCCUAUGACCGGAA 19
```

RESULT 307
ADE27133
ID ADE27133 standard; RNA; 19 BP.
XX
AC ADE27133;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:77.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 77; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 3 C; 3 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1371 GTCTGTTTATTAACTACTG 1389
              |:|:|:::|::|||:||:|
Db          1 GUCUGUUUAUUAACUACUG 19
```

RESULT 308
ADE27142
ID ADE27142 standard; RNA; 19 BP.
XX
AC ADE27142;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:86.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.

```
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 86; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 8 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1533 TCTAGGCCCATTGTCCTCC 1551
              :|:|||||||::|:||:||
Db          1 UCUAGGCCCAUUGUCCUCC 19


RESULT 309
ADE27205
ID   ADE27205 standard; RNA; 19 BP.
XX
AC   ADE27205;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:149.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 149; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2667 TAGATATTAGGTCCATTCA 2685
              :|||:|::|||:|||::||
Db          1 UAGAUAUUAGGUCCAUUCA 19


RESULT 310
ADE27225
ID   ADE27225 standard; RNA; 19 BP.
XX
AC   ADE27225;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:169.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
```

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 169; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 7 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3027 CTGAACCACTGCTTCTCTT 3045
              |:|||||||:||::|:|::
Db          1 CUGAACCACUGCUUCUCUU 19
```

RESULT 311
ADE27235
ID ADE27235 standard; RNA; 19 BP.
XX
AC ADE27235;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:179.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 179; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3207 GCACAGCCAAGCCAAGCGC 3225
              |||||||||||||||||||
Db          1 GCACAGCCAAGCCAAGCGC 19
```

RESULT 312
ADE27236
ID ADE27236 standard; RNA; 19 BP.
XX
AC ADE27236;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:180.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

```
XX
PS   Example 3; SEQ ID NO 180; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 4 C; 7 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3225 CTCATGTTGAGCCAGTGGG 3243
              |:||:|::|||||||:|||
Db          1 CUCAUGUUGAGCCAGUGGG 19


RESULT 313
ADE27251
ID   ADE27251 standard; RNA; 19 BP.
XX
AC   ADE27251;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:195.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 195; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 7 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3495 GCTGAGACCTGGGATTTGA 3513
              ||:|||||:||||:::||
Db          1 GCUGAGACCUGGGAUUUGA 19


RESULT 314
ADE27261
ID   ADE27261 standard; RNA; 19 BP.
XX
AC   ADE27261;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:205.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 205; 139pp; English.
```

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 4 C; 4 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3675 GTCTGGCTTTGCTCTATTA 3693
              |:|:|||:::||:|:|::|
Db          1 GUCUGGCUUUGCUCUAUUA 19


RESULT 315
ADE27280
ID   ADE27280 standard; RNA; 19 BP.
XX
AC   ADE27280;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:224.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 224; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4017 GATCTGATCTGTACCATGA 4035
              ||:|:||:|:|:||||:||
Db          1 GAUCUGAUCUGUACCAUGA 19


RESULT 316
ADE27300
ID   ADE27300 standard; RNA; 19 BP.
XX
AC   ADE27300;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:244.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 244; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
```

```
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4377 CAGTATCACGATTTGCAGG 4395
              |||:|:|||||:::|||||
Db          1 CAGUAUCACGAUUUGCAGG 19


RESULT 317
ADE27328
ID   ADE27328 standard; RNA; 19 BP.
XX
AC   ADE27328;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:272.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 272; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4881 AATGTCCACCATGAACTTG 4899
              ||:|:||||||:||||::|
Db          1 AAUGUCCACCAUGAACUUG 19


RESULT 318
ADE27401/c
ID   ADE27401 standard; RNA; 19 BP.
XX
AC   ADE27401;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:345.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 345; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
```

CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 4 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 975 TCGTTGCCACTTTCTTGCG 993
||||||||||||||||||||
Db 19 TCGTTGCCACTTTCTTGCG 1

RESULT 319
ADE27421/c
ID ADE27421 standard; RNA; 19 BP.
XX
AC ADE27421;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:365.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 365; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 1 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1335 TCCTTTTTCAAAAACCAGC 1353
||||||||||||||||||||
Db 19 TCCTTTTTCAAAAACCAGC 1

RESULT 320
ADE27423/c
ID ADE27423 standard; RNA; 19 BP.
XX
AC ADE27423;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:367.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 367; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or

```
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1371 GTCTGTTTATTAACTACTG 1389
              |||||||||||||||||||
Db         19 GTCTGTTTATTAACTACTG 1


RESULT 321
ADE27439/c
ID   ADE27439 standard; RNA; 19 BP.
XX
AC   ADE27439;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:383.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 383; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1659 AGCCTAAAACGAATGGTCT 1677
              |||||||||||||||||||
Db         19 AGCCTAAAACGAATGGTCT 1


RESULT 322
ADE27442/c
ID   ADE27442 standard; RNA; 19 BP.
XX
AC   ADE27442;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:386.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 386; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
```

CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 8 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1713 GAGCTTTGAAGTAGGTGGC 1731
||||||||||||||||||||
Db 19 GAGCTTTGAAGTAGGTGGC 1

RESULT 323
ADE27444/c
ID ADE27444 standard; RNA; 19 BP.
XX
AC ADE27444;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:388.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 388; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1749 CAGAATCTTCTGGGTAGTC 1767
||||||||||||||||||||
Db 19 CAGAATCTTCTGGGTAGTC 1

RESULT 324
ADE27465/c
ID ADE27465 standard; RNA; 19 BP.
XX
AC ADE27465;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:409.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 409; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

```
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 15 A; 0 C; 3 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2127 TCTTTTCTTTTTTTCTTTA 2145
              ||||||||||||||||||||
Db         19 TCTTTTCTTTTTTTCTTTA 1


RESULT 325
ADE27474/c
ID   ADE27474 standard; RNA; 19 BP.
XX
AC   ADE27474;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:418.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 418; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2289 TCAGGATATTGGTTCTTCC 2307
              ||||||||||||||||||||
Db         19 TCAGGATATTGGTTCTTCC 1


RESULT 326
ADE27478/c
ID   ADE27478 standard; RNA; 19 BP.
XX
AC   ADE27478;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:422.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 422; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 1 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2361 GATTTAAGGAGGTGAAGTC 2379
||||||||||||||||||||
Db 19 GATTTAAGGAGGTGAAGTC 1

RESULT 327
ADE27498/c
ID ADE27498 standard; RNA; 19 BP.
XX
AC ADE27498;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:442.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 442; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2721 AACTAGAAGGCTTCTCTCC 2739
||||||||||||||||||||
Db 19 AACTAGAAGGCTTCTCTCC 1

RESULT 328
ADE27500/c
ID ADE27500 standard; RNA; 19 BP.
XX
AC ADE27500;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:444.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 444; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

```
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 10 A; 3 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2757 CACTCATTTTTTTTGAGG 2775
              ||||||||||||||||||
Db         19 CACTCATTTTTTTTGAGG 1


RESULT 329
ADE27506/c
ID   ADE27506 standard; RNA; 19 BP.
XX
AC   ADE27506;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:450.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 450; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 3 C; 8 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2865 TCCTGGCTCTACCCTGTCT 2883
              ||||||||||||||||||
Db         19 TCCTGGCTCTACCCTGTCT 1


RESULT 330
ADE27552/c
ID   ADE27552 standard; RNA; 19 BP.
XX
AC   ADE27552;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:496.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 496; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
```

```
XX
SQ   Sequence 19 BP; 5 A; 4 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3693 AAGATTGGAAATGTACACT 3711
              |||||||||||||||||||
Db         19 AAGATTGGAAATGTACACT 1


RESULT 331
ADE27555/c
ID   ADE27555 standard; RNA; 19 BP.
XX
AC   ADE27555;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:499.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 499; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 9 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3747 GGAAGGGAGGAAGGCCTTT 3765
              |||||||||||||||||||
Db         19 GGAAGGGAGGAAGGCCTTT 1


RESULT 332
ADE27567/c
ID   ADE27567 standard; RNA; 19 BP.
XX
AC   ADE27567;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:511.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 511; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 0 C; 2 G; 0 T; 13 U; 0 Other;
```

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3963 TATATAAACAATAAAAACA 3981
              |||||||||||||||||||
Db         19 TATATAAACAATAAAAACA 1


RESULT 333
ADE27579/c
ID   ADE27579 standard; RNA; 19 BP.
XX
AC   ADE27579;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:523.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 523; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4179 CTCAGATCTGATCAAGAGT 4197
              |||||||||||||||||||
Db         19 CTCAGATCTGATCAAGAGT 1


RESULT 334
ADE27582/c
ID   ADE27582 standard; RNA; 19 BP.
XX
AC   ADE27582;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:526.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 526; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
```

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4233 CTGACAACTTAGCTCAGGT 4251
             |||||||||||||||||||
Db         19 CTGACAACTTAGCTCAGGT 1
```

RESULT 335
ADE27630/c
ID ADE27630 standard; RNA; 19 BP.
XX
AC ADE27630;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:574.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 574; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       5097 AGTTACTTGTGACAAAAAT 5115
             |||||||||||||||||||
Db         19 AGTTACTTGTGACAAAAAT 1
```

RESULT 336
ADE27633/c
ID ADE27633 standard; RNA; 19 BP.
XX
AC ADE27633;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:577.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 577; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 3 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       5151 AGCTAATTGTACTAATCTG 5169
             ||||||||||||||||||
Db         19 AGCTAATTGTACTAATCTG 1
```

RESULT 337
ADE27113
ID ADE27113 standard; RNA; 19 BP.
XX
AC ADE27113;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:57.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 57; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1011 ATGCCACCTGGCTGGTGAA 1029
             |:||||||:|||:||:|||
Db          1 AUGCCACCUGGCUGGUGAA 19
```

RESULT 338
ADE27123
ID ADE27123 standard; RNA; 19 BP.
XX
AC ADE27123;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:67.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 67; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 1 G; 0 T; 7 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1191 TCACCACATTCTTCATTGA 1209
```

```
              :|||||||::|::||::||
Db          1 UCACCACAUUCUUCAUUGA 19


RESULT 339
ADE27203
ID   ADE27203 standard; RNA; 19 BP.
XX
AC   ADE27203;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:147.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 147; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 1 C; 7 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2631 ACTGAGTGAGTTATTGGGA 2649
              ||:|||:|||::|::||||
Db          1 ACUGAGUGAGUUAUUGGGA 19


RESULT 340
ADE27211
ID   ADE27211 standard; RNA; 19 BP.
XX
AC   ADE27211;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:155.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 155; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 2 C; 8 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2775 GAGAAGGGGGTCTCTGTTA 2793
              ||||||||||:|:|:|::|
Db          1 GAGAAGGGGGUCUCUGUUA 19
```

```
RESULT 341
ADE27213
ID   ADE27213 standard; RNA; 19 BP.
XX
AC   ADE27213;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:157.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 157; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2811 TACAACTGCCTGGGGGGCA 2829
              :|||||:|||:||||||||
Db          1 UACAACUGCCUGGGGGGCA 19
```

```
RESULT 342
ADE27227
ID   ADE27227 standard; RNA; 19 BP.
XX
AC   ADE27227;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:171.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 171; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 7 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3063 TGCCACTTTCACGTGGCCT 3081
              :|||||:::||||:||||:
Db          1 UGCCACUUUCACGUGGCCU 19
```

RESULT 343
ADE27246
ID ADE27246 standard; RNA; 19 BP.
XX
AC ADE27246;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:190.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 190; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 3 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3405 TCACTGGGAAGAAGCAAGG 3423
:|||:|||||||||||||||
Db 1 UCACUGGGAAGAAGCAAGG 19

RESULT 344
ADE27259
ID ADE27259 standard; RNA; 19 BP.
XX
AC ADE27259;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:203.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 203; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 8 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 3639 CACTCCTGTCCCTGTAGCT 3657
|||:||:|:|||:|:|||:
Db 1 CACUCCUGUCCCUGUAGCU 19

RESULT 345
ADE27260

```
ID   ADE27260 standard; RNA; 19 BP.
XX
AC   ADE27260;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:204.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 204; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3657 TCAGTCATCAAAGCAGAAG 3675
              :|||:||:||||||||||||
Db          1 UCAGUCAUCAAAGCAGAAG 19


RESULT 346
ADE27264
ID   ADE27264 standard; RNA; 19 BP.
XX
AC   ADE27264;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:208.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 208; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 6 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3729 CTGTTGAGCCCCAGTGCTG 3747
              |:|::|||||||||:||:|
Db          1 CUGUUGAGCCCCAGUGCUG 19


RESULT 347
ADE27283
ID   ADE27283 standard; RNA; 19 BP.
XX
```

```
AC   ADE27283;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:227.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 227; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4071 GCCCCAATGTATGTGTGGC 4089
              |||||||:|:|:|:|:|||
Db          1 GCCCCAAUGUAUGUGUGGC 19


RESULT 348
ADE27301
ID   ADE27301 standard; RNA; 19 BP.
XX
AC   ADE27301;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:245.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 245; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 6 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4395 GATTCCCTTCTGGGCTTCA 4413
              ||::|||::|:||||::||
Db          1 GAUUCCCUUCUGGGCUUCA 19


RESULT 349
ADE27316
ID   ADE27316 standard; RNA; 19 BP.
XX
AC   ADE27316;
XX
```

```
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:260.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 260; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 9 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4665 CAGGGCCTCTCCAACCACT 4683
              |||||||:|:||||||||:
Db          1 CAGGGCCUCUCCAACCACU 19


RESULT 350
ADE27324
ID   ADE27324 standard; RNA; 19 BP.
XX
AC   ADE27324;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:268.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 268; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4809 ATGCTTTTTAGAAAGCATT 4827
              |:||:::::|||||||::
Db          1 AUGCUUUUUAGAAAGCAUU 19


RESULT 351
ADE27325
ID   ADE27325 standard; RNA; 19 BP.
XX
AC   ADE27325;
XX
DT   29-JAN-2004  (first entry)
XX
```

```
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:269.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 269; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4827 TTTGGGATCCTTCAGCACA 4845
              :::||||:||::|||||||
Db          1 UUUGGGAUCCUUCAGCACA 19


RESULT 352
ADE27396/c
ID   ADE27396 standard; RNA; 19 BP.
XX
AC   ADE27396;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:340.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 340; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        885 ACTACAAACCTGGCTTGCT 903
              |||||||||||||||||||
Db         19 ACTACAAACCTGGCTTGCT 1


RESULT 353
ADE27397/c
ID   ADE27397 standard; RNA; 19 BP.
XX
AC   ADE27397;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:341.
XX
```

KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 341; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 4 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 903 TGCTGATGTGCTTCATCCT 921
||||||||||||||||||||
Db 19 TGCTGATGTGCTTCATCCT 1

RESULT 354
ADE27426/c
ID ADE27426 standard; RNA; 19 BP.
XX
AC ADE27426;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:370.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 370; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 2 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1425 AACCCATTCCAGTACAGTA 1443
||||||||||||||||||||
Db 19 AACCCATTCCAGTACAGTA 1

RESULT 355
ADE27427/c
ID ADE27427 standard; RNA; 19 BP.
XX
AC ADE27427;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:371.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;

KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 371; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 0 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1443 ATTCTTTTAAAATTCAAAA 1461
||||||||||||||||||
Db 19 ATTCTTTTAAAATTCAAAA 1

RESULT 356
ADE27430/c
ID ADE27430 standard; RNA; 19 BP.
XX
AC ADE27430;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:374.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 374; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1497 AAGCTGATATTATTTCTTC 1515
||||||||||||||||||
Db 19 AAGCTGATATTATTTCTTC 1

RESULT 357
ADE27437/c
ID ADE27437 standard; RNA; 19 BP.
XX
AC ADE27437;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:381.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;

KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 381; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1623 AGTGTCCAGCTTCCAAAGC 1641
||||||||||||||||||
Db 19 AGTGTCCAGCTTCCAAAGC 1

RESULT 358
ADE27440/c
ID ADE27440 standard; RNA; 19 BP.
XX
AC ADE27440;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:384.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 384; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 2 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1677 TTTGCTCCAGATAACTCTC 1695
||||||||||||||||||
Db 19 TTTGCTCCAGATAACTCTC 1

RESULT 359
ADE27445/c
ID ADE27445 standard; RNA; 19 BP.
XX
AC ADE27445;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:389.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX

OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 389; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 2 C; 6 G; 0 T; 3 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 CCCCTGTTGATTATCTTCA 1785
              |||||||||||||||||||
Db         19 CCCCTGTTGATTATCTTCA 1
```

RESULT 360
ADE27457/c
ID ADE27457 standard; RNA; 19 BP.
XX
AC ADE27457;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:401.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 401; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 8 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1983 TTCCTTTCTCTCCTGGCTC 2001
              |||||||||||||||||||
Db         19 TTCCTTTCTCTCCTGGCTC 1
```

RESULT 361
ADE27568/c
ID ADE27568 standard; RNA; 19 BP.
XX
AC ADE27568;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:512.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX

PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 512; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 0 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3981 AACTTTCACTTCTTCCTAT 3999
||||||||||||||||||||
Db 19 AACTTTCACTTCTTCCTAT 1

RESULT 362
ADE27585/c
ID ADE27585 standard; RNA; 19 BP.
XX
AC ADE27585;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:529.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 529; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 2 C; 11 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4287 AGCCTGCCCTCACTCCCTC 4305
||||||||||||||||||||
Db 19 AGCCTGCCCTCACTCCCTC 1

RESULT 363
ADE27586/c
ID ADE27586 standard; RNA; 19 BP.
XX
AC ADE27586;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:530.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX

```
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 530; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 7 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4305 CTGCAGAATCCCTTTGCAC 4323
              ||||||||||||||||||
Db         19 CTGCAGAATCCCTTTGCAC 1


RESULT 364
ADE27120
ID   ADE27120 standard; RNA; 19 BP.
XX
AC   ADE27120;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:64.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 64; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 8 C; 1 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1137 ACCACTCCTTTCCCTATGA 1155
              |||||:||:::|||:|:||
Db          1 ACCACUCCUUUCCCUAUGA 19


RESULT 365
ADE27137
ID   ADE27137 standard; RNA; 19 BP.
XX
AC   ADE27137;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:81.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
```

```
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 81; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 2 C; 0 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1443 ATTCTTTTAAAATTCAAAA 1461
              |::|::::||||::|||||
Db          1 AUUCUUUUAAAAUUCAAAA 19


RESULT 366
ADE27141
ID   ADE27141 standard; RNA; 19 BP.
XX
AC   ADE27141;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:85.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 85; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 8 C; 0 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1515 CTCTTATCCTCTCTCTCTT 1533
              |:|::|:||:|:|:|:|::
Db          1 CUCUUAUCCUCUCUCUCUU 19


RESULT 367
ADE27146
ID   ADE27146 standard; RNA; 19 BP.
XX
AC   ADE27146;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:90.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
```

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 90; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1605 GCTGGTCAGTCTTTGCTCA 1623
              ||:||:|||:|:::||:||
Db          1 GCUGGUCAGUCUUUGCUCA 19
```

RESULT 368
ADE27174
ID ADE27174 standard; RNA; 19 BP.
XX
AC ADE27174;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:118.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 118; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 2 C; 8 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2109 TCTGCTGGGGAAGGGTTTT 2127
              :|:||:||||||||:::::
Db          1 UCUGCUGGGGAAGGGUUUU 19
```

RESULT 369
ADE27179
ID ADE27179 standard; RNA; 19 BP.
XX
AC ADE27179;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:123.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 123; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2199 TCCAGAATTGGTAAAAACA 2217
:|||||::||:|||||||
Db 1 UCCAGAAUUGGUAAAAACA 19

RESULT 370
ADE27194
ID ADE27194 standard; RNA; 19 BP.
XX
AC ADE27194;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:138.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 138; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2469 AAAACTCTGAAGGAGAGGA 2487
|||||:|:|||||||||||
Db 1 AAAACUCUGAAGGAGAGGA 19

RESULT 371
ADE27214
ID ADE27214 standard; RNA; 19 BP.
XX
AC ADE27214;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:158.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 158; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2829 AGGGTTAGGAATCTCTTCA 2847
              ||||::||||||:|:|::||
Db          1 AGGGUUAGGAAUCUCUUCA 19
```

RESULT 372
ADE27220
ID ADE27220 standard; RNA; 19 BP.
XX
AC ADE27220;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:164.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 164; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2937 TGGACAGGCAGCCTCCTTT 2955
              :|||||||||||||:||:::
Db          1 UGGACAGGCAGCCUCCUUU 19
```

RESULT 373
ADE27230
ID ADE27230 standard; RNA; 19 BP.
XX
AC ADE27230;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:174.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 174; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3117 GCCACACTGATGGCTCAAG 3135
||||||||:||:|||:||||
Db 1 GCCACACUGAUGGCUCAAG 19

RESULT 374
ADE27239
ID ADE27239 standard; RNA; 19 BP.
XX
AC ADE27239;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:183.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 183; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 7 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3279 CCCTCTCTCTGGGTCAGAA 3297
|||:|:|:|:|||:|||||
Db 1 CCCUCUCUCUGGGUCAGAA 19

RESULT 375
ADE27242
ID ADE27242 standard; RNA; 19 BP.
XX
AC ADE27242;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:186.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 186; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 6 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3333 TGAGGGTGCCCCGCCTGAG 3351
:|||||:|||||||||:|||
Db 1 UGAGGGUGCCCCGCCUGAG 19

RESULT 376
ADE27258
ID ADE27258 standard; RNA; 19 BP.
XX
AC ADE27258;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:202.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 202; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3621 AATTTGAGAACCTTGGACC 3639
||:::|||||||::|||||
Db 1 AAUUUGAGAACCUUGGACC 19

RESULT 377
ADE27292
ID ADE27292 standard; RNA; 19 BP.
XX
AC ADE27292;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:236.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.

```
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 236; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4233 CTGACAACTTAGCTCAGGT 4251
              |:||||||::|||:||||:
Db          1 CUGACAACUUAGCUCAGGU 19


RESULT 378
ADE27326
ID   ADE27326 standard; RNA; 19 BP.
XX
AC   ADE27326;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:270.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 270; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 4 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4845 AGGAATTCTCAAGACCTGA 4863
              |||||::|:|||||||:||
Db          1 AGGAAUUCUCAAGACCUGA 19


RESULT 379
ADE27330
ID   ADE27330 standard; RNA; 19 BP.
XX
AC   ADE27330;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:274.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

```
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 274; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4917 AGATGCTGTCATTAGTCTA 4935
              |||:||:|:||::||:|:|
Db          1 AGAUGCUGUCAUUAGUCUA 19


RESULT 380
ADE27338
ID   ADE27338 standard; RNA; 19 BP.
XX
AC   ADE27338;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:282.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 282; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 3 C; 6 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5061 GGGTGGGATTTTTTCCCTT 5079
              |||:||||::::::|||::
Db          1 GGGUGGGAUUUUUUCCCUU 19


RESULT 381
ADE27339
ID   ADE27339 standard; RNA; 19 BP.
XX
AC   ADE27339;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:283.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
```

```
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 283; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 0 C; 5 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5079 TTTTATGTGGGATATAGTA 5097
              ::::|:|:||||:|:||:|
Db          1 UUUUAUGUGGGAUAUAGUA 19


RESULT 382
ADE27341
ID   ADE27341 standard; RNA; 19 BP.
XX
AC   ADE27341;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:285.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 285; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 1 C; 2 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5115 TAATTTTGGAATAATTTCT 5133
              :||::::||||:||:::|:
Db          1 UAAUUUUGGAAUAAUUUCU 19


RESULT 383
ADE27434/c
ID   ADE27434 standard; RNA; 19 BP.
XX
AC   ADE27434;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:378.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
```

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 378; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 1 C; 9 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1569 TCGCCCTCCTTTCCCTTAT 1587
||||||||||||||||||||
Db 19 TCGCCCTCCTTTCCCTTAT 1

RESULT 384
ADE27447/c
ID ADE27447 standard; RNA; 19 BP.
XX
AC ADE27447;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:391.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 391; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1803 ATGGAATGGAAAAGCAACT 1821
||||||||||||||||||||
Db 19 ATGGAATGGAAAAGCAACT 1

RESULT 385
ADE27448/c
ID ADE27448 standard; RNA; 19 BP.
XX
AC ADE27448;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:392.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

XX
PS Example 3; SEQ ID NO 392; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 2 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1821 TTCATTTGACACAAAGCTT 1839
||||||||||||||||||||
Db 19 TTCATTTGACACAAAGCTT 1

RESULT 386
ADE27454/c
ID ADE27454 standard; RNA; 19 BP.
XX
AC ADE27454;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:398.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 398; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 3 C; 7 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1929 CAGACATACAGCTGCCTAC 1947
||||||||||||||||||||
Db 19 CAGACATACAGCTGCCTAC 1

RESULT 387
ADE27488/c
ID ADE27488 standard; RNA; 19 BP.
XX
AC ADE27488;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:432.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 432; 139pp; English.

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATCTAT 2559
              |||||||||||||||||||
Db         19 GCTGAGGGACAGGATCTAT 1


RESULT 388
ADE27522/c
ID   ADE27522 standard; RNA; 19 BP.
XX
AC   ADE27522;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:466.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 466; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 7 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3153 TCCCAGAAACATCTCTGGC 3171
              |||||||||||||||||||
Db         19 TCCCAGAAACATCTCTGGC 1


RESULT 389
ADE27545/c
ID   ADE27545 standard; RNA; 19 BP.
XX
AC   ADE27545;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:489.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 489; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
```

CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 5 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3567 CCCTACAGCCTAGGGCAGA 3585
||||||||||||||||||||
Db 19 CCCTACAGCCTAGGGCAGA 1

RESULT 390
ADE27593/c
ID ADE27593 standard; RNA; 19 BP.
XX
AC ADE27593;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:537.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 537; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4431 AGGGCTGCTTTTCTTAAGT 4449
||||||||||||||||||||
Db 19 AGGGCTGCTTTTCTTAAGT 1

RESULT 391
ADE27617/c
ID ADE27617 standard; RNA; 19 BP.
XX
AC ADE27617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:561.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 561; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD

CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 3 C; 0 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4863 AGTATTTTTTATAATAGGA 4881
||||||||||||||||||||
Db 19 AGTATTTTTTATAATAGGA 1

RESULT 392
ADE27116
ID ADE27116 standard; RNA; 19 BP.
XX
AC ADE27116;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:60.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 60; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 7 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1065 ACAAGAACATTAGCCCCCG 1083
|||||||||::|||||||||
Db 1 ACAAGAACAUUAGCCCCCG 19

RESULT 393
ADE27132
ID ADE27132 standard; RNA; 19 BP.
XX
AC ADE27132;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:76.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 76; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or

```
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1353 CCAGGCAGAGGTTTTAATG 1371
              ||||||||||:::::|:|
Db          1 CCAGGCAGAGGUUUUAAUG 19


RESULT 394
ADE27153
ID   ADE27153 standard; RNA; 19 BP.
XX
AC   ADE27153;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:97.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 97; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 3 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1731 CTTGAGCTAGAGATAAAAC 1749
              |::||||:|||||:|||||
Db          1 CUUGAGCUAGAGAUAAAAC 19


RESULT 395
ADE27155
ID   ADE27155 standard; RNA; 19 BP.
XX
AC   ADE27155;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:99.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 99; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
```

```
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 6 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 CCCCTGTTGATTATCTTCA 1785
              ||||:|::||::|:|::||
Db          1 CCCCUGUUGAUUAUCUUCA 19


RESULT 396
ADE27163
ID   ADE27163 standard; RNA; 19 BP.
XX
AC   ADE27163;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:107.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 107; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1911 GGAACCTCTCGCCATGATC 1929
              ||||||:|:|||||:||:|
Db          1 GGAACCUCUCGCCAUGAUC 19


RESULT 397
ADE27180
ID   ADE27180 standard; RNA; 19 BP.
XX
AC   ADE27180;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:124.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 124; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
```

```
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2217 AGCAGCTCATGGAATTTTG 2235
              |||||:||:||||::::|
Db          1 AGCAGCUCAUGGAAUUUUG 19


RESULT 398
ADE27217
ID   ADE27217 standard; RNA; 19 BP.
XX
AC   ADE27217;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:161.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 161; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 6 C; 2 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2883 TGTCCCTTTTCTTTGACCA 2901
              :|:|||::::|:::|||||
Db          1 UGUCCCUUUUCUUUGACCA 19


RESULT 399
ADE27223
ID   ADE27223 standard; RNA; 19 BP.
XX
AC   ADE27223;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:167.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 167; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

```
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 9 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2991 GGCAGCTCCCTCCTGCACA 3009
              ||||||:|||:||:|||||
Db          1 GGCAGCUCCCUCCUGCACA 19


RESULT 400
ADE27250
ID   ADE27250 standard; RNA; 19 BP.
XX
AC   ADE27250;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:194.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 194; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3477 GTGAACTGCAAAGCTTTGG 3495
              |:||||:|||||||:::||
Db          1 GUGAACUGCAAAGCUUUGG 19


RESULT 401
ADE27278
ID   ADE27278 standard; RNA; 19 BP.
XX
AC   ADE27278;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:222.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 222; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
```

```
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 0 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3981 AACTTTCACTTCTTCCTAT 3999
              |||:::|||::|::||:|:
Db          1 AACUUUCACUUCUUCCUAU 19


RESULT 402
ADE27302
ID   ADE27302 standard; RNA; 19 BP.
XX
AC   ADE27302;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:246.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 246; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 2 C; 3 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4413 ATTCTGGAAACTTTTGTTA 4431
              |::|:||||||::::|::|
Db          1 AUUCUGGAAACUUUUGUUA 19


RESULT 403
ADE27344
ID   ADE27344 standard; RNA; 19 BP.
XX
AC   ADE27344;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:288.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 288; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
```

```
XX
SQ   Sequence 19 BP; 4 A; 1 C; 5 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5169 GAGATTGTGTTTGTTCATA 5187
              ||||::|:|:::|::||:|
Db          1 GAGAUUGUGUUUGUUCAUA 19


RESULT 404
ADE27410/c
ID   ADE27410 standard; RNA; 19 BP.
XX
AC   ADE27410;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:354.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 354; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 1 C; 8 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1137 ACCACTCCTTTCCCTATGA 1155
              |||||||||||||||||||
Db         19 ACCACTCCTTTCCCTATGA 1


RESULT 405
ADE27446/c
ID   ADE27446 standard; RNA; 19 BP.
XX
AC   ADE27446;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:390.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 390; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 5 G; 0 T; 4 U; 0 Other;
```

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1785 AGCCCAGGCTTTTGCTAGA 1803
              ||||||||||||||||||||
Db         19 AGCCCAGGCTTTTGCTAGA 1

RESULT 406
ADE27468/c
ID   ADE27468 standard; RNA; 19 BP.
XX
AC   ADE27468;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:412.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 412; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 7 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2181 GTCTTGAAGTTGGGTGTTT 2199
              ||||||||||||||||||||
Db         19 GTCTTGAAGTTGGGTGTTT 1

RESULT 407
ADE27483/c
ID   ADE27483 standard; RNA; 19 BP.
XX
AC   ADE27483;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:427.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 427; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 0 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2451 AAAGAGGGATGTTTGGAAA 2469
              |||||||||||||||||||
Db         19 AAAGAGGGATGTTTGGAAA 1
```

RESULT 408
ADE27487/c
ID ADE27487 standard; RNA; 19 BP.
XX
AC ADE27487;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:431.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 431; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 9 C; 1 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2523 TGGACATGAGATGGAGAGG 2541
              |||||||||||||||||||
Db         19 TGGACATGAGATGGAGAGG 1
```

RESULT 409
ADE27499/c
ID ADE27499 standard; RNA; 19 BP.
XX
AC ADE27499;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:443.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 443; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2739 CACAGTGTTGTGCCCCTTC 2757
              |||||||||||||||||||
Db         19 CACAGTGTTGTGCCCCTTC 1
```

RESULT 410
ADE27530/c
ID ADE27530 standard; RNA; 19 BP.
XX
AC ADE27530;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:474.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 474; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3297 ACCAGAGGGCATGCTGAAT 3315
              |||||||||||||||||||
Db         19 ACCAGAGGGCATGCTGAAT 1
```

RESULT 411
ADE27531/c
ID ADE27531 standard; RNA; 19 BP.
XX
AC ADE27531;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:475.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 475; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 4 C; 7 G; 0 T; 1 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 TGCCCCCTGCTTACTTGGT 3333
```

```
                    ||||||||||||||||||||
Db         19 TGCCCCCTGCTTACTTGGT 1


RESULT 412
ADE27535/c
ID   ADE27535 standard; RNA; 19 BP.
XX
AC   ADE27535;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:479.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 479; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3387 AGTAGGAGGAAACAGTTCT 3405
              |||||||||||||||||||
Db         19 AGTAGGAGGAAACAGTTCT 1


RESULT 413
ADE27546/c
ID   ADE27546 standard; RNA; 19 BP.
XX
AC   ADE27546;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:490.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 490; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3585 ACAATAGTATAGAAGTCTG 3603
              |||||||||||||||||||
Db         19 ACAATAGTATAGAAGTCTG 1
```

```
RESULT 414
ADE27548/c
ID   ADE27548 standard; RNA; 19 BP.
XX
AC   ADE27548;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:492.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 492; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3621 AATTTGAGAACCTTGGACC 3639
              |||||||||||||||||||
Db         19 AATTTGAGAACCTTGGACC 1
```

```
RESULT 415
ADE27549/c
ID   ADE27549 standard; RNA; 19 BP.
XX
AC   ADE27549;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:493.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 493; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 8 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3639 CACTCCTGTCCCTGTAGCT 3657
              |||||||||||||||||||
Db         19 CACTCCTGTCCCTGTAGCT 1
```

RESULT 416
ADE27551/c
ID ADE27551 standard; RNA; 19 BP.
XX
AC ADE27551;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:495.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 495; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 4 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3675 GTCTGGCTTTGCTCTATTA 3693
||||||||||||||||||||
Db 19 GTCTGGCTTTGCTCTATTA 1

RESULT 417
ADE27578/c
ID ADE27578 standard; RNA; 19 BP.
XX
AC ADE27578;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:522.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 522; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 2 C; 3 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4161 TGACACATTAATGATAAAC 4179
||||||||||||||||||||
Db 19 TGACACATTAATGATAAAC 1

RESULT 418
ADE27583/c

```
ID   ADE27583 standard; RNA; 19 BP.
XX
AC   ADE27583;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:527.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 527; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 1 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4251 TGCCTTACATCTTTTCTAA 4269
             ||||||||||||||||||
Db         19 TGCCTTACATCTTTTCTAA 1


RESULT 419
ADE27590/c
ID   ADE27590 standard; RNA; 19 BP.
XX
AC   ADE27590;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:534.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 534; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4377 CAGTATCACGATTTGCAGG 4395
             ||||||||||||||||||||
Db         19 CAGTATCACGATTTGCAGG 1


RESULT 420
ADE27606/c
ID   ADE27606 standard; RNA; 19 BP.
XX
```

```
AC   ADE27606;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:550.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 550; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 9 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4665 CAGGGCCTCTCCAACCACT 4683
              |||||||||||||||||||
Db         19 CAGGGCCTCTCCAACCACT 1


RESULT 421
ADE27627/c
ID   ADE27627 standard; RNA; 19 BP.
XX
AC   ADE27627;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:571.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 571; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 5 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5043 GATGCCTTTTCTGTGATTG 5061
              |||||||||||||||||||
Db         19 GATGCCTTTTCTGTGATTG 1


RESULT 422
ADE27108
ID   ADE27108 standard; RNA; 19 BP.
XX
AC   ADE27108;
XX
```

```
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:52.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 52; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 8 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        921 TGCCCACGCTTGTGCCCTG 939
              :||||||||::|:||||:|
Db          1 UGCCCACGCUUGUGCCCUG 19


RESULT 423
ADE27150
ID   ADE27150 standard; RNA; 19 BP.
XX
AC   ADE27150;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:94.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 94; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1677 TTTGCTCCAGATAACTCTC 1695
              :::||:|||||:|||:|:|
Db          1 UUUGCUCCAGAUAACUCUC 19


RESULT 424
ADE27169
ID   ADE27169 standard; RNA; 19 BP.
XX
AC   ADE27169;
XX
DT   29-JAN-2004  (first entry)
XX
```

```
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:113.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 113; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 6 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2019 CGGTGTTTGGCAATGCTAA 2037
              |||:|:::|||||:||:||
Db          1 CGGUGUUUGGCAAUGCUAA 19


RESULT 425
ADE27197
ID   ADE27197 standard; RNA; 19 BP.
XX
AC   ADE27197;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:141.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 141; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 1 C; 9 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2523 TGGACATGAGATGGAGAGG 2541
              :|||||:||||:|||||||
Db          1 UGGACAUGAGAUGGAGAGG 19


RESULT 426
ADE27198
ID   ADE27198 standard; RNA; 19 BP.
XX
AC   ADE27198;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:142.
XX
```

```
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 142; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 7 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2541 GCTGAGGGACAGGATCTAT 2559
              ||:|||||||||||:|:|:
Db          1 GCUGAGGGACAGGAUCUAU 19


RESULT 427
ADE27210
ID   ADE27210 standard; RNA; 19 BP.
XX
AC   ADE27210;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:154.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 154; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 3 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2757 CACTCATTTTTTTTGAGG 2775
              |||:||:::::::::||||
Db          1 CACUCAUUUUUUUUUGAGG 19


RESULT 428
ADE27218
ID   ADE27218 standard; RNA; 19 BP.
XX
AC   ADE27218;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:162.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
```

KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 162; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2901 AGATCTTTCTCTTCCCTGA 2919
||||:|:::|:|::|||:||
Db 1 AGAUCUUUCUCUUCCCUGA 19

RESULT 429
ADE27222
ID ADE27222 standard; RNA; 19 BP.
XX
AC ADE27222;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:166.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 166; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2973 GTGATGACTTGCTGTCCAG 2991
|:|||:|||::||:|:||||
Db 1 GUGAUGACUUGCUGUCCAG 19

RESULT 430
ADE27238
ID ADE27238 standard; RNA; 19 BP.
XX
AC ADE27238;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:182.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;

```
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 182; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 5 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3261 GAGGGTTTATTTTCAGTCC 3279
              |||||:::|::::|||:||
Db          1 GAGGGUUUAUUUUCAGUCC 19


RESULT 431
ADE27247
ID   ADE27247 standard; RNA; 19 BP.
XX
AC   ADE27247;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:191.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 191; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3423 GGCAAGAACCCAAGTGCCT 3441
              |||||||||||||||:|||:
Db          1 GGCAAGAACCCAAGUGCCU 19


RESULT 432
ADE27291
ID   ADE27291 standard; RNA; 19 BP.
XX
AC   ADE27291;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:235.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
```

OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 235; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 0 A; 4 C; 9 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4215 CCTGCTTTGGGGGGTGTGC 4233
              ||:||:::||||||:|:||
Db          1 CCUGCUUUGGGGGGUGUGC 19
```

RESULT 433
ADE27306
ID ADE27306 standard; RNA; 19 BP.
XX
AC ADE27306;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:250.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 250; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 0 C; 3 G; 0 T; 11 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.1e+02;
Matches 8; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4485 GTATTTGATTTATAAGTTT 4503
              |:|:::||:::|:|||:::
Db          1 GUAUUUGAUUUAUAAGUUU 19
```

RESULT 434
ADE27318
ID ADE27318 standard; RNA; 19 BP.
XX
AC ADE27318;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:262.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX

PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 262; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4701 TGTGACCCTGGGCAAGTCA 4719
              :|:||||||:|||||||:||
Db          1 UGUGACCCUGGGCAAGUCA 19
```

RESULT 435
ADE27321
ID ADE27321 standard; RNA; 19 BP.
XX
AC ADE27321;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:265.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 265; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 1 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4755 AAATGGGGATAATAATACT 4773
              |||:|||||:||:||:||:
Db          1 AAAUGGGGAUAAUAAUACU 19
```

RESULT 436
ADE27416/c
ID ADE27416 standard; RNA; 19 BP.
XX
AC ADE27416;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:360.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX

PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 360; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 5 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1245 AGAAAGTCTCCAAGGCCGC 1263
||||||||||||||||||||
Db 19 AGAAAGTCTCCAAGGCCGC 1

RESULT 437
ADE27419/c
ID ADE27419 standard; RNA; 19 BP.
XX
AC ADE27419;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:363.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 363; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1299 ACTACAAGAGTGGCTGAGT 1317
||||||||||||||||||||
Db 19 ACTACAAGAGTGGCTGAGT 1

RESULT 438
ADE27429/c
ID ADE27429 standard; RNA; 19 BP.
XX
AC ADE27429;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:373.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX

PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 373; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 3 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTCTGCCTTTATGATGCTA 1497
||||||||||||||||||||
Db 19 CTCTGCCTTTATGATGCTA 1

RESULT 439
ADE27460/c
ID ADE27460 standard; RNA; 19 BP.
XX
AC ADE27460;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:404.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 404; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 2 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2037 ATTCAATGCCGCAACATAT 2055
||||||||||||||||||||
Db 19 ATTCAATGCCGCAACATAT 1

RESULT 440
ADE27462/c
ID ADE27462 standard; RNA; 19 BP.
XX
AC ADE27462;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:406.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 406; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 1 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2073 AAGAAAAGACATTTTAAGT 2091
||||||||||||||||||
Db 19 AAGAAAAGACATTTTAAGT 1

RESULT 441
ADE27463/c
ID ADE27463 standard; RNA; 19 BP.
XX
AC ADE27463;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:407.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 407; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 5 C; 1 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2091 TTTGTAGTAAAAGTGGTCT 2109
||||||||||||||||||
Db 19 TTTGTAGTAAAAGTGGTCT 1

RESULT 442
ADE27469/c
ID ADE27469 standard; RNA; 19 BP.
XX
AC ADE27469;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:413.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 413; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 3 C; 3 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2199 TCCAGAATTGGTAAAAACA 2217
||||||||||||||||||
Db 19 TCCAGAATTGGTAAAAACA 1

RESULT 443
ADE27473/c
ID ADE27473 standard; RNA; 19 BP.
XX
AC ADE27473;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:417.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 417; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 7 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2271 CTTTCTGCTCTGCCATCTT 2289
||||||||||||||||||
Db 19 CTTTCTGCTCTGCCATCTT 1

RESULT 444
ADE27475/c
ID ADE27475 standard; RNA; 19 BP.
XX
AC ADE27475;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:419.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 419; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2307 CCCTCATAGTAATAAGATG 2325
||||||||||||||||||
Db 19 CCCTCATAGTAATAAGATG 1

RESULT 445
ADE27513/c
ID ADE27513 standard; RNA; 19 BP.
XX
AC ADE27513;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:457.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 457; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 9 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2991 GGCAGCTCCCTCCTGCACA 3009
||||||||||||||||||
Db 19 GGCAGCTCCCTCCTGCACA 1

RESULT 446
ADE27533/c
ID ADE27533 standard; RNA; 19 BP.
XX
AC ADE27533;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:477.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 477; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3351 GTCAGTGCTCTCAGCTGGC 3369
||||||||||||||||||||
Db 19 GTCAGTGCTCTCAGCTGGC 1

RESULT 447
ADE27560/c
ID ADE27560 standard; RNA; 19 BP.
XX
AC ADE27560;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:504.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 504; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 4 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3837 CACCTCAGTAGAAAAGGAT 3855
||||||||||||||||||||
Db 19 CACCTCAGTAGAAAAGGAT 1

RESULT 448
ADE27561/c
ID ADE27561 standard; RNA; 19 BP.
XX
AC ADE27561;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:505.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 505; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3855 TCTAAGGGAAGATCACTGT 3873
||||||||||||||||||||
Db 19 TCTAAGGGAAGATCACTGT 1

RESULT 449
ADE27584/c
ID ADE27584 standard; RNA; 19 BP.
XX
AC ADE27584;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:528.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 528; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4269 ATCACAGTGTTGCATATGA 4287
||||||||||||||||||||
Db 19 ATCACAGTGTTGCATATGA 1

RESULT 450
ADE27591/c
ID ADE27591 standard; RNA; 19 BP.
XX
AC ADE27591;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:535.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.

```
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 535; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 4 C; 6 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4395 GATTCCCTTCTGGGCTTCA 4413
              ||||||||||||||||||
Db         19 GATTCCCTTCTGGGCTTCA 1


RESULT 451
ADE27600/c
ID   ADE27600 standard; RNA; 19 BP.
XX
AC   ADE27600;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:544.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 544; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 4 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4557 TCCTTGGTTTGCTAGTATC 4575
              |||||||||||||||||||
Db         19 TCCTTGGTTTGCTAGTATC 1


RESULT 452
ADE27608/c
ID   ADE27608 standard; RNA; 19 BP.
XX
AC   ADE27608;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:552.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

```
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 552; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4701 TGTGACCCTGGGCAAGTCA 4719
              |||||||||||||||||||
Db         19 TGTGACCCTGGGCAAGTCA 1


RESULT 453
ADE27610/c
ID   ADE27610 standard; RNA; 19 BP.
XX
AC   ADE27610;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:554.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 554; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 10 A; 2 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4737 TCAGTTTTCCTTCTGTTAA 4755
              |||||||||||||||||||
Db         19 TCAGTTTTCCTTCTGTTAA 1


RESULT 454
ADE27618/c
ID   ADE27618 standard; RNA; 19 BP.
XX
AC   ADE27618;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:562.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
```

```
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 562; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4881 AATGTCCACCATGAACTTG 4899
              |||||||||||||||||||
Db         19 AATGTCCACCATGAACTTG 1


RESULT 455
ADE27631/c
ID   ADE27631 standard; RNA; 19 BP.
XX
AC   ADE27631;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:575.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 575; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 10 A; 2 C; 1 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5115 TAATTTTGGAATAATTTCT 5133
              |||||||||||||||||||
Db         19 TAATTTTGGAATAATTTCT 1


RESULT 456
ADE27111
ID   ADE27111 standard; RNA; 19 BP.
XX
AC   ADE27111;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:55.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
```

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 55; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 6 C; 4 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 975 TCGTTGCCACTTTCTTGCG 993
:||::|||||:::|::|||
Db 1 UCGUUGCCACUUUCUUGCG 19

RESULT 457
ADE27122
ID ADE27122 standard; RNA; 19 BP.
XX
AC ADE27122;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:66.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 66; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1173 ACCGCTGGCACATCAACTT 1191
|||||:||||||:||||::
Db 1 ACCGCUGGCACAUCAACUU 19

RESULT 458
ADE27162
ID ADE27162 standard; RNA; 19 BP.
XX
AC ADE27162;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:106.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

```
XX
PS   Example 3; SEQ ID NO 106; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 9 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1893 GAGGGAAGCGAAGCAAGAG 1911
              |||||||||||||||||||
Db          1 GAGGGAAGCGAAGCAAGAG 19


RESULT 459
ADE27185
ID   ADE27185 standard; RNA; 19 BP.
XX
AC   ADE27185;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:129.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 129; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 4 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2307 CCCTCATAGTAATAAGATG 2325
              |||:||:||:||:||||:|
Db          1 CCCUCAUAGUAAUAAGAUG 19


RESULT 460
ADE27191
ID   ADE27191 standard; RNA; 19 BP.
XX
AC   ADE27191;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:135.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 135; 139pp; English.
```

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 3 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2415 GCTTAGAACGTTAAACTAT 2433
              ||::||||||::||||:|:
Db          1 GCUUAGAACGUUAAACUAU 19


RESULT 461
ADE27192
ID   ADE27192 standard; RNA; 19 BP.
XX
AC   ADE27192;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:136.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 136; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2433 TTAGAGTATTTCCCTTCCA 2451
              ::||||:|:::|||::|||
Db          1 UUAGAGUAUUUCCCUUCCA 19


RESULT 462
ADE27199
ID   ADE27199 standard; RNA; 19 BP.
XX
AC   ADE27199;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:143.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 143; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
```

```
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2559 TAGGCAGCTTCTAAGAGCG 2577
              :|||||||::|:|||||||
Db          1 UAGGCAGCUUCUAAGAGCG 19


RESULT 463
ADE27206
ID   ADE27206 standard; RNA; 19 BP.
XX
AC   ADE27206;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:150.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 150; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 2 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2685 ATTAATTAGTTCCAGTTTC 2703
              |::||::||::||||:::|
Db          1 AUUAAUUAGUUCCAGUUUC 19


RESULT 464
ADE27226
ID   ADE27226 standard; RNA; 19 BP.
XX
AC   ADE27226;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:170.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 170; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
```

```
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3045 TTTGAAAGTAGAGCTAGCT 3063
              :::||||||:|||||:|||:
Db          1 UUUGAAAGUAGAGCUAGCU 19


RESULT 465
ADE27229
ID   ADE27229 standard; RNA; 19 BP.
XX
AC   ADE27229;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:173.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 173; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 10 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3099 ACACCCCTGTGCTCCCCTG 3117
              |||||||:|:||:||||:|
Db          1 ACACCCCUGUGCUCCCCUG 19


RESULT 466
ADE27233
ID   ADE27233 standard; RNA; 19 BP.
XX
AC   ADE27233;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:177.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 177; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
```

```
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 9 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3171 CCCAGAAAGCCTCTCTCTC 3189
              ||||||||||:|:|:|:|
Db          1 CCCAGAAAGCCUCUCUCUC 19


RESULT 467
ADE27253
ID   ADE27253 standard; RNA; 19 BP.
XX
AC   ADE27253;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:197.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 197; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes; in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3531 TGAACACAGTGTCTGTTCA 3549
              :|||||||:|:|:|::||
Db          1 UGAACACAGUGUCUGUUCA 19


RESULT 468
ADE27270
ID   ADE27270 standard; RNA; 19 BP.
XX
AC   ADE27270;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:214.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 214; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
```

```
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3837 CACCTCAGTAGAAAAGGAT 3855
              ||||:|||:|||||||||:
Db          1 CACCUCAGUAGAAAAGGAU 19


RESULT 469
ADE27272
ID   ADE27272 standard; RNA; 19 BP.
XX
AC   ADE27272;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:216.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 216; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 3 C; 4 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3873 TAGTTTAGTTCTGTTGACC 3891
              :||:::||::|:|::||||
Db          1 UAGUUUAGUUCUGUUGACC 19


RESULT 470
ADE27295
ID   ADE27295 standard; RNA; 19 BP.
XX
AC   ADE27295;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:239.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 239; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
```

```
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 11 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4287 AGCCTGCCCTCACTCCCTC 4305
              ||||:||||:|||:|||:|
Db          1 AGCCUGCCCUCACUCCCUC 19


RESULT 471
ADE27310
ID   ADE27310 standard; RNA; 19 BP.
XX
AC   ADE27310;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:254.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 254; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 4 C; 4 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4557 TCCTTGGTTTGCTAGTATC 4575
              :||::||:::||:||:|:|
Db          1 UCCUUGGUUUGCUAGUAUC 19


RESULT 472
ADE27336
ID   ADE27336 standard; RNA; 19 BP.
XX
AC   ADE27336;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:280.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 280; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 5 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5025 CCACGGAAACATACAGAGG 5043
||||||||||:|||||||
Db 1 CCACGGAAACAUACAGAGG 19

RESULT 473
ADE27403/c
ID ADE27403 standard; RNA; 19 BP.
XX
AC ADE27403;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:347.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 347; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 ATGCCACCTGGCTGGTGAA 1029
||||||||||||||||||||
Db 19 ATGCCACCTGGCTGGTGAA 1

RESULT 474
ADE27407/c
ID ADE27407 standard; RNA; 19 BP.
XX
AC ADE27407;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:351.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 351; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 GGGAGAATATCCTGGTTTC 1101
||||||||||||||||||||
Db 19 GGGAGAATATCCTGGTTTC 1

RESULT 475
ADE27420/c
ID ADE27420 standard; RNA; 19 BP.
XX
AC ADE27420;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:364.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 364; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 6 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1317 TTTGGGGTCCCTCAGGTTT 1335
||||||||||||||||||||
Db 19 TTTGGGGTCCCTCAGGTTT 1

RESULT 476
ADE27441/c
ID ADE27441 standard; RNA; 19 BP.
XX
AC ADE27441;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:385.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 385; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.

```
XX
SQ   Sequence 19 BP; 9 A; 5 C; 4 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1695 CTTTCCTTGAGCTGTTGTG 1713
             |||||||||||||||||||
Db         19 CTTTCCTTGAGCTGTTGTG 1

RESULT 477
ADE27458/c
ID   ADE27458 standard; RNA; 19 BP.
XX
AC   ADE27458;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:402.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 402; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2001 CGGGGTAAAAAGTGGCTGC 2019
             |||||||||||||||||||
Db         19 CGGGGTAAAAAGTGGCTGC 1

RESULT 478
ADE27479/c
ID   ADE27479 standard; RNA; 19 BP.
XX
AC   ADE27479;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:423.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 423; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 2 G; 0 T; 10 U; 0 Other;
```

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2379 CGGGTCAAAAATAAAATAT 2397
              |||||||||||||||||||
Db         19 CGGGTCAAAAATAAAATAT 1


RESULT 479
ADE27503/c
ID   ADE27503 standard; RNA; 19 BP.
XX
AC   ADE27503;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:447.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 447; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 7 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2811 TACAACTGCCTGGGGGGCA 2829
              |||||||||||||||||||
Db         19 TACAACTGCCTGGGGGGCA 1


RESULT 480
ADE27520/c
ID   ADE27520 standard; RNA; 19 BP.
XX
AC   ADE27520;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:464.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 464; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
```

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3117 GCCACACTGATGGCTCAAG 3135
              ||||||||||||||||||
Db         19 GCCACACTGATGGCTCAAG 1
```

RESULT 481
ADE27526/c
ID ADE27526 standard; RNA; 19 BP.
XX
AC ADE27526;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:470.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 470; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3225 CTCATGTTGAGCCAGTGGG 3243
              ||||||||||||||||||
Db         19 CTCATGTTGAGCCAGTGGG 1
```

RESULT 482
ADE27532/c
ID ADE27532 standard; RNA; 19 BP.
XX
AC ADE27532;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:476.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 476; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3333 TGAGGGTGCCCCGCCTGAG 3351
              ||||||||||||||||||||
Db         19 TGAGGGTGCCCCGCCTGAG 1
```

RESULT 483
ADE27537/c
ID ADE27537 standard; RNA; 19 BP.
XX
AC ADE27537;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:481.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 481; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 5 C; 6 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       3423 GGCAAGAACCCAAGTGCCT 3441
              ||||||||||||||||||||
Db         19 GGCAAGAACCCAAGTGCCT 1
```

RESULT 484
ADE27542/c
ID ADE27542 standard; RNA; 19 BP.
XX
AC ADE27542;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:486.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 486; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 2 C; 7 G; 0 T; 7 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       3513 AGATACCACAAACCCTGCT 3531
```

```
                    ||||||||||||||||||||
Db         19 AGATACCACAAACCCTGCT 1
```

RESULT 485
ADE27547/c
ID ADE27547 standard; RNA; 19 BP.
XX
AC ADE27547;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:491.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 491; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 0 A; 3 C; 2 G; 0 T; 14 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3603 GGAAAAAAACAAAAACAGA 3621
              ||||||||||||||||||||
Db         19 GGAAAAAAACAAAAACAGA 1
```

RESULT 486
ADE27564/c
ID ADE27564 standard; RNA; 19 BP.
XX
AC ADE27564;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:508.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 508; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 5 C; 2 G; 0 T; 4 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3909 GAAATGTCTGCTGGTATTT 3927
              ||||||||||||||||||||
Db         19 GAAATGTCTGCTGGTATTT 1
```

```
RESULT 487
ADE27569/c
ID   ADE27569 standard; RNA; 19 BP.
XX
AC   ADE27569;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:513.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 513; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 6 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3999 TTGTAATCGTGTGCCATGG 4017
              |||||||||||||||||||
Db         19 TTGTAATCGTGTGCCATGG 1
```

```
RESULT 488
ADE27576/c
ID   ADE27576 standard; RNA; 19 BP.
XX
AC   ADE27576;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:520.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 520; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4125 GAACACGATTTTCAAGATT 4143
              |||||||||||||||||||
Db         19 GAACACGATTTTCAAGATT 1
```

RESULT 489
ADE27598/c
ID ADE27598 standard; RNA; 19 BP.
XX
AC ADE27598;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:542.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 542; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4521 AAAAGATGGTTGTAGCATT 4539
||||||||||||||||||||
Db 19 AAAAGATGGTTGTAGCATT 1

RESULT 490
ADE27604/c
ID ADE27604 standard; RNA; 19 BP.
XX
AC ADE27604;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:548.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 548; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4629 AAAGCGAGGTGGCCATGTT 4647
||||||||||||||||||||
Db 19 AAAGCGAGGTGGCCATGTT 1

RESULT 491
ADE27621/c

```
ID   ADE27621 standard; RNA; 19 BP.
XX
AC   ADE27621;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:565.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 565; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4935 ATATGGTTCTCCAAGAAAC 4953
              |||||||||||||||||||
Db         19 ATATGGTTCTCCAAGAAAC 1


RESULT 492
ADE27632/c
ID   ADE27632 standard; RNA; 19 BP.
XX
AC   ADE27632;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:576.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 576; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 1 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5133 TATTAATATCAACTCTGAA 5151
              |||||||||||||||||||
Db         19 TATTAATATCAACTCTGAA 1


RESULT 493
ADE27110
ID   ADE27110 standard; RNA; 19 BP.
XX
```

```
AC   ADE27110;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:54.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 54; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        957 CTTTTCAAAACAGTGTGTT 975
              |::::||||||||:|:|::
Db          1 CUUUUCAAAACAGUGUGUU 19


RESULT 494
ADE27127
ID   ADE27127 standard; RNA; 19 BP.
XX
AC   ADE27127;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:71.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 71; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1263 CCATCTTGGCCAGGATTAA 1281
              |||:|::||||||||::||
Db          1 CCAUCUUGGCCAGGAUUAA 19


RESULT 495
ADE27129
ID   ADE27129 standard; RNA; 19 BP.
XX
AC   ADE27129;
XX
```

```
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:73.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 73; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1299 ACTACAAGAGTGGCTGAGT 1317
              ||:|||||||:|||:|||:
Db          1 ACUACAAGAGUGGCUGAGU 19


RESULT 496
ADE27139
ID   ADE27139 standard; RNA; 19 BP.
XX
AC   ADE27139;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:83.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 83; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 5 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CTCTGCCTTTATGATGCTA 1497
              |:|:|||:::|:||:||:|
Db          1 CUCUGCCUUUAUGAUGCUA 19


RESULT 497
ADE27148
ID   ADE27148 standard; RNA; 19 BP.
XX
AC   ADE27148;
XX
DT   29-JAN-2004  (first entry)
XX
```

```
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:92.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 92; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1641 CCTAGACAACCTTTCTGTA 1659
              ||:||||||||:::|:|:|
Db          1 CCUAGACAACCUUUCUGUA 19


RESULT 498
ADE27173
ID   ADE27173 standard; RNA; 19 BP.
XX
AC   ADE27173;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:117.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 117; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 1 C; 5 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2091 TTTGTAGTAAAAGTGGTCT 2109
              :::|:||:|||||:||:|:
Db          1 UUUGUAGUAAAAGUGGUCU 19


RESULT 499
ADE27187
ID   ADE27187 standard; RNA; 19 BP.
XX
AC   ADE27187;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:131.
XX
```

KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 131; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 3 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2343 CATCCAAAAAAAGGGAAGG 2361
||:||||||||||||||||
Db 1 CAUCCAAAAAAAGGGAAGG 19

RESULT 500
ADE27209
ID ADE27209 standard; RNA; 19 BP.
XX
AC ADE27209;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:153.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 153; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 7 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2739 CACAGTGTTGTGCCCCTTC 2757
|||||:|::|:|||||::|
Db 1 CACAGUGUUGUGCCCCUUC 19

RESULT 501
ADE27224
ID ADE27224 standard; RNA; 19 BP.
XX
AC ADE27224;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:168.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;

KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 168; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3009 ACAGAATGCTCAGGGTCAC 3027
              ||||||:||:|||||:|||
Db          1 ACAGAAUGCUCAGGGUCAC 19
```

RESULT 502
ADE27277
ID ADE27277 standard; RNA; 19 BP.
XX
AC ADE27277;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:221.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 221; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 13 A; 2 C; 0 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3963 TATATAAACAATAAAAACA 3981
              :|:|:|||||||:|||||||
Db          1 UAUAUAAACAAUAAAAACA 19
```

RESULT 503
ADE27290
ID ADE27290 standard; RNA; 19 BP.
XX
AC ADE27290;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:234.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;

```
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 234; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4197 TCCGGATTTCTAACAGTCC 4215
              :|||||:::|:|||||:||
Db          1 UCCGGAUUUCUAACAGUCC 19


RESULT 504
ADE27298
ID   ADE27298 standard; RNA; 19 BP.
XX
AC   ADE27298;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:242.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 242; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 1 C; 9 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4341 TGGCTGGTAGAAAAAGGGG 4359
              :|||:||:||||||||||||
Db          1 UGGCUGGUAGAAAAAGGGG 19


RESULT 505
ADE27337
ID   ADE27337 standard; RNA; 19 BP.
XX
AC   ADE27337;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:281.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
```

OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 281; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 3 C; 5 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 2.1e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 5043 GATGCCTTTTCTGTGATTG 5061
||:|||::::|:|:||::|
Db 1 GAUGCCUUUUCUGUGAUUG 19

RESULT 506
ADE27415/c
ID ADE27415 standard; RNA; 19 BP.
XX
AC ADE27415;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:359.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 359; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1227 GTCTGGCCTATGACCGGAA 1245
|||||||||||||||||||
Db 19 GTCTGGCCTATGACCGGAA 1

RESULT 507
ADE27418/c
ID ADE27418 standard; RNA; 19 BP.
XX
AC ADE27418;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:362.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX

PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 362; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 6 C; 2 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1281 AAAGAACCGGAGATGGAAA 1299
||||||||||||||||||||
Db 19 AAAGAACCGGAGATGGAAA 1

RESULT 508
ADE27449/c
ID ADE27449 standard; RNA; 19 BP.
XX
AC ADE27449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:393.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 393; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1839 TCTAAAGCAGGTAAATTGT 1857
||||||||||||||||||||
Db 19 TCTAAAGCAGGTAAATTGT 1

RESULT 509
ADE27467/c
ID ADE27467 standard; RNA; 19 BP.
XX
AC ADE27467;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:411.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX

PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 411; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2163 TAGTTCATATATCAAGAAG 2181
||||||||||||||||||||
Db 19 TAGTTCATATATCAAGAAG 1

RESULT 510
ADE27559/c
ID ADE27559 standard; RNA; 19 BP.
XX
AC ADE27559;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:503.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 503; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 3 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3819 CTTGTCTTTTGAGCTATTC 3837
||||||||||||||||||||
Db 19 CTTGTCTTTTGAGCTATTC 1

RESULT 511
ADE27572/c
ID ADE27572 standard; RNA; 19 BP.
XX
AC ADE27572;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:516.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX

```
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 516; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 8 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4053 TGGCACCTCAGGCTGAGGG 4071
              |||||||||||||||||||
Db         19 TGGCACCTCAGGCTGAGGG 1


RESULT 512
ADE27573/c
ID   ADE27573 standard; RNA; 19 BP.
XX
AC   ADE27573;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:517.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 517; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4071 GCCCCAATGTATGTGTGGC 4089
              |||||||||||||||||||
Db         19 GCCCCAATGTATGTGTGGC 1


RESULT 513
ADE27592/c
ID   ADE27592 standard; RNA; 19 BP.
XX
AC   ADE27592;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:536.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
```

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 536; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 3 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4413 ATTCTGGAAACTTTTGTTA 4431
||||||||||||||||||||
Db 19 ATTCTGGAAACTTTTGTTA 1

RESULT 514
ADE27594/c
ID ADE27594 standard; RNA; 19 BP.
XX
AC ADE27594;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:538.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 538; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4449 TGCCCACATTTGATGGAGG 4467
||||||||||||||||||||
Db 19 TGCCCACATTTGATGGAGG 1

RESULT 515
ADE27614/c
ID ADE27614 standard; RNA; 19 BP.
XX
AC ADE27614;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:558.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

```
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 558; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 3 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4809 ATGCTTTTTAGAAAGCATT 4827
              |||||||||||||||||||
Db         19 ATGCTTTTTAGAAAGCATT 1


RESULT 516
ADE27136
ID   ADE27136 standard; RNA; 19 BP.
XX
AC   ADE27136;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:80.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 80; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1425 AACCCATTCCAGTACAGTA 1443
              ||||||::||||:||||:|
Db          1 AACCCAUUCCAGUACAGUA 19


RESULT 517
ADE27143
ID   ADE27143 standard; RNA; 19 BP.
XX
AC   ADE27143;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:87.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
```

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 87; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 1 G; 0 T; 11 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.1e+02;
Matches 8; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1551 CTTTTCACTTTATTGCTAT 1569
              |::::|||:::|::||:|:
Db          1 CUUUUCACUUUAUUGCUAU 19
```

RESULT 518
ADE27161
ID ADE27161 standard; RNA; 19 BP.
XX
AC ADE27161;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:105.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 105; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 0 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1875 ATGTATGAATGTAAGGATG 1893
              |:|:|:|||:|:|||||:|
Db          1 AUGUAUGAAUGUAAGGAUG 19
```

RESULT 519
ADE27165
ID ADE27165 standard; RNA; 19 BP.
XX
AC ADE27165;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:109.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 109; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1947 CCTAATGAGGACTTCAAGC 1965
||:||:|||||||::|||||
Db 1 CCUAAUGAGGACUUCAAGC 19

RESULT 520
ADE27177
ID ADE27177 standard; RNA; 19 BP.
XX
AC ADE27177;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:121.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 121; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 2 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2163 TAGTTCATATATCAAGAAG 2181
:||::||:|:|:|||||||
Db 1 UAGUUCAUAUAUCAAGAAG 19

RESULT 521
ADE27202
ID ADE27202 standard; RNA; 19 BP.
XX
AC ADE27202;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:146.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

```
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 146; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 2 C; 8 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2613 CAGGGGCTTGAGAAGGTTA 2631
              ||||||::|||||||::|
Db          1 CAGGGGCUUGAGAAGGUUA 19


RESULT 522
ADE27237
ID   ADE27237 standard; RNA; 19 BP.
XX
AC   ADE27237;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:181.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 181; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 6 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3243 GCCAGCCACAGAGCAAAAG 3261
              |||||||||||||||||||
Db          1 GCCAGCCACAGAGCAAAAG 19


RESULT 523
ADE27244
ID   ADE27244 standard; RNA; 19 BP.
XX
AC   ADE27244;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:188.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
```

```
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 188; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3369 CAGTGCAATGCTTGTAGAA 3387
              |||:||||:||::|:||||
Db          1 CAGUGCAAUGCUUGUAGAA 19


RESULT 524
ADE27248
ID   ADE27248 standard; RNA; 19 BP.
XX
AC   ADE27248;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:192.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 192; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 7 C; 5 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3441 TCACCTCGAAAGGAGGCCC 3459
              :||||:|||||||||||||
Db          1 UCACCUCGAAAGGAGGCCC 19


RESULT 525
ADE27249
ID   ADE27249 standard; RNA; 19 BP.
XX
AC   ADE27249;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:193.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
```

```
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 193; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 5 C; 7 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3459 CTGTTCCCTGGAGTCAGGG 3477
              |:|::|||:||||:|||||
Db          1 CUGUUCCCUGGAGUCAGGG 19


RESULT 526
ADE27254
ID   ADE27254 standard; RNA; 19 BP.
XX
AC   ADE27254;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:198.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 198; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 6 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3549 AGCAAACTAACCAGCATTC 3567
              ||||||||:|||||||||::|
Db          1 AGCAAACUAACCAGCAUUC 19


RESULT 527
ADE27262
ID   ADE27262 standard; RNA; 19 BP.
XX
AC   ADE27262;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:206.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
```

```
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 206; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3693 AAGATTGGAAATGTACACT 3711
              ||||::|||||:|:||||:
Db          1 AAGAUUGGAAAUGUACACU 19


RESULT 528
ADE27268
ID   ADE27268 standard; RNA; 19 BP.
XX
AC   ADE27268;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:212.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 212; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3801 GCCTGGACTAAAGGCATCC 3819
              |||:||||:|||||||:||
Db          1 GCCUGGACUAAAGGCAUCC 19


RESULT 529
ADE27273
ID   ADE27273 standard; RNA; 19 BP.
XX
AC   ADE27273;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:217.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
```

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 217; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 8 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3891 CTGTGCACCTACCCCTTGG 3909
|:|:|||||:|||||::||
Db 1 CUGUGCACCUACCCCUUGG 19

RESULT 530
ADE27307
ID ADE27307 standard; RNA; 19 BP.
XX
AC ADE27307;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:251.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 251; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 0 C; 3 G; 0 T; 15 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 21.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 4503 TTTTTTTTTTTTTGGGTTA 4521
:::::::::::::|||::|
Db 1 UUUUUUUUUUUUUGGGUUA 19

RESULT 531
ADE27312
ID ADE27312 standard; RNA; 19 BP.
XX
AC ADE27312;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:256.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

```
XX
PS   Example 3; SEQ ID NO 256; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 2 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4593 AAGTGTAGCTCAAATAGGT 4611
              |||:|:|||:||||:|||:
Db          1 AAGUGUAGCUCAAAUAGGU 19


RESULT 532
ADE27320
ID   ADE27320 standard; RNA; 19 BP.
XX
AC   ADE27320;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:264.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 264; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 4 C; 2 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   47.4%;  Pred. No. 2.1e+02;
  Matches    9;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4737 TCAGTTTTCCTTCTGTTAA 4755
              :|||::::||::|:|::||
Db          1 UCAGUUUUCCUUCUGUUAA 19


RESULT 533
ADE27340
ID   ADE27340 standard; RNA; 19 BP.
XX
AC   ADE27340;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:284.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 284; 139pp; English.
```

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5097 AGTTACTTGTGACAAAAAT 5115
              ||::||::|:||||||||:
Db          1 AGUUACUUGUGACAAAAAU 19


RESULT 534
ADE27342
ID   ADE27342 standard; RNA; 19 BP.
XX
AC   ADE27342;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:286.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 286; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 3 C; 1 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 2.1e+02;
  Matches   12;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5133 TATTAATATCAACTCTGAA 5151
              :|::||:|:||||:|:|||
Db          1 UAUUAAUAUCAACUCUGAA 19


RESULT 535
ADE27399/c
ID   ADE27399 standard; RNA; 19 BP.
XX
AC   ADE27399;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:343.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 343; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
```

CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 7 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 939 GGTATTTCTGGGGTGAAAC 957
||||||||||||||||||||
Db 19 GGTATTTCTGGGGTGAAAC 1

RESULT 536
ADE27404/c
ID ADE27404 standard; RNA; 19 BP.
XX
AC ADE27404;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:348.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 348; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 ACAGTGCTGCCCACCTCTT 1047
||||||||||||||||||||
Db 19 ACAGTGCTGCCCACCTCTT 1

RESULT 537
ADE27450/c
ID ADE27450 standard; RNA; 19 BP.
XX
AC ADE27450;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:394.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 394; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD

```
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 9 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1857 TCGGGGGAGAGAGTTAGCA 1875
              |||||||||||||||||||
Db         19 TCGGGGGAGAGAGTTAGCA 1

RESULT 538
ADE27451/c
ID   ADE27451 standard; RNA; 19 BP.
XX
AC   ADE27451;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:395.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 395; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 6 C; 0 G; 0 T; 7 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1875 ATGTATGAATGTAAGGATG 1893
              |||||||||||||||||||
Db         19 ATGTATGAATGTAAGGATG 1

RESULT 539
ADE27452/c
ID   ADE27452 standard; RNA; 19 BP.
XX
AC   ADE27452;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:396.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 396; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
```

```
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 0 A; 9 C; 2 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1893 GAGGGAAGCGAAGCAAGAG 1911
              ||||||||||||||||||
Db         19 GAGGGAAGCGAAGCAAGAG 1


RESULT 540
ADE27476/c
ID   ADE27476 standard; RNA; 19 BP.
XX
AC   ADE27476;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:420.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 420; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2325 GGCTGTGGCATTTCCAAAC 2343
              ||||||||||||||||||
Db         19 GGCTGTGGCATTTCCAAAC 1


RESULT 541
ADE27477/c
ID   ADE27477 standard; RNA; 19 BP.
XX
AC   ADE27477;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:421.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 421; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
```

CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 5 C; 3 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2343 CATCCAAAAAAAGGGAAGG 2361
||||||||||||||||||||
Db 19 CATCCAAAAAAAGGGAAGG 1

RESULT 542
ADE27497/c
ID ADE27497 standard; RNA; 19 BP.
XX
AC ADE27497;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:441.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 441; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 3 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2703 CTCCTTGAAATGAGTAAAA 2721
||||||||||||||||||||
Db 19 CTCCTTGAAATGAGTAAAA 1

RESULT 543
ADE27508/c
ID ADE27508 standard; RNA; 19 BP.
XX
AC ADE27508;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:452.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 452; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

```
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 2 C; 6 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2901 AGATCTTTCTCTTCCCTGA 2919
              ||||||||||||||||||||
Db         19 AGATCTTTCTCTTCCCTGA 1


RESULT 544
ADE27509/c
ID   ADE27509 standard; RNA; 19 BP.
XX
AC   ADE27509;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:453.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 453; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 10 A; 1 C; 6 G; 0 T; 2 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2919 AACGTTTTCTTCTTTCCCT 2937
              ||||||||||||||||||||
Db         19 AACGTTTTCTTCTTTCCCT 1


RESULT 545
ADE27510/c
ID   ADE27510 standard; RNA; 19 BP.
XX
AC   ADE27510;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:454.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 454; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
```

CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2937 TGGACAGGCAGCCTCCTTT 2955
||||||||||||||||||||
Db 19 TGGACAGGCAGCCTCCTTT 1

RESULT 546
ADE27518/c
ID ADE27518 standard; RNA; 19 BP.
XX
AC ADE27518;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:462.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 462; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3081 TCCGCAGTGTCTCCACCTA 3099
||||||||||||||||||||
Db 19 TCCGCAGTGTCTCCACCTA 1

RESULT 547
ADE27528/c
ID ADE27528 standard; RNA; 19 BP.
XX
AC ADE27528;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:472.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 472; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

```
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3261 GAGGGTTTATTTTCAGTCC 3279
              ||||||||||||||||||
Db         19 GAGGGTTTATTTTCAGTCC 1


RESULT 548
ADE27597/c
ID   ADE27597 standard; RNA; 19 BP.
XX
AC   ADE27597;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:541.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 541; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 15 A; 3 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGGGTTA 4521
              ||||||||||||||||||
Db         19 TTTTTTTTTTTTTGGGTTA 1


RESULT 549
ADE27613/c
ID   ADE27613 standard; RNA; 19 BP.
XX
AC   ADE27613;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:557.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 557; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
```

XX
SQ Sequence 19 BP; 6 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4791 AGTTTTGAGGCATGACTAA 4809
||||||||||||||||||||
Db 19 AGTTTTGAGGCATGACTAA 1

RESULT 550
ADE27626/c
ID ADE27626 standard; RNA; 19 BP.
XX
AC ADE27626;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:570.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 570; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX

SQ Sequence 19 BP; 1 A; 5 C; 5 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5025 CCACGGAAACATACAGAGG 5043
||||||||||||||||||||
Db 19 CCACGGAAACATACAGAGG 1

RESULT 551
ADE27107
ID ADE27107 standard; RNA; 19 BP.
XX
AC ADE27107;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:51.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 51; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 5 C; 4 G; 0 T; 8 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        903 TGCTGATGTGCTTCATCCT 921
              :||:||:|:||::||:||:
Db          1 UGCUGAUGUGCUUCAUCCU 19


RESULT 552
ADE27117
ID   ADE27117 standard; RNA; 19 BP.
XX
AC   ADE27117;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:61.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 61; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 6 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1083 GGGAGAATATCCTGGTTTC 1101
              |||||||:|:||:||:::|
Db          1 GGGAGAAUAUCCUGGUUUC 19


RESULT 553
ADE27128
ID   ADE27128 standard; RNA; 19 BP.
XX
AC   ADE27128;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:72.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 72; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 10 A; 2 C; 6 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
```

```
  Best Local Similarity   94.7%;  Pred. No. 2.1e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1281 AAAGAACCGGAGATGGAAA 1299
              ||||||||||||||:|||||
Db          1 AAAGAACCGGAGAUGGAAA 19
```

RESULT 554
ADE27131
ID ADE27131 standard; RNA; 19 BP.
XX
AC ADE27131;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:75.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 75; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1335 TCCTTTTTCAAAAACCAGC 1353
              :||:::::|||||||||||
Db          1 UCCUUUUUCAAAAACCAGC 19
```

RESULT 555
ADE27195
ID ADE27195 standard; RNA; 19 BP.
XX
AC ADE27195;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:139.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 139; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 2 C; 7 G; 0 T; 5 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2487 AGGAATTAGTTGGGATGCC 2505
              |||||::||::||||:|||
Db          1 AGGAAUUAGUUGGGAUGCC 19
```

RESULT 556
ADE27204
ID ADE27204 standard; RNA; 19 BP.
XX
AC ADE27204;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:148.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 148; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 2 C; 1 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2649 AGTCTTAATAAAATAAACT 2667
              ||:|::||:||||:||||:
Db          1 AGUCUUAAUAAAAUAAACU 19
```

RESULT 557
ADE27228
ID ADE27228 standard; RNA; 19 BP.
XX
AC ADE27228;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:172.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 172; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 5 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3081 TCCGCAGTGTCTCCACCTA 3099
```

```
                  :||||||:|:|:|||||:|
Db          1 UCCGCAGUGUCUCCACCUA 19
```

RESULT 558
ADE27287
ID ADE27287 standard; RNA; 19 BP.
XX
AC ADE27287;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:231.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 231; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4143 TCTAAAGCTCAATTCAAGT 4161
              :|:||||||:|||::||||:
Db          1 UCUAAAGCUCAAUUCAAGU 19
```

RESULT 559
ADE27323
ID ADE27323 standard; RNA; 19 BP.
XX
AC ADE27323;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:267.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 267; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 2 C; 5 G; 0 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4791 AGTTTTGAGGCATGACTAA 4809
              ||::::||||||:|||:||
Db          1 AGUUUUGAGGCAUGACUAA 19
```

```
RESULT 560
ADE27331
ID   ADE27331 standard; RNA; 19 BP.
XX
AC   ADE27331;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:275.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 275; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 4 C; 3 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4935 ATATGGTTCTCCAAGAAAC 4953
              |:|:||::|:||||||||||
Db          1 AUAUGGUUCUCCAAGAAAC 19
```

```
RESULT 561
ADE27332
ID   ADE27332 standard; RNA; 19 BP.
XX
AC   ADE27332;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:276.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 276; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4953 CTGAATGAATCCATTGGAG 4971
              |:|||:|||:|||::||||
Db          1 CUGAAUGAAUCCAUUGGAG 19
```

RESULT 562
ADE27402/c
ID ADE27402 standard; RNA; 19 BP.
XX
AC ADE27402;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:346.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 346; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 993 GATATGCTGTGGTGCTTAA 1011
||||||||||||||||||
Db 19 GATATGCTGTGGTGCTTAA 1

RESULT 563
ADE27406/c
ID ADE27406 standard; RNA; 19 BP.
XX
AC ADE27406;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:350.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 350; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 3 C; 7 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1065 ACAAGAACATTAGCCCCCG 1083
||||||||||||||||||
Db 19 ACAAGAACATTAGCCCCCG 1

RESULT 564
ADE27435/c

```
ID   ADE27435 standard; RNA; 19 BP.
XX
AC   ADE27435;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:379.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 379; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 5 C; 7 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1587 TTGCCTCCCAGGCAAGCAG 1605
              ||||||||||||||||||||
Db         19 TTGCCTCCCAGGCAAGCAG 1

RESULT 565
ADE27455/c
ID   ADE27455 standard; RNA; 19 BP.
XX
AC   ADE27455;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:399.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 399; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1947 CCTAATGAGGACTTCAAGC 1965
              ||||||||||||||||||||
Db         19 CCTAATGAGGACTTCAAGC 1

RESULT 566
ADE27484/c
ID   ADE27484 standard; RNA; 19 BP.
XX
```

```
AC   ADE27484;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:428.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 428; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 6 C; 2 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2469 AAAACTCTGAAGGAGAGGA 2487
              |||||||||||||||||||
Db         19 AAAACTCTGAAGGAGAGGA 1


RESULT 567
ADE27489/c
ID   ADE27489 standard; RNA; 19 BP.
XX
AC   ADE27489;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:433.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 433; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2559 TAGGCAGCTTCTAAGAGCG 2577
              |||||||||||||||||||
Db         19 TAGGCAGCTTCTAAGAGCG 1


RESULT 568
ADE27496/c
ID   ADE27496 standard; RNA; 19 BP.
XX
AC   ADE27496;
XX
```

DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:440.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 440; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2685 ATTAATTAGTTCCAGTTTC 2703
||||||||||||||||||||
Db 19 ATTAATTAGTTCCAGTTTC 1

RESULT 569
ADE27511/c
ID ADE27511 standard; RNA; 19 BP.
XX
AC ADE27511;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:455.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 455; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 7 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2955 TGTGTGTATTCAGAGGCAG 2973
||||||||||||||||||||
Db 19 TGTGTGTATTCAGAGGCAG 1

RESULT 570
ADE27515/c
ID ADE27515 standard; RNA; 19 BP.
XX
AC ADE27515;
XX
DT 29-JAN-2004 (first entry)
XX

```
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:459.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 459; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 7 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3027 CTGAACCACTGCTTCTCTT 3045
              |||||||||||||||||||
Db         19 CTGAACCACTGCTTCTCTT 1


RESULT 571
ADE27525/c
ID   ADE27525 standard; RNA; 19 BP.
XX
AC   ADE27525;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:469.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 469; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 0 A; 5 C; 8 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3207 GCACAGCCAAGCCAAGCGC 3225
              |||||||||||||||||||
Db         19 GCACAGCCAAGCCAAGCGC 1


RESULT 572
ADE27553/c
ID   ADE27553 standard; RNA; 19 BP.
XX
AC   ADE27553;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:497.
XX
```

KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 497; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 1 C; 8 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3711 TACCAAACACTCAGTCCAC 3729
||||||||||||||||||
Db 19 TACCAAACACTCAGTCCAC 1

RESULT 573
ADE27556/c
ID ADE27556 standard; RNA; 19 BP.
XX
AC ADE27556;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:500.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 500; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 4 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3765 TCTTCTGTGTTAATTGCGT 3783
||||||||||||||||||
Db 19 TCTTCTGTGTTAATTGCGT 1

RESULT 574
ADE27557/c
ID ADE27557 standard; RNA; 19 BP.
XX
AC ADE27557;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:501.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;

KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 501; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3783 TAGAGGCTACAGGGGTTAG 3801
||||||||||||||||||||
Db 19 TAGAGGCTACAGGGGTTAG 1

RESULT 575
ADE27566/c
ID ADE27566 standard; RNA; 19 BP.
XX
AC ADE27566;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:510.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 510; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3945 CAGATGCCTGCTTGATAAT 3963
||||||||||||||||||||
Db 19 CAGATGCCTGCTTGATAAT 1

RESULT 576
ADE27571/c
ID ADE27571 standard; RNA; 19 BP.
XX
AC ADE27571;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:515.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;

KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 515; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4035 ACCCTACATAAGGCTGGAT 4053
||||||||||||||||||||
Db 19 ACCCTACATAAGGCTGGAT 1

RESULT 577
ADE27607/c
ID ADE27607 standard; RNA; 19 BP.
XX
AC ADE27607;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:551.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 551; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 5 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4683 TGTGCCACTGACTTGCTGT 4701
||||||||||||||||||||
Db 19 TGTGCCACTGACTTGCTGT 1

RESULT 578
ADE27634/c
ID ADE27634 standard; RNA; 19 BP.
XX
AC ADE27634;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:578.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX

OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 578; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 5 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5169 GAGATTGTGTTTGTTCATA 5187
||||||||||||||||||||
Db 19 GAGATTGTGTTTGTTCATA 1

RESULT 579
ADE27115
ID ADE27115 standard; RNA; 19 BP.
XX
AC ADE27115;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:59.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 59; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 2.1e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 TCGGATATCGTCCTTATGA 1065
:||||:|:||:||::|:||
Db 1 UCGGAUAUCGUCCUUAUGA 19

RESULT 580
ADE27126
ID ADE27126 standard; RNA; 19 BP.
XX
AC ADE27126;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:70.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX

PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 70; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1245 AGAAAGTCTCCAAGGCCGC 1263
|||||| :|:|||||||||||
Db 1 AGAAAGUCUCCAAGGCCGC 19

RESULT 581
ADE27130
ID ADE27130 standard; RNA; 19 BP.
XX
AC ADE27130;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:74.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 74; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 4 C; 6 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1317 TTTGGGGTCCCTCAGGTTT 1335
::: |||| :||| :|||| :::
Db 1 UUUGGGGUCCCUCAGGUUU 19

RESULT 582
ADE27138
ID ADE27138 standard; RNA; 19 BP.
XX
AC ADE27138;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:82.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX

```
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 82; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1461 AGTATTGAAAGCCAACAAC 1479
              ||:|::|||||||||||||
Db          1 AGUAUUGAAAGCCAACAAC 19


RESULT 583
ADE27144
ID   ADE27144 standard; RNA; 19 BP.
XX
AC   ADE27144;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:88.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 88; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 9 C; 1 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 2.1e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1569 TCGCCCTCCTTTCCCTTAT 1587
              :|||||:||:::|||::|:
Db          1 UCGCCCUCCUUUCCCUUAU 19


RESULT 584
ADE27182
ID   ADE27182 standard; RNA; 19 BP.
XX
AC   ADE27182;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:126.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
```

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PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 126; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 6 C; 1 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2253 TCATTACAGTTCTTTCCTC 2271
              :||::||||::|:::||:|
Db          1 UCAUUACAGUUCUUUCCUC 19


RESULT 585
ADE27183
ID   ADE27183 standard; RNA; 19 BP.
XX
AC   ADE27183;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:127.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 127; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 7 C; 2 G; 0 T; 9 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 2.1e+02;
  Matches   10;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2271 CTTTCTGCTCTGCCATCTT 2289
              |:::|:||:|:||||:|::
Db          1 CUUUCUGCUCUGCCAUCUU 19


RESULT 586
ADE27184
ID   ADE27184 standard; RNA; 19 BP.
XX
AC   ADE27184;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:128.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 128; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 4 C; 4 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.1e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2289 TCAGGATATTGGTTCTTCC 2307
:|||||:|::||::|::||
Db 1 UCAGGAUAUUGGUUCUUCC 19

RESULT 587
ADE27189
ID ADE27189 standard; RNA; 19 BP.
XX
AC ADE27189;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:133.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 133; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 2 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2379 CGGGTCAAAAATAAAATAT 2397
||||:||||||:||||:|:
Db 1 CGGGUCAAAAAUAAAAUAU 19

RESULT 588
ADE27193
ID ADE27193 standard; RNA; 19 BP.
XX
AC ADE27193;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:137.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 137; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 8 A; 0 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2451 AAAGAGGGATGTTTGGAAA 2469
||||||||:|:::|||||
Db 1 AAAGAGGGAUGUUUGGAAA 19

RESULT 589
ADE27240
ID ADE27240 standard; RNA; 19 BP.
XX
AC ADE27240;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:184.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 184; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3297 ACCAGAGGGCATGCTGAAT 3315
||||||||||:||:|||:
Db 1 ACCAGAGGGCAUGCUGAAU 19

RESULT 590
ADE27243
ID ADE27243 standard; RNA; 19 BP.
XX
AC ADE27243;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:187.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 187; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3351 GTCAGTGCTCTCAGCTGGC 3369
|:|||:||:|:||||:|||
Db 1 GUCAGUGCUCUCAGCUGGC 19

RESULT 591
ADE27257
ID ADE27257 standard; RNA; 19 BP.
XX
AC ADE27257;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:201.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 201; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 14 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3603 GGAAAAAAACAAAAACAGA 3621
||||||||||||||||||
Db 1 GGAAAAAAACAAAAACAGA 19

RESULT 592
ADE27265
ID ADE27265 standard; RNA; 19 BP.
XX
AC ADE27265;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:209.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 209; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 2 C; 9 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3747 GGAAGGGAGGAAGGCCTTT 3765
              |||||||||||||||:::
Db          1 GGAAGGGAGGAAGGCCUUU 19
```

RESULT 593
ADE27281
ID ADE27281 standard; RNA; 19 BP.
XX
AC ADE27281;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:225.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 225; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4035 ACCCTACATAAGGCTGGAT 4053
              ||||:|||:|||||:|||:
Db          1 ACCCUACAUAAGGCUGGAU 19
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RESULT 594
ADE27288
ID ADE27288 standard; RNA; 19 BP.
XX
AC ADE27288;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:232.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

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XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 232; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 9 A; 3 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4161 TGACACATTAATGATAAAC 4179
              :|||||||::||:||:||||
Db          1 UGACACAUUAAUGAUAAAC 19


RESULT 595
ADE27299
ID   ADE27299 standard; RNA; 19 BP.
XX
AC   ADE27299;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:243.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 243; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 3 C; 7 G; 0 T; 5 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4359 GCCTGAGTGGAGGATTATC 4377
              |||:|||:||||||::|:|
Db          1 GCCUGAGUGGAGGAUUAUC 19


RESULT 596
ADE27305
ID   ADE27305 standard; RNA; 19 BP.
XX
AC   ADE27305;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:249.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
```

XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 249; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 0 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 4467 GGTGGAAATAATTTGAATG 4485
||:|||||:||:::|||:|
Db 1 GGUGGAAAUAAUUUGAAUG 19

RESULT 597
ADE27431/c
ID ADE27431 standard; RNA; 19 BP.
XX
AC ADE27431;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:375.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 375; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 10 A; 0 C; 8 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1515 CTCTTATCCTCTCTCTCTT 1533
|||||||||||||||||||
Db 19 CTCTTATCCTCTCTCTCTT 1

RESULT 598
ADE27459/c
ID ADE27459 standard; RNA; 19 BP.
XX
AC ADE27459;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:403.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;

XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 403; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2019 CGGTGTTTGGCAATGCTAA 2037
||||||||||||||||||||
Db 19 CGGTGTTTGGCAATGCTAA 1

RESULT 599
ADE27486/c
ID ADE27486 standard; RNA; 19 BP.
XX
AC ADE27486;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:430.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 430; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 1 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2505 CAATTTCCTCTCCACTGCT 2523
||||||||||||||||||||
Db 19 CAATTTCCTCTCCACTGCT 1

RESULT 600
ADE27492/c
ID ADE27492 standard; RNA; 19 BP.
XX
AC ADE27492;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:436.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.

XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 436; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2613 CAGGGGCTTGAGAAGGTTA 2631
||||||||||||||||||||
Db 19 CAGGGGCTTGAGAAGGTTA 1

RESULT 601
ADE27494/c
ID ADE27494 standard; RNA; 19 BP.
XX
AC ADE27494;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:438.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 438; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 1 C; 2 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2649 AGTCTTAATAAAATAAACT 2667
||||||||||||||||||||
Db 19 AGTCTTAATAAAATAAACT 1

RESULT 602
ADE27495/c
ID ADE27495 standard; RNA; 19 BP.
XX
AC ADE27495;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:439.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 439; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 7 A; 3 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2667 TAGATATTAGGTCCATTCA 2685
||||||||||||||||||||
Db 19 TAGATATTAGGTCCATTCA 1

RESULT 603
ADE27524/c
ID ADE27524 standard; RNA; 19 BP.
XX
AC ADE27524;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:468.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 468; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 9 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3189 CCCTCCCTCTCTCATGAGG 3207
||||||||||||||||||||
Db 19 CCCTCCCTCTCTCATGAGG 1

RESULT 604
ADE27543/c
ID ADE27543 standard; RNA; 19 BP.
XX
AC ADE27543;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:487.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

XX
PS Example 3; SEQ ID NO 487; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 6 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3531 TGAACACAGTGTCTGTTCA 3549
||||||||||||||||||||
Db 19 TGAACACAGTGTCTGTTCA 1

RESULT 605
ADE27554/c
ID ADE27554 standard; RNA; 19 BP.
XX
AC ADE27554;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:498.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 498; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 6 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3729 CTGTTGAGCCCCAGTGCTG 3747
||||||||||||||||||||
Db 19 CTGTTGAGCCCCAGTGCTG 1

RESULT 606
ADE27635/c
ID ADE27635 standard; RNA; 19 BP.
XX
AC ADE27635;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:579.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 579; 139pp; English.

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 4 A; 4 C; 1 G; 0 T; 10 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5187 AATAAAAGTGAAGTGAATC 5205
              |||||||||||||||||||
Db         19 AATAAAAGTGAAGTGAATC 1


RESULT 607
AAQ75609
ID   AAQ75609 standard; DNA; 21 BP.
XX
AC   AAQ75609;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGGGT 21


RESULT 608
ADE27648/c
ID   ADE27648 standard; RNA; 21 BP.
XX
AC   ADE27648;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:592.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 592; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 2 A; 5 C; 6 G; 2 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4774 GACCTACCTCAAAGGGCAG 4792
              ||||||||||||||||||
Db         19 GACCTACCTCAAAGGGCAG 1
```

RESULT 609
ADE27641
ID ADE27641 standard; RNA; 21 BP.
XX
AC ADE27641;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:585.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 585; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 3 A; 2 C; 6 G; 2 T; 8 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 21;
Best Local Similarity 57.9%; Pred. No. 2.3e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

```
Qy        995 TATGCTGTGGTGCTTAATG 1013
              :|:||:|:||::||:|
Db          1 UAUGCUGUGGUGCUUAAUG 19
```

RESULT 610
ADE27642
ID ADE27642 standard; RNA; 21 BP.
XX
AC ADE27642;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:586.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 586; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.3e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2520 TGCTGGACATGAGATGGAG 2538
```

```
           :||:|||||:||||:||||
Db         1 UGCUGGACAUGAGAUGGAG 19
```

RESULT 611
ADG30278/c
ID ADG30278 standard; RNA; 21 BP.
XX
AC ADG30278;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD-targeted siNA DNA-RNA hybrid - SEQ ID 844.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX
PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 844; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA DNA-
CC RNA hybrid of the invention.
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 2 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4774 GACCTACCTCAAAGGGCAG 4792
              |||||||||||||||||||
Db         19 GACCTACCTCAAAGGGCAG 1
```

RESULT 612
ADG30286/c
ID ADG30286 standard; RNA; 21 BP.
XX
AC ADG30286;
XX
DT 26-FEB-2004 (first entry)
XX
DE SCD-targeted siNA DNA-RNA hybrid - SEQ ID 852.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX
PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 852; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA DNA-
CC RNA hybrid of the invention.
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 2 T; 6 U; 0 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4774 GACCTACCTCAAAGGGCAG 4792
              ||||||||||||||||||||
Db         19 GACCTACCTCAAAGGGCAG 1


RESULT 613
ADG30280
ID   ADG30280 standard; RNA; 21 BP.
XX
AC   ADG30280;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 846.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 846; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2520 TGCTGGACATGAGATGGAG 2538
              :||:|||||:||||:||||
Db          1 UGCUGGACAUGAGAUGGAG 19


RESULT 614
ADG30279
ID   ADG30279 standard; RNA; 21 BP.
XX
AC   ADG30279;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 845.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 845; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 3 A; 2 C; 6 G; 2 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 21;
```

Best Local Similarity 57.9%; Pred. No. 2.3e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

```
Qy        995 TATGCTGTGGTGCTTAATG 1013
              :|:||:|:||:||::||:|
Db          1 UAUGCUGUGGUGCUUAAUG 19
```

RESULT 615
ADE27662/c
ID ADE27662 standard; RNA; 22 BP.
XX
AC ADE27662;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:606.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 606; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 1 Other;

Query Match 0.4%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2520 TGCTGGACATGAGATGGAG 2538
              ||||||||||||||||||
Db         19 TGCTGGACATGAGATGGAG 1
```

RESULT 616
ADE27654/c
ID ADE27654 standard; RNA; 22 BP.
XX
AC ADE27654;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:598.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 598; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 1 Other;

Query Match 0.4%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2520 TGCTGGACATGAGATGGAG 2538
             ||||||||||||||||||
Db         19 TGCTGGACATGAGATGGAG 1
```

RESULT 617
ADE27657
ID ADE27657 standard; RNA; 23 BP.
XX
AC ADE27657;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:601.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 601; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 23 BP; 3 A; 2 C; 6 G; 2 T; 8 U; 2 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   57.9%;  Pred. No. 2.6e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        995 TATGCTGTGGTGCTTAATG 1013
              :|:||:|:||:||::||:|
Db          2 UAUGCUGUGGUGCUUAAUG 20
```

RESULT 618
ADE27649
ID ADE27649 standard; RNA; 23 BP.
XX
AC ADE27649;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:593.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 593; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 23 BP; 3 A; 2 C; 6 G; 2 T; 8 U; 2 Other;

```
  Query Match             0.4%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   57.9%;  Pred. No. 2.6e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        995 TATGCTGTGGTGCTTAATG 1013
```

```
                :|:||:|:||:||::||:|
Db          2 UAUGCUGUGGUGCUUAAUG 20


RESULT 619
ADG30272
ID   ADG30272 standard; RNA; 23 BP.
XX
AC   ADG30272;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 838.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 838; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 23 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 2 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   78.9%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2520 TGCTGGACATGAGATGGAG 2538
                :||:|||||:||||:||||
Db          2 UGCUGGACAUGAGAUGGAG 20


RESULT 620
ADG30271
ID   ADG30271 standard; RNA; 23 BP.
XX
AC   ADG30271;
XX
DT   26-FEB-2004  (first entry)
XX
DE   SCD-targeted siNA DNA-RNA hybrid - SEQ ID 837.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; SCD.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 837; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 23 BP; 3 A; 2 C; 6 G; 2 T; 8 U; 2 Other;

  Query Match             0.4%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   57.9%;  Pred. No. 2.6e+02;
  Matches   11;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        995 TATGCTGTGGTGCTTAATG 1013
              :|:||:|:||:||::||:|
Db          2 UAUGCUGUGGUGCUUAAUG 20
```

RESULT 621
ABZ89487/c
ID ABZ89487 standard; DNA; 20 BP.
XX
AC ABZ89487;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4729; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| ||||
Db         20 TTTTTTTTTTTTTTTGGTT 1
```

RESULT 622
ABD25717/c
ID ABD25717 standard; DNA; 20 BP.
XX
AC ABD25717;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI034360-derived oligonucleotide SEQ ID 4729.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4729; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

```
CC   transplantation rejection, pulmonary infections, bronchitis or cancer.
CC   The reduced adenosine content of the anti-sense oligos corresponding to
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| ||||
Db         20 TTTTTTTTTTTTTTTTGGTT 1


RESULT 623
ADL59750/c
ID   ADL59750 standard; DNA; 20 BP.
XX
AC   ADL59750;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1999.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1999; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| ||
Db         20 TTTTTTTTTTTTTTTGGCTT 1


RESULT 624
AAQ75617
ID   AAQ75617 standard; DNA; 21 BP.
XX
AC   AAQ75617;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 2.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| ||||
Db          2 TTTTTTTTTTTTTTTTGGTT 21
```

```
RESULT 625
ADF83488/c
ID   ADF83488 standard; DNA; 21 BP.
XX
AC   ADF83488;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human MC1R gene-specific primer #4.
XX
KW   Predisposition; melanoma; human; cyclin dependent kinase inhibitor 2A;
KW   CDKN2A; mutant allele; melanocortin-1 receptor; MC1R; variant allele;
KW   gene-specific; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2003175721-A1.
XX
PD   18-SEP-2003.
XX
PF   28-MAR-2002; 2002US-00108732.
XX
PR   28-MAR-2001; 2001US-0279515P.
XX
PA   (BOXN/) BOX N F.
PA   (DUFF/) DUFFY D L.
PA   (HAYW/) HAYWARD N K.
PA   (MART/) MARTIN N G.
PA   (STUR/) STURM R A.
PA   (GRUI/) GRUIS N A.
PA   (VVEL/) VAN DER VELDEN P A.
PA   (BERG/) BERGMAN W.
PA   (FRAN/) FRANTS R R.
XX
PI   Box NF,  Duffy DL,  Hayward NK,  Martin NG,  Sturm RA,  Gruis NA;
PI   Van Der Velden PA,  Bergman W,  Frants RR;
XX
DR   WPI; 2003-898522/82.
XX
PT   Identifying a predisposition to melanoma comprises determining whether an
PT   individual carrying a cyclin dependent kinase inhibitor 2A (CDKN2A)
PT   mutant allele also carries a melanocortin-1 receptor (MC1R) variant
PT   allele.
XX
PS   Claim 14; SEQ ID NO 42; 30pp; English.
XX
CC   The present invention relates to a method of identifying a predisposition
CC   to melanoma. The method comprises determining whether a human individual
CC   carrying a cyclin dependent kinase inhibitor 2A (CDKN2A) mutant allele
CC   also carries a melanocortin-1 receptor (MC1R) variant allele, where the
CC   presence of a MC1R variant allele indicates a predisposition of the
CC   individual to melanoma greater than that expected as a consequence of the
CC   CDKN2A mutant allele alone. Also disclosed is a kit for identifying a
CC   predisposition to melanoma. The kit comprises MC1R gene-specific primers
CC   and/or CDKN2A gene-specific primers and MC1R variant allele-specific
CC   probes and/or CDKN2A mutant allele-specific probes. The kit further
CC   comprises MC1R sequencing primers and/or CDKN2A sequencing primers. The
CC   method is useful for identifying a predisposition to melanoma. The
CC   present sequence represents a gene-specific primer that can be used in
CC   the method of the present invention.
XX
SQ   Sequence 21 BP; 6 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 2.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4695 TTGCTGTGTGACCCTGGGCA 4714
              || |||||||||||||||||
Db         20 TTCCTGTGTGACCCTGGGCA 1
```

```
RESULT 626
AAQ75028/c
ID   AAQ75028 standard; DNA; 23 BP.
XX
AC   AAQ75028;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 2.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 23;
  Best Local Similarity   95.0%;  Pred. No. 3.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||||||| |
Db         20 TTTTTTTTTTTTTTTGGGGT 1
```

```
RESULT 627
AAQ75029
ID   AAQ75029 standard; RNA; 23 BP.
XX
AC   AAQ75029;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1995  (first entry)
XX
DE   LCR oligo 3.
XX
KW   Synthetic oligo; solid phase immunoassay; ss.
XX
OS   Synthetic.
```

```
XX
PN   WO9426932-A1.
XX
PD   24-NOV-1994.
XX
PF   13-MAY-1994;   94WO-US005407.
XX
PR   13-MAY-1993;   93US-00061694.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fields HA,  Khudyakov YE;
XX
DR   WPI; 1995-006819/01.
XX
PT   Solid phase immunoassay using oligo:nucleotide as label - also new
PT   conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT   diagnosing hepatitis C or E virus infection.
XX
PS   Example; Page 13; 34pp; English.
XX
CC   AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC   They are used in a method for detecting an antigen in a subject. The
CC   method involves binding the antigen to a solid support and then reacting
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
CC   AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 23;
  Best Local Similarity   20.0%;  Pred. No. 3.2e+02;
  Matches    4;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ::::::::::::::::||| |
Db          4 UUUUUUUUUUUUUUUGGGGT 23


RESULT 628
AAV54171
ID   AAV54171 standard; cDNA; 18 BP.
XX
AC   AAV54171;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 8.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTGG 18


RESULT 629
AAZ90641
ID   AAZ90641 standard; DNA; 18 BP.
XX
AC   AAZ90641;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #2.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTGG 18
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```
RESULT 630
AAQ75559
ID   AAQ75559 standard; DNA; 20 BP.
XX
AC   AAQ75559;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGGG 20


RESULT 631
AAQ75607
ID   AAQ75607 standard; DNA; 21 BP.
XX
AC   AAQ75607;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGGG 20


RESULT 632
AAQ75608
ID   AAQ75608 standard; DNA; 21 BP.
XX
AC   AAQ75608;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
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SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGGG 20


RESULT 633
AAQ75610
ID   AAQ75610 standard; DNA; 21 BP.
XX
AC   AAQ75610;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGGG 20


RESULT 634
ADK01302
ID   ADK01302 standard; DNA; 21 BP.
XX
AC   ADK01302;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Rat DNA microarray capture oligonucleotide #22.
XX
KW   ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW   blood; nerve; germ cell; food additive; food supplement.
XX
OS   Rattus sp.
XX
PN   DE10208794-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2002; 2002DE-01008794.
XX
PR   28-FEB-2002; 2002DE-01008794.
XX
PA   (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI   Boekenkamp D,  Dieck HT,  Hoppe H;
XX
DR   WPI; 2003-714082/68.
XX
PT   Sorting single-stranded nucleic acid, useful for analyzing expression
PT   patterns and screening active agents, uses capture agent with variable
PT   and constant regions.
XX
PS   Example; Page 5; 8pp; German.
XX
CC   This invention describes a novel method for sorting single-stranded
CC   nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC   reading out, where the nucleic acids are selectively bound using capture
CC   agents that are (a) immobilised on the surface of a solid matrix and (b)
CC   comprise variable and non-variable regions. The capture oligonucleotides
CC   have a 5'-invariable anchor region, the complement of which is present at
CC   least once in each nucleic acid and a 3'-variable, discriminatory region
CC   that comprises all possible combinations of up to 10 nucleotides to allow
CC   binding of particular sorts of single stranded nucleic acids. The capture
CC   agents are particularly locked nucleic acids (LNA) and the anchor region
CC   comprises a sequence of 10-50, particularly 15-25, T residues. The
CC   capture oligonucleotides are biotinylated and immobilised on a surface by
CC   interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC   metal, resin, gel, crystalline material and/or membrane, having semi-
CC   conducting properties and especially in the form of a chip. Its surface
CC   is particularly a layer of (bio)molecular filaments and binding of single
CC   stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC   physical, stimulated by an electrical field or through a molecular sieve.
CC   The method is used (i) for analysis of patterns, especially in mucosal,
CC   hair root, blood, nerve or germ cells and (ii) for determining the
CC   activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC   additives or supplements, especially minerals, trace elements, organic
CC   acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC   mixtures. The method provides rapid, inexpensive and reproducible
CC   representation of differences in pools of nucleic acids from cells. It
CC   allows imaging of the complete pattern of all nucleic acid in a cell, and
CC   can detect very small differences in the nucleic acid pool. Since the
CC   method is based on comparison of nucleic acid pools, not individual
CC   genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC   capture probes used in the method of the invention.
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGGG 21


RESULT 635
ACA89735/c
ID   ACA89735 standard; DNA; 22 BP.
XX
AC   ACA89735;
XX
```

```
DT   09-JUL-2003  (first entry)
XX
DE   Herbicide resistance polymorphic marker related primer #34.
XX
KW   Polymorphic marker; herbicide resistance; herbicide susceptible plant;
KW   herbicide resistant plant; Conyza canadensis; Lolium rigidum; goosegrass;
KW   glyphosate; paraquat; sulfonyl urea moiety; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003031937-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032637.
XX
PR   12-OCT-2001; 2001US-0328750P.
XX
PA   (MORP-) MORPHOTEK INC.
XX
PI   Chao Q,  Grasso L,  Nicolaides NC,  Sass PM;
XX
DR   WPI; 2003-430273/40.
XX
PT   Identifying polymorphic markers of herbicide resistance in a plant, by
PT   analyzing genomic DNA of herbicide resistant and susceptible plants, and
PT   identifying difference that correlate with resistance or susceptibility.
XX
PS   Example 6; Page 38; 168pp; English.
XX
CC   The invention describes a method of identifying polymorphic markers of
CC   herbicide resistance in a plant. The method involves: isolating genomic
CC   DNA from an herbicide susceptible plant and an herbicide resistant plant
CC   of the same species, performing genetic analysis and identifying
CC   differences between their genomic DNA, identifying the difference that
CC   correlate with herbicide resistance or susceptibility, thus identifying
CC   polymorphic markers. The method is useful for identifying polymorphic
CC   markers of herbicide resistance in a plant e.g. Conyza canadensis, Lolium
CC   rigidum and goosegrass species, where the herbicides include glyphosate,
CC   paraquat and sulfonyl urea moieties. This sequence represents a primer
CC   associated with the identification of polymorphic markers of herbicide
CC   resistance
XX
SQ   Sequence 22 BP; 10 A; 0 C; 11 G; 0 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 3.6e+02;
  Matches   19;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3180 CCTCTCTCTCCCTCCCTCTCTC 3201
              :||||||||| ||| |||||||
Db         22 VCTCTCTCTCTCTCTCTCTCTC 1


RESULT 636
AAQ75648
ID   AAQ75648 standard; DNA; 21 BP.
XX
AC   AAQ75648;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 3.7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTTA 4521
              |||||||||||||||  ||||
Db          1 TTTTTTTTTTTTTTTTTGTTA 21


RESULT 637
AAQ75777
ID   AAQ75777 standard; DNA; 21 BP.
XX
AC   AAQ75777;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
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```
XX
SQ   Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 3.7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTTT 2144
              |||| |||| ||||||||||||
Db          1 TTTTTTTTTTTTTTTTCTTT 21


RESULT 638
AAF99703
ID   AAF99703 standard; DNA; 22 BP.
XX
AC   AAF99703;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #819.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 3.9e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTC 21


RESULT 639
ABS78424
ID   ABS78424 standard; DNA; 22 BP.
XX
AC   ABS78424;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #908.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 3.9e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTC 21


RESULT 640
ACH03242
ID   ACH03242 standard; DNA; 22 BP.
```

XX
AC ACH03242;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #877.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 32; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 641
ADB37205
ID ADB37205 standard; DNA; 22 BP.
XX
AC ADB37205;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #819.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3181 CTCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 CTCTCTCTCTCTCTCTCTC 21

RESULT 642
ADK61705
ID ADK61705 standard; DNA; 22 BP.
XX
AC ADK61705;
XX
DT 06-MAY-2004 (first entry)
XX
DE Base containing SSR sequence #9.
XX
KW rice variety; amplification genetic marker; ds.
XX
OS Oryza sp.
XX
PN JP2003319782-A.
XX
PD 11-NOV-2003.
XX
PF 02-MAY-2002; 2002JP-00130645.
XX
PR 02-MAY-2002; 2002JP-00130645.
XX
PA (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
PA (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
XX
DR WPI; 2004-003560/01.
XX
PT Identifying rice variety using base sequence containing SSR sequence and
PT amplifying genetic marker.
XX
PS Claim 34; SEQ ID NO 9; 30pp; Japanese.
XX
CC The present invention relates to identifying a rice variety as
CC amplification genetic marker and identifying whether test rice variety is
CC any one of the 32 rice varieties e.g., Kasalath, breath which came or
CC Hayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USSR22,
CC Nihonbare. The method is useful for identifying rice variety and

```
CC   identifies excellent rice variety. The present sequence represents a base
CC   - containing SSR sequence of the invention.
XX
SQ   Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 3.9e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db          1 CTCTCTCTCTCTCTCTCTCTC 21


RESULT 643
ADK61713/c
ID   ADK61713 standard; DNA; 22 BP.
XX
AC   ADK61713;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Base containing SSR sequence #17.
XX
KW   rice variety; amplification genetic marker; ds.
XX
OS   Oryza sp.
XX
PN   JP2003319782-A.
XX
PD   11-NOV-2003.
XX
PF   02-MAY-2002; 2002JP-00130645.
XX
PR   02-MAY-2002; 2002JP-00130645.
XX
PA   (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
PA   (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
XX
DR   WPI; 2004-003560/01.
XX
PT   Identifying rice variety using base sequence containing SSR sequence and
PT   amplifying genetic marker.
XX
PS   Claim 65; SEQ ID NO 17; 30pp; Japanese.
XX
CC   The present invention relates to identifying a rice variety as
CC   amplification genetic marker and identifying whether test rice variety is
CC   any one of the 32 rice varieties e.g., Kasalath, breath which came or
CC   Hayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USSR22,
CC   Nihonbare. The method is useful for identifying rice variety and
CC   identifies excellent rice variety. The present sequence represents a base
CC   - containing SSR sequence of the invention.
XX
SQ   Sequence 22 BP; 11 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 3.9e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db         22 CTCTCTCTCTCTCTCTCTCTC 2


RESULT 644
ADR23192/c
ID   ADR23192 standard; DNA; 22 BP.
XX
AC   ADR23192;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human D16S475.R11 allele dinucleotide repeat region.
XX
KW   Alcoholism; alcohol tolerance; diagnosis; marker; D16S475; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004067763-A2.
XX
PD   12-AUG-2004.
XX
PF   27-JAN-2004; 2004WO-US002406.
XX
PR   27-JAN-2003; 2003US-0443072P.
XX
PA   (COLS ) UNIV COLORADO.
XX
PI   Tabakoff B,  Martinez L,  Hoffman P;
XX
DR   WPI; 2004-581008/56.
XX
PT   Identifying individuals predisposed to alcohol tolerance and dependence
PT   comprises screening the sample for a biomarker based on polymorphism.
XX
PS   Example 9; SEQ ID NO 4; 99pp; English.
XX
CC   The present sequence is that of the dinucleotide repeat region of the
CC   human D16S475.R11 allele ADR23191. Case-control association studies for
CC   alcohol abuse, alcohol consumption and alcohol dependence were performed
CC   using polymorphic markers in the human 16p13.3 locus and in the human
CC   16q12.2 locus. Chi-square analysis showed a negative association between
CC   multiple subject characteristics and the D16S475.R11 allele. However,
CC   upon further more sophisticated statistical analysis, this relationship
CC   could not be confirmed. The invention relates to compositions and methods
CC   for determining whether an individual is predisposed to or protected from
CC   alcoholism. It provides genetic markers useful for the diagnosis,
CC   characterisation, and treatment or prevention of alcohol tolerance, abuse
CC   and/or dependence.
XX
SQ   Sequence 22 BP; 11 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 3.9e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCTC 3201
              ||||||||| ||| |||||||
Db         21 CTCTCTCTCTCTCTCTCTCTC 1


RESULT 645
ADN34219/c
ID   ADN34219 standard; RNA; 19 BP.
XX
AC   ADN34219;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Upper strand of cyclin D1 targeted double stranded siNA #239.
XX
KW   short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic;
KW   cancer; cell-proliferation disorder; restenosis; drug screening;
KW   genetic engineering; pharmacogenomics; gene mapping;
KW   single nucleotide polymorphisms; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003072705-A2.
XX
PD   04-SEP-2003.
XX
PF   06-FEB-2003; 2003WO-US003662.
XX
PR   20-FEB-2002; 2002US-0358580P.
```

PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 17-SEP-2002; 2002US-0411275P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson J, Mcswiggen J, Beigelman L;
XX
DR WPI; 2003-689983/65.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer and restenosis, down regulates expression of at least
PT one cyclin gene.
XX
PS Example 3; SEQ ID NO 239; 144pp; English.
XX
CC The present invention relates to a short interfering nucleic acid (siNA)
CC that down regulates expression of at least one cyclin gene by RNA
CC interference. siNA are used to modulate expression of cyclin genes, in
CC cells, tissue explants or organisms, e.g. for treating a wide range of
CC cancers and other cell-proliferation disorders such as restenosis, but
CC also for drug screening, diagnosis, target identification and validation;
CC genetic engineering, pharmacogenomics, studying gene function and gene
CC mapping (e.g. of single-nucleotide polymorphisms). The present sequence
CC represents the upper strand of cyclin D1 targeted double stranded siNA
CC which is identical to the cyclin D1 transcript target sequence.
XX
SQ Sequence 19 BP; 15 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
||||||||||||||| ||||
Db 19 TTTTTTTTTTTTTTGGGGT 1

RESULT 646
ADN34458
ID ADN34458 standard; RNA; 19 BP.
XX
AC ADN34458;
XX
DT 01-JUL-2004 (first entry)
XX
DE Lower strand of cyclin D1 targeted double stranded siNA #239.
XX
KW short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic;
KW cancer; cell-proliferation disorder; restenosis; drug screening;
KW genetic engineering; pharmacogenomics; gene mapping;
KW single nucleotide polymorphisms; ss.
XX
OS Homo sapiens.
XX
PN WO2003072705-A2.
XX
PD 04-SEP-2003.
XX
PF 06-FEB-2003; 2003WO-US003662.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 17-SEP-2002; 2002US-0411275P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson J, Mcswiggen J, Beigelman L;
XX
DR WPI; 2003-689983/65.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer and restenosis, down regulates expression of at least
PT one cyclin gene.
XX
PS Example 3; SEQ ID NO 478; 144pp; English.
XX
CC The present invention relates to a short interfering nucleic acid (siNA)
CC that down regulates expression of at least one cyclin gene by RNA
CC interference. siNA are used to modulate expression of cyclin genes, in
CC cells, tissue explants or organisms, e.g. for treating a wide range of
CC cancers and other cell-proliferation disorders such as restenosis, but
CC also for drug screening, diagnosis, target identification and validation;
CC genetic engineering, pharmacogenomics, studying gene function and gene
CC mapping (e.g. of single-nucleotide polymorphisms). The present sequence
CC represents the lower strand of cyclin D1 targeted double stranded siNA.
XX
SQ Sequence 19 BP; 0 A; 0 C; 4 G; 0 T; 15 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 15.8%; Pred. No. 3.9e+02;
Matches 3; Conservative 15; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
:::::::::::::: |||:
Db 1 UUUUUUUUUUUUUUGGGGU 19

RESULT 647
ADK70862/c
ID ADK70862 standard; DNA; 19 BP.
XX
AC ADK70862;
XX
DT 06-MAY-2004 (first entry)
XX
DE 5' mRNA DNA preparation method related tag DNA sequence #30.
XX
KW DNA preparation; 5' mRNA; linker synthesis; primer synthesis;
KW gene regulation; gene expression; ss; tag.
XX
OS Unidentified.
XX
PN WO2003106672-A2.
XX
PD 24-DEC-2003.
XX
PF 12-JUN-2003; 2003WO-JP007514.
XX
PR 12-JUN-2002; 2002JP-00171851.
PR 12-AUG-2002; 2002JP-00235294.
XX
PA (RIKE) RIKEN KK.
PA (DNAF-) DNAFORM KK.
XX
PI Hayashizaki Y, Carninci P, Harbers MT;
XX
DR WPI; 2004-082194/08.
XX
PT Preparing DNA fragment corresponding to nucleotide sequence of 5' end
PT region of mRNA, by preparing nucleic acid corresponding to nucleotide
PT sequence of 5' end of mRNA, cleaving nucleic acid with restriction
PT enzyme.
XX
PS Example 5; SEQ ID NO 62; 121pp; English.
XX
CC The invention comprises a method for preparing a DNA fragment

```
CC   corresponding to a nucleotide sequence of a 5' end of an mRNA. The method
CC   is useful for synthesising a nucleotide sequence to be used as a linker
CC   or primer and selectively collecting multiple nucleic acid fragments
CC   containing information on the nucleotide sequences at the 5' end of
CC   multiple mRNA in a sample. The method is also useful for identifying
CC   regions in the genome, which are required for gene regulation and gene
CC   expression. The present DNA sequence was used in an example of the
CC   invention.
XX
SQ   Sequence 19 BP; 16 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 3.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||| |
Db         19 AGTTTTTTTTTTTTTTTG 1


RESULT 648
AAQ75561
ID   AAQ75561 standard; DNA; 20 BP.
XX
AC   AAQ75561;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||| |||
Db          2 TTTTTTTTTTTTTTTTGGT 20


RESULT 649
AAQ97426
ID   AAQ97426 standard; DNA; 20 BP.
XX
AC   AAQ97426;
XX
DT   20-MAR-1996  (first entry)
XX
DE   Phage lambda (1841-1860) complementary downstream PCR primer CF1005.
XX
KW   PCR amplification; thermostable DNA polymerase; combination;
KW   large fragment; genomic mapping; sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   EP669401-A2.
XX
PD   30-AUG-1995.
XX
PF   16-FEB-1995;   95EP-00102141.
XX
PR   25-FEB-1994;   94US-00203198.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Cheng S;
XX
DR   WPI; 1995-294352/39.
XX
PT   PCR amplification of long nucleic acid sequences - using a combination of
PT   the Thermus thermophilus and pref. Thermococcus litoralis DNA polymerase.
XX
PS   Example 2; Page 13; 25pp; English.
XX
CC   A set of primers (Q97424-Q97445) was designed to enable the PCR
CC   amplification of phage lambda target sequences ranging in size from 1.5-
CC   42.2 kb in length. Each primer of the set was designed to have approx.
CC   the same optimal annealing temp. (Tm= ca.68 deg.C), formimg a hybrid of
CC   12 G-C pairings and 8-11 A-T pairings. A new method was used to amplify
CC   the large genomic sequences in which Thermus thermophilus DNA polymerase
CC   was used in combination with a second DNA polymerase from Thermococcus
CC   litoralis, Pyrococcus sp. or Thermatoga maritima. Amplified products of
CC   22.8 kb, 39 kb and (at lower yields) 42.2 kb were observed. The present
CC   sequence (primer CF1005) is complementary to nucleotides 1841-1860 of the
CC   phage lambda genome sequence (Genbank Acc.No. M17233) and has a Tm of 66
CC   deg.C
XX
SQ   Sequence 20 BP; 1 A; 9 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2269 CTCTTTCTGCTCTGCCATC 2287
              ||||||| ||||||||||
Db          2 CTCTTTCCGCTCTGCCATC 20


RESULT 650
ABL57547/c
ID   ABL57547 standard; DNA; 20 BP.
XX
AC   ABL57547;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly n.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
```

XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2384 CAAAAATAAAATATATATA 2402
              |||||| ||||||||||||
Db         19 CAAAAAAAAAATATATATA 1
```

RESULT 651
AAI70284
ID AAI70284 standard; DNA; 20 BP.
XX
AC AAI70284;
XX
DT 07-JAN-2002 (first entry)
XX
DE Phage lambda genome downstream PCR primer CF1005.
XX
KW DNA polymerase; phage lambda; PCR primer; ss.
XX
OS Bacteriophage lambda.
XX
PN EP1130118-A2.
XX
PD 05-SEP-2001.
XX
PF 16-FEB-1995; 2001EP-00113936.
XX
PR 25-FEB-1994; 94US-00203198.
PR 16-FEB-1995; 95EP-00102141.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Cheng S;
XX
DR WPI; 2001-640282/74.
XX
PT New DNA polymerase composition consisting of a combination of a first DNA
PT polymerase and a second DNA polymerase, useful for amplifying nucleic
PT acids, particularly long nucleic acid sequences by PCR.
XX
PS Example 1; Page 13; 26pp; English.
XX
CC The invention provides a DNA polymerase composition for the PCR
CC amplification of long (over 10 kb) nucleic acid sequences. The
CC composition includes the DNA polymerase of Thermus thermophilus and a
CC second, thermostable, DNA polymerase that provides 3'-to-5' exonuclease
CC activity. Use of the composition was demonstrated for the amplification
CC of phage lambda genomic sequences of 1.5-42.2 kb, with the second DNA
CC polymerase provided by Thermotoga maritima. Upstream primers (see
CC AAI70282-83) were designed to be used with each of a set of downstream
CC primers (see AAI70284-303) including the present primer, CF1005,
CC resulting in a series of target sequences increasing in length by 1-3 kb.
CC Each primer was designed to have approximately the same optimal annealing
CC temperature (68 degree C) by selecting primer sequences of 20-23 bp
CC length such that the hybrid duplex formed between the primer and target
CC sequence would have an overall composition of 12 G-C pairings and 8-11 A-
CC T pairings. Primer CF1005 is complementary to nucleotides 1841-1860 of
CC the phage lambda genome
XX
SQ Sequence 20 BP; 1 A; 9 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2269 CTCTTTCTGCTCTGCCATC 2287
              ||||||| ||||||||||||
Db          2 CTCTTTCCGCTCTGCCATC 20
```

RESULT 652
ABL45057
ID ABL45057 standard; DNA; 20 BP.
XX
AC ABL45057;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:2101.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.

XX
PT Arraying genome clones.
XX
PS Claim 4; Page 46; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4705 ACCCTGGGCAAGTCACTTA 4723
||||||||||| |||||||
Db 2 ACCCTGGGCAACTCACTTA 20

RESULT 653
ABA97632/c
ID ABA97632 standard; DNA; 20 BP.
XX
AC ABA97632;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly n nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2384 CAAAAATAAAATATATATA 2402
|||||| ||||||||||||
Db 19 CAAAAAAAAAATATATATA 1

RESULT 654
ADB25743
ID ADB25743 standard; DNA; 20 BP.
XX
AC ADB25743;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse connective tissue growth factor antisense oligo DNA (SeqID 136).
XX
KW antisense; mouse; murine; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rP2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003053340-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
XX
PT New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
PS Claim 3; Page 89; 139pp; English.
XX
CC This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2,

CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC mouse CTGF of the invention.
XX
SQ Sequence 20 BP; 11 A; 1 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2392 AAATATATATACATATATA 2410
||||||||||| |||||||
Db 2 AAATATATATATATATATA 20

RESULT 655
ABZ85669
ID ABZ85669 standard; DNA; 20 BP.
XX
AC ABZ85669;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 911; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTTCTTTTTTTCT 2142
|||| ||||||||||||||
Db 2 TTTTTTTTTCTTTTTTTCT 20

RESULT 656
ABZ85532/c
ID ABZ85532 standard; DNA; 20 BP.
XX
AC ABZ85532;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 774; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
||||||||||||||||| |
Db 19 TTTTTTTTTTTTTTTGGCT 1

RESULT 657
ABZ89014/c
ID ABZ89014 standard; DNA; 20 BP.
XX
AC ABZ89014;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4256; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
||||||||||||||||| |||
Db 20 TTTTTTTTTTTTTTTAGGT 2

RESULT 658
ABD21762/c
ID ABD21762 standard; DNA; 20 BP.
XX
AC ABD21762;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stanniocalcin-derived oligo SEQ ID 774.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 774; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
||||||||||||||||| |
Db 19 TTTTTTTTTTTTTTTGGCT 1

RESULT 659
ABD25244/c
ID ABD25244 standard; DNA; 20 BP.
XX
AC ABD25244;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI051839-derived oligonucleotide SEQ ID 4256.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4256; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
||||||||||||||| |||
Db 20 TTTTTTTTTTTTTTTAGGT 2

RESULT 660
ABD21899
ID ABD21899 standard; DNA; 20 BP.
XX
AC ABD21899;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stanniocalcin-derived oligo SEQ ID 911.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 911; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTTCTTTTTTTCT 2142
|||| ||||||||||||||||
Db 2 TTTTTTTTTCTTTTTTTCT 20

RESULT 661
ADG86989/c
ID ADG86989 standard; cDNA; 20 BP.
XX
AC ADG86989;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PPAR antisense oligonucleotoide target sequence #51.
XX
KW Human; ss; PPAR delta; peroxisome proliferative activated receptor delta;
KW antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer;
KW osteoporosis; diabetes; endocrine disorder.
XX
OS Homo sapiens.
XX
PN US2003224514-A1.
XX
PD 04-DEC-2003.
XX
PF 31-MAY-2002; 2002US-00160807.
XX
PR 31-MAY-2002; 2002US-00160807.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde W, Freier SM, Watt AT;
XX
DR WPI; 2004-022078/02.
XX
PT New antisense oligonucleotides of 8-80 nucleobases, useful for treating
PT cancer, diabetes, osteoporosis or various endocrine disorders.
XX
PS Example 16; SEQ ID NO 225; 155pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising 8-80
CC nucleobases in length targeted to the coding region of a nucleic acid
CC molecule encoding PPAR-delta (peroxisome proliferative activated receptor
CC delta), where the antisense compound inhibits the expression of the PPAR-
CC delta and has any of the 66 sequences of 20 amino acids fully defined in
CC the specification. Also included are a compound of 8-80 nucleobases in
CC length that specifically hybridises with at least an 8-nucleobase portion
CC of a preferred target region on a nucleic acid molecule encoding PPAR-
CC delta and a composition comprising the antisense oligonucleotide and a
CC carrier. The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage (preferably a phosphorothioate linkage), at least
CC one sugar moiety (preferably 2'-O-methoxyethyl moiety) and at least one
CC modified nucleobase (which is a 5-methyl cytosine). The antisense
CC compounds are useful for treating cancer, osteoporosis, diabetes or
CC various endocrine disorders. The Human PPAR delta gene is located on
CC chromosome 6p21. The present sequence is a human PPAR delta cDNA target
CC sequence for the antisense oligonucleotides of the invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3274 CAGTCCCCTCTCTCTGGGT 3292
||| ||||||||||||||||
Db 19 CAGGCCCCTCTCTCTGGGT 1

RESULT 662
ADG86844
ID ADG86844 standard; DNA; 20 BP.
XX
AC ADG86844;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PPAR antisense oligonucleotide ISIS 136923.
XX
KW Human; ss; PPAR delta; peroxisome proliferative activated receptor delta;
KW antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer;
KW osteoporosis; diabetes; endocrine disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages and all cytidines are 5

```
FT                   -methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residue"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residue"
XX
PN   US2003224514-A1.
XX
PD   04-DEC-2003.
XX
PF   31-MAY-2002; 2002US-00160807.
XX
PR   31-MAY-2002; 2002US-00160807.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Gaarde W,  Freier SM,  Watt AT;
XX
DR   WPI; 2004-022078/02.
XX
PT   New antisense oligonucleotides of 8-80 nucleobases, useful for treating
PT   cancer, diabetes, osteoporosis or various endocrine disorders.
XX
PS   Claim 1; SEQ ID NO 80; 155pp; English.
XX
CC   The invention relates to an antisense oligonucleotide comprising 8-80
CC   nucleobases in length targeted to the coding region of a nucleic acid
CC   molecule encoding PPAR-delta (peroxisome proliferative activated receptor
CC   delta), where the antisense compound inhibits the expression of the PPAR-
CC   delta and has any of the 66 sequences of 20 amino acids fully defined in
CC   the specification. Also included are a compound of 8-80 nucleobases in
CC   length that specifically hybridises with at least an 8-nucleobase portion
CC   of a preferred target region on a nucleic acid molecule encoding PPAR-
CC   delta and a composition comprising the antisense oligonucleotide and a
CC   carrier. The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage (preferably a phosphorothioate linkage), at least
CC   one sugar moiety (preferably 2'-O-methoxyethyl moiety) and at least one
CC   modified nucleobase (which is a 5-methyl cytosine). The antisense
CC   compounds are useful for treating cancer, osteoporosis, diabetes or
CC   various endocrine disorders. The Human PPAR delta gene is located on
CC   chromosome 6p21. The present sequence is an antisense oligonucleotide of
CC   the invention targeting human PPAR delta.
XX
SQ   Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db          2 CAGGCCCCTCTCTCTGGGT 20


RESULT 663
ADH70655/c
ID   ADH70655 standard; DNA; 20 BP.
XX
AC   ADH70655;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #445.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 849; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2126 TTCTTTTCTTTTTTTCTTT 2144
              ||||||| ||||||||||
Db         20 TTCTTTTTTTTTTTTCTTT 2


RESULT 664
ADJ25433
ID   ADJ25433 standard; DNA; 20 BP.
XX
AC   ADJ25433;
XX
DT   20-MAY-2004  (first entry)
XX
```

```
DE   Human endothelial lipase antisense oligonucleotide, SEQ ID 3831.
XX
KW   Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW   Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW   cardiovascular disorder; metabolic syndrome X; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 4 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2004009541-A2.
XX
PD   29-JAN-2004.
XX
PF   18-JUL-2003; 2003WO-US022410.
XX
PR   19-JUL-2002; 2002US-0397106P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Bhat BG;
XX
DR   WPI; 2004-132912/13.
XX
PT   New antisense oligonucleotide for modulating endothelial lipase
PT   expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT   high density lipoprotein or cardiovascular disorders.
XX
PS   Claim 3; SEQ ID NO 3831; 1007pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADJ21603-
CC   ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC   (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC   with and inhibits the expression of EL. The antisense oligonucleotides
CC   are useful for modulating the expression of endothelial lipase in cells
CC   or tissues to treat diseases associated with EL expression, such as
CC   dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC   disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC   used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ   Sequence 20 BP; 11 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match              0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4753 TAAAATGGGGATAATAATA 4771
              |||||| ||||||||||||
Db          1 TAAAATAGGGATAATAATA 19


RESULT 665
ADJ25040
ID   ADJ25040 standard; DNA; 20 BP.
XX
AC   ADJ25040;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human endothelial lipase antisense oligonucleotide, SEQ ID 3438.
XX
KW   Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW   Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW   cardiovascular disorder; metabolic syndrome X; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 4 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2004009541-A2.
XX
PD   29-JAN-2004.
XX
PF   18-JUL-2003; 2003WO-US022410.
XX
PR   19-JUL-2002; 2002US-0397106P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Bhat BG;
XX
DR   WPI; 2004-132912/13.
XX
PT   New antisense oligonucleotide for modulating endothelial lipase
PT   expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT   high density lipoprotein or cardiovascular disorders.
XX
PS   Claim 3; SEQ ID NO 3438; 1007pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADJ21603-
CC   ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC   (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC   with and inhibits the expression of EL. The antisense oligonucleotides
CC   are useful for modulating the expression of endothelial lipase in cells
CC   or tissues to treat diseases associated with EL expression, such as
CC   dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC   disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC   used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ   Sequence 20 BP; 11 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match              0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4753 TAAAATGGGGATAATAATA 4771
              |||||| ||||||||||||
Db          2 TAAAATAGGGATAATAATA 20


RESULT 666
ADL59745/c
ID   ADL59745 standard; DNA; 20 BP.
XX
AC   ADL59745;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1994.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
```

```
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate backbone. All cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1994; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||||| ||
Db         20 TTTTTTTTTTTTTTGGCTT 2


RESULT 667
ADL59751/c
ID   ADL59751 standard; DNA; 20 BP.
XX
AC   ADL59751;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 2000.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 2000; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 16 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGGT 4519
              |||||||||||||||| |
Db         19 TTTTTTTTTTTTTTGGCT 1


RESULT 668
ADL34927/c
ID   ADL34927 standard; DNA; 20 BP.
XX
AC   ADL34927;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human PPAR-delta target site ID 50043.
XX
KW   antisense; PPAR-delta; human; hybridisation; inhibitor;
KW   phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   US2004063129-A1.
XX
PD   01-APR-2004.
XX
PF   05-SEP-2003; 2003US-00655847.
XX
PR   31-MAY-2002; 2002US-00160807.
XX
PA   (GAAR/) GAARDE W.
PA   (FREI/) FREIER S M.
PA   (WATT/) WATT A T.
```

```
XX
PI   Gaarde W,  Freier SM,  Watt AT;
XX
DR   WPI; 2004-282460/26.
XX
PT   New antisense oligonucleotide, having a sequence targeted to a nucleic
PT   acid encoding PPAR-delta, useful for preparing a composition for treating
PT   hyperproliferative disorder, e.g., cancer.
XX
PS   Example 16; SEQ ID NO 225; 0pp; English.
XX
CC   This invention describes novel antisense oligonucleotides targeted to a
CC   nucleic acid encoding PPAR-delta, which specifically hybridise to and
CC   inhibit expression of PPAR-delta. The oligonucleotide specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on the
CC   nucleic acid molecule encoding the PPAR-delta and comprises at least one
CC   modified internucleoside linkage, which is a phosphorothioate linkage, at
CC   least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar
CC   moiety or at least one modified nucleobase, which is a 5-methylcytosine.
CC   The antisense oligonucleotides are useful for preparing a composition for
CC   treating hyperproliferative disorders, e.g., cancer. The oligonucleotides
CC   of the invention have cytostatic activity and can be used for gene
CC   therapy.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db         19 CAGGCCCCTCTCTCTGGGT 1


RESULT 669
ADL34782
ID   ADL34782 standard; DNA; 20 BP.
XX
AC   ADL34782;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Antisense oligonucleotide ISIS 136923.
XX
KW   antisense; PPAR-delta; human; hybridisation; inhibitor;
KW   phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; gene therapy; ss;
KW   primer.
XX
OS   Synthetic.
XX
PN   US2004063129-A1.
XX
PD   01-APR-2004.
XX
PF   05-SEP-2003; 2003US-00655847.
XX
PR   31-MAY-2002; 2002US-00160807.
XX
PA   (GAAR/) GAARDE W.
PA   (FREI/) FREIER S M.
PA   (WATT/) WATT A T.
XX
PI   Gaarde W,  Freier SM,  Watt AT;
XX
DR   WPI; 2004-282460/26.
XX
PT   New antisense oligonucleotide, having a sequence targeted to a nucleic
PT   acid encoding PPAR-delta, useful for preparing a composition for treating
PT   hyperproliferative disorder, e.g., cancer.
XX
PS   Example 15; SEQ ID NO 80; 0pp; English.
XX
CC   This invention describes novel antisense oligonucleotides targeted to a
CC   nucleic acid encoding PPAR-delta, which specifically hybridise to and
CC   inhibit expression of PPAR-delta. The oligonucleotide specifically
CC   hybridises with at least an 8-nucleobase portion of an active site on the
CC   nucleic acid molecule encoding the PPAR-delta and comprises at least one
CC   modified internucleoside linkage, which is a phosphorothioate linkage, at
CC   least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar
CC   moiety or at least one modified nucleobase, which is a 5-methylcytosine.
CC   The antisense oligonucleotides are useful for preparing a composition for
CC   treating hyperproliferative disorders, e.g., cancer. The oligonucleotides
CC   of the invention have cytostatic activity and can be used for gene
CC   therapy.
XX
SQ   Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3274 CAGTCCCCTCTCTCTGGGT 3292
              ||| ||||||||||||||||
Db          2 CAGGCCCCTCTCTCTGGGT 20


RESULT 670
AAQ61989
ID   AAQ61989 standard; DNA; 21 BP.
XX
AC   AAQ61989;
XX
DT   25-MAR-2003  (revised)
DT   04-NOV-1994  (first entry)
XX
DE   HIV replication inhibiting oligomer, T13G4T4.
XX
KW   Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
KW   human cytomegalovirus; influenza virus; inflammation; telomere length;
KW   neurological disorders; phospholipase A2 activity; hyperproliferation;
KW   malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /note= "Labeled with 32P"
XX
PN   WO9408053-A1.
XX
PD   14-APR-1994.
XX
PF   29-SEP-1993;   93WO-US009297.
XX
PR   29-SEP-1992;   92US-00954185.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Hanecak RC,  Anderson KP,  Bennett CF,  Chiang M,  Brown-Driver VL;
PI   Ecker DJ,  Vickers TA,  Wyatt JR,  Imbach JL;
XX
DR   WPI; 1994-135613/16.
XX
PT   New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT   of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT   of chromosomes.
XX
PS   Example 21; Page 60; 144pp; English.
XX
CC   This sequence may be used for inhibiting replication of human immuno-
CC   deficiency virus (HIV). Oligonucleotides such as this may also be used
CC   for inhibiting activity of HSV, human cytomegalovirus or influenza virus,
CC   or for treating inflammatory and neurological disorders caused by
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CC   phospholipase A2 activity in cases of hyper- proliferation, malignancy,
CC   cardiovascular disease and snake bite. They may also be used for
CC   inhibiting division of malignant cells by modualting telomere length,
CC   which may also retard aging. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTTGGGGTT 19


RESULT 671
AAQ75657
ID   AAQ75657 standard; DNA; 21 BP.
XX
AC   AAQ75657;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              |||||||||||||||| ||
Db          3 TTTTTTTTTTTTTTTGCGT 21


RESULT 672
AAQ75618
ID   AAQ75618 standard; DNA; 21 BP.
XX
AC   AAQ75618;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              |||||||||||||||| |||
Db          2 TTTTTTTTTTTTTTTTGGT 20


RESULT 673
AAQ75625
ID   AAQ75625 standard; DNA; 21 BP.
XX
AC   AAQ75625;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
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DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||| ||
Db          3 TTTTTTTTTTTTTTTGAGT 21


RESULT 674
AAQ75641
ID   AAQ75641 standard; DNA; 21 BP.
XX
AC   AAQ75641;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||| ||
Db          3 TTTTTTTTTTTTTTTGTGT 21


RESULT 675
AAQ75615
ID   AAQ75615 standard; DNA; 21 BP.
XX
AC   AAQ75615;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||| |||
Db          2 TTTTTTTTTTTTTTTTGGT 20


RESULT 676
AAQ75705
ID   AAQ75705 standard; DNA; 21 BP.
XX
AC   AAQ75705;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
```

```
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||| |||
Db          3 TTTTTTTTTTTTTTTAGGT 21


RESULT 677
AAQ75737
ID   AAQ75737 standard; DNA; 21 BP.
XX
AC   AAQ75737;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||| |||
Db          3 TTTTTTTTTTTTTTTCGGT 21


RESULT 678
AAQ75621
ID   AAQ75621 standard; DNA; 21 BP.
XX
AC   AAQ75621;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||| |
Db          3 TTTTTTTTTTTTTTTGGCT 21


RESULT 679
AAQ75613
ID   AAQ75613 standard; DNA; 21 BP.
XX
AC   AAQ75613;
```

```
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||| |
Db          3 TTTTTTTTTTTTTTTGGAT 21


RESULT 680
AAQ75616
ID   AAQ75616 standard; DNA; 21 BP.
XX
AC   AAQ75616;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGT 4519
              ||||||||||||||||| |||
Db          2 TTTTTTTTTTTTTTTTGGT 20


RESULT 681
AAT35001
ID   AAT35001 standard; DNA; 21 BP.
XX
AC   AAT35001;
XX
DT   25-MAR-2003  (revised)
DT   03-DEC-1996  (first entry)
XX
DE   HIV inhibitor #4.
XX
KW   HIV; infection inhibitor; triplex forming; purine rich promoter; V3 loop;
KW   transcription inhibitor; gp120 protein; viral growth; enzyme inhibitor;
KW   PLA2; telomere length; glove coating; condom; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .21
FT                   /*tag=  a
FT                   /note= "phosphorothioate nucleotides"
XX
PN   US5523389-A.
XX
PD   04-JUN-1996.
XX
PF   28-SEP-1993;   93US-00128011.
XX
PR   29-SEP-1992;   92US-00954185.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Imbach JL,  Ecker DJ,  Wyatt JR;
XX
DR   WPI; 1996-285782/29.
XX
PT   New octa:nucleotide with guanosine quartet and phosphoro:thioate links -
PT   is inhibitor of HIV infection by binding to the V3 loop.
XX
PS   Example 3; Col 8; 14pp; English.
XX
CC   AAT34998-T35001 represent HIV inhibitors. Sequences containing only G and
CC   T residues (such as these sequences) are triplex forming
CC   oligonucleotides, and form purine rich promoter elements used to inhibit
CC   transcription. These sequences bind to the HIV gp120 protein at the V3
CC   loop via the internal guanosine quartet. This binding prevents cell-to-
CC   cell and virus-to-cell infection. The sequences may also be used for
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CC   inhibiting viral growth, and other viral genes, for inhibiting the enzyme
CC   PLA2, and to modulate telomere length. In some cases these sequences need
CC   to be chemically modified. The chemically modified oligonucleotides
CC   preferably include at least one phosphorothioate linkage. Other modified
CC   intersugar links, or 2'-modified sugar residues can also be used. These
CC   oligonucleotides can be used for coating gloves, condoms, etc, or for
CC   topical application. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| |||||
Db          1 TTTTTTTTTTTTTTGGGGTT 19


RESULT 682
AAT76098
ID   AAT76098 standard; DNA; 21 BP.
XX
AC   AAT76098;
XX
DT   12-SEP-1997  (first entry)
XX
DE   Human histidine decarboxylase antisense oligonucleotide HUMHDCAS2.
XX
KW   Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW   chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS   Synthetic.
XX
PN   WO9640162-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009306.
XX
PR   07-JUN-1995;   95US-00474497.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW,  Metzger WJ;
XX
DR   WPI; 1997-051871/05.
XX
PT   Treatment of airway diseases such as asthma - by topically applying
PT   adenosine-free antisense oligo:nucleotide to airway epithelium of
PT   subject.
XX
PS   Claim 5; Page 26; 71pp; English.
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide HUMHDCAS2
CC   specific for the human histidine decarboxylase. The method can be used to
CC   treat airway diseases such as cystic fibrosis, asthma, chronic
CC   obstructive pulmonary disease, bronchitis and other airway diseases
CC   characterised by an inflammatory response. By eliminating adenosine from
CC   the antisense ON, its liberation upon antisense degradation is prevented,
CC   thereby preventing adenosine- induced bronchoconstriction in patients
CC   with hyper-reactive airways
XX
SQ   Sequence 21 BP; 0 A; 10 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCT 3200
              ||||||||||||| ||||||
Db          1 TCTCTCTCCCTCTCTCTCT 19


RESULT 683
AAX53903
ID   AAX53903 standard; DNA; 21 BP.
XX
AC   AAX53903;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Histidine decarboxylase receptor antisense oligonucleotide.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 45; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 21 BP; 0 A; 10 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3182 TCTCTCTCCCTCCCTCTCT 3200
              ||||||||||||| ||||||
Db          1 TCTCTCTCCCTCTCTCTCT 19


RESULT 684
AAA33346
ID   AAA33346 standard; DNA; 21 BP.
XX
AC   AAA33346;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1035.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Claim 18; Page 394; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 21 BP; 0 A; 10 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match              0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCT 3200
              ||||||||||||| ||||||
Db          1 TCTCTCTCCCTCTCTCTCT 19


RESULT 685
AAF19468
ID   AAF19468 standard; DNA; 21 BP.
XX
AC   AAF19468;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human histidine decarboxylase polynucleotide fragment #1035.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 141; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
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CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 21 BP; 0 A; 10 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCT 3200
              ||||||||||||| ||||||
Db          1 TCTCTCTCCCTCTCTCTCT 19


RESULT 686
ABS98544/c
ID   ABS98544 standard; DNA; 21 BP.
XX
AC   ABS98544;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human acetyl choline muscarinic receptor 3 polymorphic sequence #10.
XX
KW   Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 28; Page 160; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   polymorphic DNA sequence of the invention
XX
SQ   Sequence 21 BP; 10 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 4.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2392 AAATATATATACATATATA 2410
              | ||||||||||||||||||
Db         20 ATATATATATACATATATA 2


RESULT 687
ABZ95162
ID   ABZ95162 standard; DNA; 21 BP.
XX
AC   ABZ95162;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human histidine decarboxylase antisense fragment no.1025.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
```

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10404; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 0 A; 10 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3182 TCTCTCTCCCTCCCTCTCT 3200
||||||||||||| ||||||
Db 1 TCTCTCTCCCTCTCTCTCT 19

RESULT 688
ADK01304
ID ADK01304 standard; DNA; 21 BP.
XX
AC ADK01304;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #24.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGT 4519
|||||||||||||||| |||
Db 3 TTTTTTTTTTTTTTTTGGT 21

RESULT 689
ABD19062
ID ABD19062 standard; DNA; 21 BP.
XX
AC ABD19062;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human histidine decarboxylase DNA fragment 1025.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.

XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 10404; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 21 BP; 0 A; 10 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3182 TCTCTCTCCCTCCCTCTCT 3200
||||||||||| ||||||
Db 1 TCTCTCTCCCTCTCTCTCT 19

RESULT 690
AAA30181
ID AAA30181 standard; DNA; 17 BP.
XX
AC AAA30181;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15G used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 691
AAZ35714
ID AAZ35714 standard; DNA; 17 BP.
XX
AC AAZ35714;
XX
DT 31-JAN-2000 (first entry)
XX
DE Murine gene anchor PCR primer SEQ ID NO:3.
XX
KW Rare expressed gene; analysis; expression; nucleic acid sample;
KW PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN EP959141-A2.
XX
PD 24-NOV-1999.
XX
PF 18-MAY-1999; 99EP-00109795.
XX
PR 20-MAY-1998; 98JP-00153651.

XX
PA (HITA) HITACHI LTD.
XX
PI Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;
XX
DR WPI; 2000-001284/01.
XX
PT Preparation of nucleic acid sample, useful for analysis of rare expressed
PT genes.
XX
PS Disclosure; Page 11; 22pp; English.
XX
CC The present invention describes a process for the preparation of a
CC nucleic acid sample comprising: (a) providing a nucleic acid sample
CC having a plurality of species of sequences, and providing one or a
CC plurality of kinds of probes having a known sequence substantially
CC complementary to a portion of sequence of the nucleic acid sample; (b)
CC mixing and hybridizing the nucleic acid sample with probes; (c)
CC subsequently recovering nucleic acid molecules; or (i) providing a
CC nucleic acid sample having a plurality of species of sequences, and
CC providing one or a plurality of kinds of probes having a known sequence
CC substantially complementary to a portion of sequence of the nucleic acid
CC sample; (ii) mixing and hybridizing the nucleic acid sample with the
CC probes; (iii) treating the product of (ii) with nuclease activity of an
CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic
CC acid molecules not digested by the nuclease activity in (iii); or (I)
CC providing a nucleic acid sample having a plurality of species of
CC sequences and oligonucleotides primer having predetermined sequences for
CC synthesizing DNA strands; (II) providing one or a plurality of kinds of
CC probes having a known sequence substantially complementary to a portion
CC of a sequence of the nucleic acid sample having such a structure to
CC prevent a polymerase reaction from its 3' end and a nuclease reaction
CC from its 5' end; (III) mixing and hybridizing the nucleic acid sample
CC with the primers and probes; (IV) executing polymerase chain reaction for
CC the samples prepared in (III); and (V) subsequently recovering nucleic
CC acid molecules synthesized in (IV). The method is useful for the
CC preparation of a nucleic acid sample for the analysis of rare expressed
CC genes. The present sequence represents a PCR primer used in the
CC exemplification of the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 692
AAX82721
ID AAX82721 standard; DNA; 17 BP.
XX
AC AAX82721;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IgA nephropathy-associated cDNA primer #62.
XX
KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002855.
XX
PR 02-JUN-1998; 98JP-00152603.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
PT DNA sequences preferentially expressed in IgA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins.
XX
PS Claim 3; Page 170; 180pp; Japanese.
XX
CC This invention describes novel DNA sequences preferentially expressed in
CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IgA nephropathy
CC incorporating the antisense sequences; the treatment of IgA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IgA nephropathy containing the antibodies; and compositions
CC for the treatment of IgA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IgA nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human IgA nephropathy-associated proteins
CC described in the method of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 693
AAZ36740
ID AAZ36740 standard; DNA; 17 BP.
XX
AC AAZ36740;
XX
DT 13-MAR-2000 (first entry)
XX
DE Anchored oligo(dT) primer GT15G used for modified differential display.
XX
KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS Synthetic.
XX
PN WO9955913-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US009119.
XX
PR 27-APR-1998; 98US-0083331P.
PR 27-AUG-1998; 98US-0098070P.
PR 04-FEB-1999; 99US-0118624P.
XX
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI Mcclelland M, Welsh J, Trenkle T;
XX
DR WPI; 2000-086388/07.

XX
PT Measuring expression of low abundance reduced complexity target nucleic
PT acid molecules.
XX
PS Example 3; Page 91; 187pp; English.
XX
CC AAZ36739-41 represent oligo(dT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in a
CC target. The method comprises contacting a probe with an arbitrarily or
CC statistically sampled target and detecting the amount of specific binding
CC of the target to the probe. The methods can be used to identify
CC differentially expressed nucleic acid molecules associated with disease
CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 694
AAA25448
ID AAA25448 standard; DNA; 17 BP.
XX
AC AAA25448;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTTT 4515
|||||||||||||||||
Db 1 AGTTTTTTTTTTTTTTT 17

RESULT 695
AAC64204
ID AAC64204 standard; DNA; 17 BP.
XX
AC AAC64204;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
XX
KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065046-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002730.
XX
PR 27-APR-1999; 99JP-00120489.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687339/67.
XX
PT Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 70; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using

CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis gene 373; expression constructs and
CC host cells comprising pollinosis-associated gene 373 nucleic acids;
CC pollinosis-associated gene 373 primers and probes; antibodies against the
CC protein encoded by the gene; methods of detection of pollinosis-
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC diseases via the detection of pollinosis-associated gene 373 nucleic
CC acids. The invention additionally encompasses methods of screening drug
CC candidates for the treatment of allergic disease by measuring the
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC T-cells in the presence of a test compound relative to a control.
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC diseases and in the screening of drug candidates for the treatment of
CC such diseases. The present sequence represents a PCR primer used in the
CC isolation of human pollinosis-associated gene 373 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 696
AAC64183
ID AAC64183 standard; DNA; 17 BP.
XX
AC AAC64183;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 50; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 697
AAC64173
ID AAC64173 standard; DNA; 17 BP.
XX
AC AAC64173;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 39; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of

```
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 513 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 698
AAC64163
ID   AAC64163 standard; DNA; 17 BP.
XX
AC   AAC64163;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX
KW   Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065048-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002732.
XX
PR   27-APR-1999;   99JP-00120492.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687341/67.
XX
PT   Pollenosis-associated gene 581 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 40; 69pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 581 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis-associated gene 581; to expression
CC   constructs and host cells comprising pollinosis-associated gene 581
CC   nucleic acids; pollinosis-associated gene 581 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 581 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 581 nucleic acids. The invention additionally encompasses methods of
CC   screening drug candidates for the treatment of allergic disease by
CC   measuring the expression of pollinosis-associated gene 581 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 699
AAC64215
ID   AAC64215 standard; DNA; 17 BP.
XX
AC   AAC64215;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.
XX
KW   Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065051-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002735.
XX
PR   27-APR-1999;   99JP-00120493.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687344/67.
XX
PT   Pollinosis-associated gene 627 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 42; 51pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 627 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates to methods of
CC   detection of pollinosis-associated gene 627 nucleic acids; a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 627 nucleic acids; and a method of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis-associated gene 627
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 627 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

```
RESULT 700
AAC64232
ID   AAC64232 standard; DNA; 17 BP.
XX
AC   AAC64232;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
XX
KW   Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW   immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW   detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065050-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002734.
XX
PR   27-APR-1999;   99JP-00120494.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2000-687343/67.
XX
PT   Pollinosis-associated gene 795 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Page 46; Example 6; 73pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 795 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. Pollinosis-associated gene 795 has
CC   homology with the human vimentin gene. The invention also relates also
CC   relates to the protein encoded by pollinosis gene 795; to expression
CC   constructs and host cells comprising pollinosis-associated gene 795
CC   nucleic acids; pollinosis-associated gene 795 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 795 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 795 nucleic acids. The invention additionally encompasses methods of
CC   screening drug candidates for the treatment of allergic disease by
CC   measuring the expression of pollinosis-associated gene 795 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 701
AAC92294
ID   AAC92294 standard; DNA; 17 BP.
XX
AC   AAC92294;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 44; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 702
AAC91721
ID   AAC91721 standard; DNA; 17 BP.
XX
AC   AAC91721;
XX
DT   27-MAR-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
KW   Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW   reduced expression; detection; diagnosis; drug screening;
KW   allergic disease; PCR primer; ss.
```

XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 41; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 703
AAC82876
ID AAC82876 standard; DNA; 17 BP.
XX
AC AAC82876;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #3.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 36; 42pp; Japanese.
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 704
AAH47128
ID AAH47128 standard; DNA; 17 BP.
XX
AC AAH47128;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of primer GT15G.
XX
KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200165259-A1.
XX
PD 07-SEP-2001.
XX
PF 23-FEB-2001; 2001WO-JP001372.
XX
PR 02-MAR-2000; 2000JP-00061832.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX
DR WPI; 2001-557789/62.
XX
PT Diagnosis of allergies including atopic dermatitis.
XX
PS Example 6; Page 66; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151

CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 705
ABK49636
ID ABK49636 standard; DNA; 17 BP.
XX
AC ABK49636;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 57; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 706
ABL59040
ID ABL59040 standard; DNA; 17 BP.
XX
AC ABL59040;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15G.
XX
KW Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-00291316.
XX
PR 25-SEP-2000; 2000JP-00291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR WPI; 2002-439993/47.
XX
PT Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.
XX
PS Example 1; Page 17; 20pp; Japanese.
XX
CC The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergosis. The present sequence represents a PCR primer, which is used
CC in the course of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 707
ABN99831
ID ABN99831 standard; DNA; 17 BP.
XX
AC ABN99831;
XX
DT 15-AUG-2002 (first entry)
XX

DE Human allergic disease related PCR primer SEQ ID NO: 20.
XX
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX
PD 25-APR-2002.
XX
PF 28-SEP-2001; 2001WO-JP008574.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX
DR WPI; 2002-372311/40.
XX
PT Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
PS Example 1; Page 110; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 708
AAL49950
ID AAL49950 standard; DNA; 17 BP.
XX
AC AAL49950;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human B1153 expression in allergic disease related PCR primer GT15G.
XX
KW Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN WO200250269-A1.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-JP011286.
XX
PR 21-DEC-2000; 2000JP-00389476.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX
DR WPI; 2002-713252/77.
XX
PT Examination of allergic diseases comprises detecting gene B1153 over-
PT expressed in T cells of allergy patients for diagnosis treatment and
PT investigation of atopic skin inflammation and asthma.
XX
PS Example 6; Page 82; 102pp; Japanese.
XX
CC The present invention relates to a method of examining allergic diseases
CC which comprises comparing the expression level of gene B1153 in allergy
CC patients with the expression level in healthy subjects. The method is
CC useful for the treatment, prevention, diagnosis and study of allergic
CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 709
AAL47236
ID AAL47236 standard; DNA; 17 BP.
XX
AC AAL47236;
XX
DT 22-AUG-2002 (first entry)
XX
DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX
KW Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW atopic dermatitis; human; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200233122-A1.
XX
PD 25-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008937.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX
DR WPI; 2002-372313/40.
XX
PT Method for examining allergic diseases by differential display of
PT intersectin 2 gene showing different expression particularly significant
PT increase in eosinophils in patients.
XX
PS Example 1; Page 53; 90pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC with intersectin 2 gene or a gene with equivalent function of intersectin

CC 2 as an indicator gene, which comprises determining the expression level
CC of the gene in the eosinophils in a patient, and comparing the expression
CC level with that in the eosinophils of a healthy individual. The method is
CC for examining allergic diseases, particularly atopic dermatitis, which is
CC also applicable in screening candidate compounds for remedies. The
CC present sequence is an anchor primer described in the exemplification of
CC the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 710
ABK49758
ID ABK49758 standard; DNA; 17 BP.
XX
AC ABK49758;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15g.
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15g.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 55; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15g PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTTG 4516
||||||||||||||||||
Db 1 GTTTTTTTTTTTTTTTG 17

RESULT 711
ADB42614/c
ID ADB42614 standard; DNA; 17 BP.
XX
AC ADB42614;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2937.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 375; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 5 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4819 GAAAGCATTTTGGGATC 4835

```
                  ||||||||||||||||
Db         17 GAAAGCATTTTGGGATC 1
```

```
RESULT 712
ADB44070
ID   ADB44070 standard; DNA; 17 BP.
XX
AC   ADB44070;
XX
DT   18-DEC-2003  (revised)
DT   04-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #4393.
XX
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
PD   15-MAY-2003.
XX
PF   17-SEP-2002; 2002WO-IB004219.
XX
PR   17-SEP-2001; 2001FR-00011981.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-441574/41.
XX
PT   New nucleic acid encoding human prostate membrane-specific antigen,
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 545; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1926 GATCAGACATACAGCTG 1942
                ||||||||||||||||
Db          1 GATCAGACATACAGCTG 17
```

```
RESULT 713
ADC84470
ID   ADC84470 standard; DNA; 17 BP.
XX
AC   ADC84470;
XX
DT   01-JAN-2004  (first entry)
XX
DE   PCR primer for amplifying  plant blastogenesis specific gene #SEQ ID 3.
XX
KW   Plant blastogenesis; transformation; gene expression; tissue specific;
KW   PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2003159071-A.
XX
PD   03-JUN-2003.
XX
PF   22-NOV-2001; 2001JP-00358366.
XX
PR   22-NOV-2001; 2001JP-00358366.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-818678/77.
XX
PT   New naturally derived DNA specifically expressed during blastogenesis of
PT   a plant, useful for producing a transformed plant and for compulsive
PT   expression of a protein.
XX
PS   Example 3; SEQ ID NO 3; 43pp; Japanese.
XX
CC   The invention relates to naturally derived DNA specifically expressed
CC   during plant blastogenesis. The DNA of the invention is useful for
CC   producing a transformed plant. Methods of the invention are also useful
CC   for compulsive expression of this DNA. Methods of the invention are
CC   useful for plant tissue specific expression of genes. Also, the growth
CC   stage of a plant can be controlled specifically. The current sequence
CC   represents a PCR primer for amplifying a plant blastogenesis specific
CC   gene of the invention.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
                ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17
```

```
RESULT 714
ADE30798
ID   ADE30798 standard; DNA; 17 BP.
XX
AC   ADE30798;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Cholesterol homeostasis/adipogenesis related DNA seq id 185.
XX
KW   expression vector; anorectic; antiarteriosclerotic; cardiant;
KW   antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;
KW   obesity; athersclerosis; diabetes mellitus;
KW   coronary artery heart disease; cholesterol homeostasis; ss;
KW   differntial expression.
XX
OS   Homo sapiens.
XX
PN   US2003180764-A1.
```

XX
PD 25-SEP-2003.
XX
PF 08-JAN-2003; 2003US-00339793.
XX
PR 09-JAN-2002; 2002US-0347286P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Shang J, Bowen B;
XX
DR WPI; 2003-830986/77.
XX
PT Polynucleotides differentially regulated in response to cholesterol and
PT adipogenesis are useful to detect and treat associated conditions such as
PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart
PT disease.
XX
PS Claim 8; SEQ ID NO 185; 59pp; English.
XX
CC The invention describes a composition comprising at least one expression
CC vector comprising a polynucleotide of the invention. The composition has
CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.
CC The invention is used to detect and treat conditions associated with
CC elevated cholesterol and lipid or during adipogenesis, particularly
CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart
CC disease. This sequence represents a polynucleotide differentially
CC expressed during cholesterol homeostasis and adipogenesis.
XX
SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4832 GATCCTTCAGCACAGGA 4848
||||||||||||||||
Db 1 GATCCTTCAGCACAGGA 17

RESULT 715
ADI50896
ID ADI50896 standard; DNA; 17 BP.
XX
AC ADI50896;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID3399.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 3399; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 4 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3865 GATCACTGTAGTTTAGT 3881
|||||||||||||||||
Db 1 GATCACTGTAGTTTAGT 17

RESULT 716
ACC53202
ID ACC53202 standard; DNA; 17 BP.
XX
AC ACC53202;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #1969.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 495; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The

```
CC   invention is used to diagnose or treat viral disease or disease
CC   characterized by development of tumour cells or cellular degeneration
XX
SQ   Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGGA 4848
              |||||||||||||||||
Db          1 GATCCTTCAGCACAGGA 17


RESULT 717
ACC51607
ID   ACC51607 standard; DNA; 17 BP.
XX
AC   ACC51607;
XX
DT   27-JUN-2003  (first entry)
XX
DE   Human tumour suppressor sequence #374.
XX
KW   ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW   tumour regression; apoptosis; virus resistance; diagnosis;
KW   cellular degeneration.
XX
OS   Homo sapiens.
XX
PN   FR2826373-A1.
XX
PD   27-DEC-2002.
XX
PF   20-JUN-2001; 2001FR-00008139.
XX
PR   20-JUN-2001; 2001FR-00008139.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Tuijnder M,  Telerman A,  Amson R;
XX
DR   WPI; 2003-250498/25.
XX
PT   New nucleic acid sequences associated with tumor suppression, regression,
PT   apoptosis or virus resistance are useful to diagnose and treat viral
PT   disease, development of tumor cells and cell degeneration.
XX
PS   Claim 1; Page 126; 798pp; French.
XX
CC   This sequence represents an isolated nucleic acid sequence associated
CC   with tumour suppression or regression, apoptosis or virus resistance. The
CC   invention relates to these sequences or sequences having at least 80%
CC   identity to them, and polypeptides encoded by the sequences or
CC   polypeptides having 80% identity to the polypeptide sequences. The
CC   invention is used to diagnose or treat viral disease or disease
CC   characterized by development of tumour cells or cellular degeneration
XX
SQ   Sequence 17 BP; 4 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3865 GATCACTGTAGTTTAGT 3881
              |||||||||||||||||
Db          1 GATCACTGTAGTTTAGT 17


RESULT 718
ADI13011
ID   ADI13011 standard; DNA; 17 BP.
XX
AC   ADI13011;
XX
DT   22-APR-2004  (first entry)
XX
DE   PCR primer GT15G used to amplify human NOR-1 (MINOR) DNA SeqID 5.
XX
KW   human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;
KW   atopic dermatitis; antiallergic; antiinflammatory; dermatological;
KW   primer.
XX
OS   Homo sapiens.
XX
PN   WO2004003198-A1.
XX
PD   08-JAN-2004.
XX
PF   27-JUN-2003; 2003WO-JP008199.
XX
PR   27-JUN-2002; 2002JP-00188490.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN AGENCY NATION.
XX
PI   Hashida R,  Kagaya S,  Yayoi Y,  Sugita Y,  Saito H;
XX
DR   WPI; 2004-083057/08.
XX
PT   Examining allergic diseases e.g. atopic dermatitis by differential
PT   display based on gene expression of NOR-1 receptor protein, also
PT   applicable in screening compounds for treatment of allergic diseases.
XX
PS   Example 1; SEQ ID NO 5; 155pp; Japanese.
XX
CC   This invention relates to a novel method for examining allergic diseases
CC   that comprises comparing the expression levels of a gene encoding the NOR
CC   -1 receptor protein between patients and healthy individuals.
CC   Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in
CC   the specialist white blood cells known as eosinophils and is involved in
CC   mediating an allergic reaction. The present invention describes a
CC   differential display method that can identify the expression level of
CC   this gene in order to identify its usefulness in diagnosing allergic
CC   diseases such as atopic dermatitis. Furthermore, compositions can also be
CC   used to screen compounds for the treatment of allergic diseases.
CC   Accordingly, they exhibit various activities including antiallergic,
CC   antiinflammatory and dermatological. This oligonucleotide sequence is a
CC   PCR primer used to amplify human NOR-1 DNA in an exemplification of the
CC   invention.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 719
AAV54168
ID   AAV54168 standard; cDNA; 18 BP.
XX
AC   AAV54168;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 5.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
```

```
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 720
AAV54174
ID   AAV54174 standard; cDNA; 18 BP.
XX
AC   AAV54174;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 11.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 721
AAV54165
ID   AAV54165 standard; cDNA; 18 BP.
XX
AC   AAV54165;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 2.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 47; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTG 4516
              |||||||||||||||||
Db          1 GTTTTTTTTTTTTTTTG 17


RESULT 722
AAZ90644
ID   AAZ90644 standard; DNA; 18 BP.
XX
```

```
AC   AAZ90644;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #5.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 723
AAZ90650
ID   AAZ90650 standard; DNA; 18 BP.
XX
AC   AAZ90650;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #11.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17


RESULT 724
AAZ90647
ID   AAZ90647 standard; DNA; 18 BP.
XX
AC   AAZ90647;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #8.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTG 17
```

```
RESULT 725
AAQ75547
ID   AAQ75547 standard; DNA; 19 BP.
XX
AC   AAQ75547;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 726
AAQ75560
ID   AAQ75560 standard; DNA; 20 BP.
XX
AC   AAQ75560;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 727
AAQ75562
ID   AAQ75562 standard; DNA; 20 BP.
XX
AC   AAQ75562;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
```

```
  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 728
AAT04917
ID   AAT04917 standard; cDNA; 20 BP.
XX
AC   AAT04917;
XX
DT   25-MAR-2003  (revised)
DT   15-MAY-1996  (first entry)
XX
DE   Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KW   Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW   thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW   transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS   Synthetic.
XX
PN   EP676470-A1.
XX
PD   11-OCT-1995.
XX
PF   04-OCT-1990;   95EP-00105391.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselman RA,  Martin FH;
XX
DR   WPI; 1995-346090/45.
XX
PT   New stem cell factor polypeptide(s) - for stimulating the growth of
PT   primitive progenitor cells, esp. for treating disorders involving blood
PT   cells.
XX
PS   Example 3; Fig 12C; 127pp; English.
XX
CC   AAT04915-T04922 are oligonucleotide primers and probes used for the
CC   amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC   naturally occuring SCF and C-terminally truncated polypeptides, having
CC   amino acid sequences sufficiently duplicative of naturally ocurring SCF,
CC   stimulate growth of primitive progenitors such as haematopoietic
CC   progenitor cells, neural stem cells and primordial germ stem cells. The
CC   peptides can be used in a composition for treating leucopenia, anaemia or
CC   thrombocytopenia, for enhancing engraftment of bone marrow during
CC   transplantation or for bone marrow recovery after chemotherapy or
CC   radiation-induced bone marrow aplasia or myelosuppression. They can also
CC   be used for treating neoplasia, nerve damage, infertlilty, intestinal
CC   damage or myeloproliferative disorders. Antibodies may be raised against
CC   the peptides for use in detection or neutralisation of SCF in serum. SCF
CC   may be useful for the treatment of AIDS and severe combined
CC   immunodeficiency (SCID) states alone or in combination with other factors
CC   such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 729
AAV15104
ID   AAV15104 standard; DNA; 20 BP.
XX
AC   AAV15104;
XX
DT   20-MAY-1998  (first entry)
XX
DE   Human VEGF antisense oligonucleotide U0370T-S.
XX
KW   Human; vascular endothelial cell growth factor; VEGF; diagnosis;
KW   antisense oligonucleotide; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   JP10052285-A.
XX
PD   24-FEB-1998.
XX
PF   20-MAY-1997;   97JP-00129767.
XX
PR   23-MAY-1996;   96JP-00128192.
XX
PA   (TOAG ) TOA GOSEI CHEM IND LTD.
XX
DR   WPI; 1998-200633/18.
XX
PT   Preparation of anti-sense nucleic acid - by assigning numerical value to
PT   target mRNA region and preparing new molecule with nucleic acid
PT   complementary to sequence with low value.
XX
PS   Example 3; Page 9; 19pp; Japanese.
XX
CC   The present sequence represents an antisense oligonucleotide for human
CC   derived vascular endothelial cell growth factor (VEGF), used in an
CC   example of the present invention. The present invention describes the
CC   preparation of an antisense nucleic acid (ANA). The method comprises: (a)
CC   using an mRNA sequence of varying regions in which a numerical value (NV)
CC   is assigned to a target region, where the size of NV depends on the
CC   possibility of forming a truly complementary double strand (DS) between
CC   two regions, and (b) preparing ANA with a nucleic acid containing a base
CC   sequence which is truly complementary to a sequence which has a low NV,
CC   where NV assigned to the ability to form DS is based on the difference of
CC   the complementary base sequence to the target. ANA can be used for the
CC   preparation of diagnostic and therapeutic agents. The method can easily
CC   predict ANA target site, therefore enabling easy and rapid preparation of
CC   ANA
XX
SQ   Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGCT 2279
              |||||||||||||||||
Db          4 TCTTTCCTCTTTCTGCT 20


RESULT 730
AAZ09195/c
ID   AAZ09195 standard; DNA; 20 BP.
XX
AC   AAZ09195;
XX
DT   19-OCT-1999  (first entry)
```

XX
DE Oligonucleotide 7 for DNA analysis.
XX
KW Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS Synthetic.
XX
PN JP11196874-A.
XX
PD 27-JUL-1999.
XX
PF 14-JAN-1998; 98JP-00005399.
XX
PR 14-JAN-1998; 98JP-00005399.
XX
PA (HITA) HITACHI LTD.
XX
DR WPI; 1999-496652/42.
XX
PT Analysis of DNA fragment - comprises addition of known common
PT oligonucleotide, amplification of resultant DNA fragment and analysis and
PT labelling of amplified DNA.
XX
PS Example 1; Page 12; 17pp; Japanese.
XX
CC This invention descibes a novel method for the analysis of a DNA fragment
CC which comprises: (i) addition of a known common oligonucleotide sequence
CC to at least one terminal of each DNA fragment, (ii) amplification of the
CC resultant DNA fragment as a primer using a first common primer containing
CC a complementary nucleotide sequence to the above mentioned known common
CC oligonucleotide sequence, a second common primer containing a
CC complementary nucleotide sequence to the prepared known common
CC oligonucleotide sequence optionally having been introduced with
CC complementary nucleotide sequence at a terminal, and a specific primer
CC capable of hybridisation with a DNA fragment containing whole or part of
CC the gene having known sequence, to give amplified DNA, (iii) analysis of
CC the amplified DNA to find the information of the DNA fragment, in which
CC the specific primer is designed to prepare fragments of the common first
CC and second primers and to give short fragment of amplified DNA and (iv)
CC labelling them to make their differentiation. Differentiation of
CC informations of known and unknown genes readily provides information of
CC unknown gene and simultaneous monitoring of signals derived from minor
CC genes. Furthermore, labelling of DNAs according to functions of known
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC used to illustrate the method of the invention
XX
SQ Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 20 TTTTTTTTTTTTTTTGG 4

RESULT 731
AAX15599/c
ID AAX15599 standard; cDNA to mRNA; 20 BP.
XX
AC AAX15599;
XX
DT 07-MAY-1999 (first entry)
XX
DE Fragment of upstream sequence of coding region for VEGF.
XX
KW Vascular endothelial cell growth factor; VEGF; antisense oligonucleotide;
KW solid tumor growth; anticancer agent; rheumatic arthritis;
KW diabetic retinitis; ss.
XX
OS Unidentified.
XX
PN JP11042091-A.
XX
PD 16-FEB-1999.
XX
PF 25-JUL-1997; 97JP-00213838.
XX
PR 25-JUL-1997; 97JP-00213838.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 1999-197823/17.
XX
PT An antisense nucleic acid compound against vascular endothelial cell
PT growth factor (VEGF) - useful as an anticancer agent, and for treatment
PT of rheumatic arthritis and diabetic retinitis.
XX
PS Example 2; Page 11; 16pp; English.
XX
CC The present sequence represents the a fragment of the upstream sequence
CC of the coding region for vascular endothelial cell growth factor (VEGF).
CC Antisense oligonucleotides targeted to this region inhibit at least 50 %
CC of VEGF expression by the cell. The antisense oligonucleotides can
CC inhibit the growth of solid tumor and are useful as anticancer agents and
CC for treating rheumatic arthritis and diabetic retinitis
XX
SQ Sequence 20 BP; 10 A; 1 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2263 TCTTTCCTCTTTCTGCT 2279
|||||||||||||||||
Db 17 TCTTTCCTCTTTCTGCT 1

RESULT 732
AAX15764
ID AAX15764 standard; cDNA to mRNA; 20 BP.
XX
AC AAX15764;
XX
DT 07-MAY-1999 (first entry)
XX
DE Antisense oligonucleotide targeted to upstream sequence of VEGF.
XX
KW Vascular endothelial cell growth factor; VEGF; antisense oligonucleotide;
KW solid tumor growth; anticancer agent; rheumatic arthritis;
KW diabetic retinitis; ss.
XX
OS Synthetic.
XX
PN JP11042091-A.
XX
PD 16-FEB-1999.
XX
PF 25-JUL-1997; 97JP-00213838.
XX
PR 25-JUL-1997; 97JP-00213838.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 1999-197823/17.
XX
PT An antisense nucleic acid compound against vascular endothelial cell
PT growth factor (VEGF) - useful as an anticancer agent, and for treatment
PT of rheumatic arthritis and diabetic retinitis.
XX
PS Example 1; Page 7; 16pp; English.
XX
CC AAX15764-81 represent antisense oligonucleotides targeted to the upstream
CC sequence of the coding region for vascular endothelial cell growth factor
CC (VEGF). Antisense oligonucleotides targeted to this region inhibit at

```
CC   least 50 % of VEGF expression by the cell. The antisense oligonucleotides
CC   can inhibit the growth of solid tumor and are useful as anticancer agents
CC   and for treating rheumatic arthritis and diabetic retinitis
XX
SQ   Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2263 TCTTTCCTCTTTCTGCT 2279
              |||||||||||||||||
Db          4 TCTTTCCTCTTTCTGCT 20


RESULT 733
AAA13752
ID   AAA13752 standard; DNA; 20 BP.
XX
AC   AAA13752;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Stem cell factor universal oligonucleotide 220-3.
XX
KW   Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW   primitive progenitor cell; haematopoietic disorder; syngeneic;
KW   allogeneic; autologous bone marrow transplant; gene therapy;
KW   transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   EP992579-A1.
XX
PD   12-APR-2000.
XX
PF   04-OCT-1990;   99EP-00122861.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   28-SEP-1990;   90WO-US005548.
PR   01-OCT-1990;   90US-00589701.
PR   04-OCT-1990;   90EP-00310899.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Suggs SV,  Bosselmann RA,  Martin FH;
XX
DR   WPI; 2000-259135/23.
XX
PT   Production of hematopoietic cells suitable for administration to a
PT   subject using progenitor cells and expanding the cells using stem cell
PT   factor.
XX
PS   Example 3; Fig 12C; 123pp; English.
XX
CC   A method has been developed of making haematopoietic cells suitable for
CC   administration to a subject. The method comprises: (a) obtaining
CC   haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC   by adding to the cells a haematopoietically effective dose of a
CC   polypeptide product having at least part of the primary structural
CC   confirmation and one or more of the biological properties of naturally
CC   occurring stem cell factor (SCF). The method is useful for stimulating
CC   primitive progenitor cells including early haematopoietic progenitor
CC   cells which are capable of maturing to erythroid, megakaryocyte,
CC   granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC   increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC   SCF is useful for treating haematopoietic disorders. The method is useful
CC   for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC   or autologous bone marrow transplant. SCF is useful for enhancing the
CC   efficiency of gene therapy based on transfecting haematopoietic stem
CC   cells. SCF is also useful for combating the myelosuppressive effects of
CC   anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC   after acute blood loss and as a boost to the immune system for fighting
CC   neoplasia (cancer). The present sequence represents a universal
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 734
AAH41331
ID   AAH41331 standard; DNA; 20 BP.
XX
AC   AAH41331;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
XX
KW   Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW   gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS   Synthetic.
XX
PN   US6207454-B1.
XX
PD   27-MAR-2001.
XX
PF   31-DEC-1998;   98US-00224681.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
PR   24-MAY-1995;   95US-00449653.
PR   12-JAN-1998;   98US-00005893.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-366062/38.
XX
PT   Enhancing efficiency of transfer of polynucleotide into a target
PT   mammalian cell in vitro, involves exposing cell that expresses a stem
PT   cell factor receptor to stem cell factor, and introducing polynucleotide
PT   into cell in vitro.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present invention describes a method for enhancing (E) the efficiency
CC   of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC   vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC   receptor to a biologically active SCF, its analogue or fragment, which
CC   induces cell proliferation, and introducing (I) to (II) in vitro.
CC   Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC   The method is useful for enhancing the efficiency of the transfer of a
CC   polynucleotide into a target mammalian cell in vitro. The method is
CC   useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC   AAB98390 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
```

```
  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20
```

RESULT 735
AAS04111
ID AAS04111 standard; DNA; 20 BP.
XX
AC AAS04111;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6207417-B1.
XX
PD 27-MAR-2001.
XX
PF 07-JUN-1995; 95US-00482918.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 21-DEC-1993; 93US-00172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-298941/31.
XX
PT Novel nucleic acids encoding stem cell factor useful for treating
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
PT disease, Kala azar, anemia and septicemia.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC disorders such as piebaldism and vitiligo
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20
```

RESULT 736
AAF89091
ID AAF89091 standard; DNA; 20 BP.
XX
AC AAF89091;
XX
DT 13-JUL-2001 (first entry)
XX
DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.
XX
KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency; PCR primer; ss.
XX
OS Mammalia.
XX
PN US6207802-B1.
XX
PD 27-MAR-2001.
XX
PF 09-NOV-1994; 94US-00336728.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2001-353108/37.
XX
PT Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early hematopoietic progenitor cells, useful for
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis.
XX
PS Example 3; Fig 12C; 209pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20
```

RESULT 737

```
AAH23889
ID   AAH23889 standard; DNA; 20 BP.
XX
AC   AAH23889;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6204363-B1.
XX
PD   20-MAR-2001.
XX
PF   25-NOV-1992;   92US-00982255.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-256683/26.
XX
PT   New stem cell factor polypeptides and their analogs which stimulate
PT   growth of early hematopoietic progenitors, useful for treating aplastic
PT   anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT   disease.
XX
PS   Example 3; Fig 12C; 166pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
CC   polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC   including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
CC   (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
CC   B12 and folic acid deficiency, pyridoxine deficiency, and
CC   hypopigmentation disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 738
AAS04212
ID   AAS04212 standard; DNA; 20 BP.
XX
AC   AAS04212;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX
KW   Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW   blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW   anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218148-B1.
XX
PD   17-APR-2001.
XX
PF   21-DEC-1993;   93US-00172329.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   25-NOV-1992;   92US-00982255.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-281051/29.
XX
PT   Isolated DNA sequence, encoding polypeptide product useful for
PT   stimulating growth of early hematopoietic progenitor cells.
XX
PS   Example 3; Fig 12C; 167pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 8 universal
CC   oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
CC   SCF (stem cell factor) cDNA sequence. The present invention relates to
CC   novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
CC   and the polynucleotides encoding them. SCF stimulate primitive progenitor
CC   cells including early haematopoietic progenitor cells. The invention also
CC   describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
CC   (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
CC   The polynucleotide encoding SCF is useful for producing SCF and useful in
CC   gene therapy. It is useful for treating disorders involving blood cells
CC   such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC   myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC   congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC   disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
CC   and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
CC   disorders such as piebaldism and vitiligo
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 739
AAS10447
ID   AAS10447 standard; DNA; 20 BP.
XX
AC   AAS10447;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
```

```
XX
KW   Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW   blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW   hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6248319-B1.
XX
PD   19-JUN-2001.
XX
PF   24-MAY-1995;   95US-00449653.
XX
PR   16-OCT-1989;   89US-00422383.
PR   11-JUN-1990;   90US-00537198.
PR   24-AUG-1990;   90US-00573616.
PR   01-OCT-1990;   90US-00589701.
PR   10-APR-1991;   91US-00684535.
PR   25-NOV-1992;   92US-00982255.
PR   21-DEC-1993;   93US-00172329.
XX
PA   (ZSEB/) ZSEBO K M.
PA   (BOSS/) BOSSELMAN R A.
PA   (SUGG/) SUGGS S V.
PA   (MART/) MARTIN F H.
XX
PI   Zsebo KM,  Bosselman RA,  Suggs SV,  Martin FH;
XX
DR   WPI; 2001-407312/43.
XX
PT   Increasing the number of early hematopoietic progenitor cells in the
PT   peripheral blood useful for the treatment of blood disorders including
PT   Hodgkin's disease comprises the administration of human stem cell factor.
XX
PS   Example 3; Fig 12C; 210pp; English.
XX
CC   The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
CC   primers (AAS10435-AAS10453) used to amplify various portions of the human
CC   SCF cDNA sequence. The sequence is described in an invention relating to
CC   novel stem cell factors, the polynucleotides encoding them and methods
CC   for producing the stem cell factors. The methods involve increasing the
CC   number of early haematopoietic progenitor cells in human peripheral blood
CC   by administering a haematopoietically effective human stem cell factor
CC   polypeptide. The methods are useful for the treatment of blood disorders,
CC   including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
CC   carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC   lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC   disorders i.e. piebaldism and viral induced disorders, including AIDS
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 740
ABL57070/c
ID   ABL57070 standard; DNA; 20 BP.
XX
AC   ABL57070;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .20
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 1-20 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 2; Page 26; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         17 AGTTTTTTTTTTTTTTT 1


RESULT 741
AAD35464
ID   AAD35464 standard; DNA; 20 BP.
XX
AC   AAD35464;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Rat SCF 5' cDNA amplifying PCR primer, 220-3.
XX
KW   Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW   anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW   infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
KW   metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW   Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW   Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW   Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia;
```

KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopaenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTGG 20

RESULT 742
ABS73848
ID ABS73848 standard; DNA; 20 BP.
XX
AC ABS73848;
XX
DT 05-DEC-2002 (first entry)
XX
DE SCF universal oligonucleotide 220-3.
XX
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW haematopoietic system; metastatic carcinoma; acute leukaemia;
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
KW disseminated fungus disease; haematopoietic; tuberculostatic;
KW antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS Synthetic.
XX
PN EP1241258-A2.
XX
PD 18-SEP-2002.
XX
PF 04-OCT-1990; 2002EP-00008587.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
PR 04-OCT-1990; 90EP-00310899.
PR 04-OCT-1990; 95EP-00105391.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI; 2002-684093/74.
XX
PT Production of a human stem cell factor (SCF) polypeptide for treating
PT disorders involving blood cells, such as leukemia, comprises culturing
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT encoding the human SCF.
XX
PS Example 3; Fig 12C; 120pp; English.
XX
CC The present invention relates to novel stem cell factors (SCFs),
CC polynucleotide sequences encoding the SCFs, and methods of producing
CC them. SCFs are involved in the blood-forming (haematopoietic) system in
CC mammals, particularly humans. The method of the invention is useful for
CC the production of human SCF. The stem cell factors are useful to treat
CC disorders involving blood cells e.g. metastatic carcinoma, acute
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus
CC disease, malaria, and vitiligo. The present sequence representing a
CC universal oligonucleotide for SCF DNA is used in the examples of the
CC present invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTGG 20

RESULT 743
AAD57844/c
ID AAD57844 standard; DNA; 20 BP.
XX
AC AAD57844;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target oligonucleotide #1 used in nonlinear optical technique.

XX
KW Nonlinear optical technique; screening; ss.
XX
OS Unidentified.
XX
PN WO2003064991-A2.
XX
PD 07-AUG-2003.
XX
PF 17-JUL-2002; 2002WO-US022681.
XX
PR 17-JUL-2001; 2001US-0306040P.
PR 23-OCT-2001; 2001US-0347821P.
PR 06-FEB-2002; 2002US-0354668P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-646172/61.
XX
PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase,
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
XX
PS Disclosure; Fig 20B; 146pp; English.
XX
CC The present invention relates to a method for detecting interactions
CC between biological components using a nonlinear optical technique. The
CC invention is used for screening candidate binding partner(s) for binding
CC to test molecule. It can also be used to detect changes in orientation or
CC conformation of the probe and/or target. The present sequence is a target
CC oligonucleotide used in nonlinear optical technique
XX
SQ Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 17 AGTTTTTTTTTTTTTTT 1

RESULT 744
ADE52460
ID ADE52460 standard; DNA; 20 BP.
XX
AC ADE52460;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stem cell factor (SCF) related DNA #31.
XX
KW Stem cell factor; SCF; haematopoietic activity; infertility;
KW intestinal damage; myeloproliferative disorder; leucopenia;
KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW miliary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS Synthetic.
XX
PN US2002031491-A1.
XX
PD 14-MAR-2002.
XX
PF 31-DEC-1998; 98US-00224683.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449653.
PR 12-JAN-1998; 98US-00005893.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2003-851459/79.
XX
PT New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT immune deficiency, also related nucleic acid and antibodies.
XX
PS Disclosure; SEQ ID NO 32; 217pp; English.
XX
CC The invention relates to stem cell factor (SCF) polypeptides with
CC haematopoietic activity and the polynucleotides encoding them. The
CC polypeptides are used for treating infertility, intestinal damage,
CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC for improving engraftment of bone marrow transplants, for enhancing bone
CC marrow recovery after radiotherapy or chemotherapy and in treatment of
CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC also used to expand haematopoietic progenitor cells for transplantation
CC and to prepare such cells for transfection with a gene. The SCF
CC polynucleotides can be used for recombinant expression of the
CC polypeptides and also as probes for mapping of the SCF gene, for
CC identifying SCF-related diseases and as a marker for neighbouring genes.
CC Antibodies raised against the polypeptides are useful in diagnosis and to
CC remove SCF from blood. This sequence represents SCF related DNA of the
CC invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTGG 20

RESULT 745
ADF23330/c
ID ADF23330 standard; DNA; 20 BP.
XX
AC ADF23330;
XX
DT 12-FEB-2004 (first entry)
XX
DE Binding partner sceening method molecular beacon analogue #1.
XX
KW binding partner screening; light beam; nonlinear optical light beam; ss;
KW molecular beacon analogue.
XX
OS Synthetic.
XX
PN US2003148391-A1.
XX
PD 07-AUG-2003.
XX
PF 06-JUN-2002; 2002US-00164915.
XX
PR 24-JAN-2002; 2002US-0351879P.
PR 06-FEB-2002; 2002US-0354668P.
PR 06-FEB-2002; 2002US-0354679P.

PR 05-MAR-2002; 2002US-0362003P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-897567/82.
XX
PT Screening of candidate binding partners for binding to test molecule
PT comprises illuminating sample with light beams and measuring physical
PT properties of nonlinear optical light beam emanating from sample.
XX
PS Disclosure; SEQ ID NO 1; 58pp; English.
XX
CC The invention describes screening a candidate binding partner by
CC illuminating the sample with light beams at fundamental frequencies to
CC binding partners, and measuring physical properties of a nonlinear
CC optical light beam emanating from sample. On binding to the test molecule
CC the properties change relative to that in absence of exposure of the test
CC molecule. The invention is used in the screening of candidate binding
CC partners for binding to test molecule. This sequence represents a
CC molecular beacon analogue, an exemplary test molecule of the invention.
XX
SQ Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 17 AGTTTTTTTTTTTTTTT 1

RESULT 746
ABZ85535/c
ID ABZ85535 standard; DNA; 20 BP.
XX
AC ABZ85535;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 777; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTTCTTTTTTT 2140
||||||||||||||||
Db 18 TTTTCTTTTCTTTTTTT 2

RESULT 747
ABD21765/c
ID ABD21765 standard; DNA; 20 BP.
XX
AC ABD21765;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stanniocalcin-derived oligo SEQ ID 777.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and

```
PT   bronchodilating agent.
XX
PS   Claim 15; SEQ ID NO 777; 763pp; English.
XX
CC   This invention describes a novel composition (a) a first active agent,
CC   comprising oligonucleotides, effective for alleviating
CC   bronchoconstriction, respiratory tract inflammation, allergies and
CC   reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC   surfactant depletion or hyposecretion, when administered to a mammal. The
CC   oligonucleotides are derived from a gene encoding or regulating
CC   expression of a target polypeptide associated with lung airway or lung
CC   dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC   The invention also describes a kit, that comprises: (a) a delivery
CC   device, in separate containers, (b) the oligonucleotides, (c)
CC   instructions for adding a carrier and for use of the kit. The composition
CC   of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC   analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC   beta-adrenergic agonist. The composition is useful for preventing or
CC   treating a respiratory, lung or malignant disease. The administered
CC   composition comprises oligo and is administered to reduce the production
CC   or availability, or to increase the degradation of the target mRNA or to
CC   reduce the amount of target polypeptide present in the lungs. The
CC   pulmonary obstruction, and/or bronchoconstriction and/or lung
CC   inflammation, allergies and/or surfactant hypoproduction are associated
CC   with a disease or condition such as pulmonary vasoconstriction,
CC   inflammation, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC   transplantation rejection, pulmonary infections, bronchitis or cancer.
CC   The reduced adenosine content of the anti-sense oligos corresponding to
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTT 2140
              |||||||||||||||||
Db         18 TTTTCTTTTCTTTTTTT 2


RESULT 748
ADL59746/c
ID   ADL59746 standard; DNA; 20 BP.
XX
AC   ADL59746;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1995.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1995; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 15 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTGG 2


RESULT 749
ADL59742/c
ID   ADL59742 standard; DNA; 20 BP.
XX
AC   ADL59742;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1991.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
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```
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1991; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTGG 1


RESULT 750
ADM14803
ID   ADM14803 standard; DNA; 20 BP.
XX
AC   ADM14803;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:990.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 990; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTGG 17


RESULT 751
ADM14429
ID   ADM14429 standard; DNA; 20 BP.
```

```
XX
AC   ADM14429;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:616.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 616; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 1 A; 1 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          2 TTTTTTTTTTTTTTTGG 18


RESULT 752
ADM14371
ID   ADM14371 standard; DNA; 20 BP.
XX
AC   ADM14371;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:558.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 558; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
```

```
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 753
ADM14467
ID   ADM14467 standard; DNA; 20 BP.
XX
AC   ADM14467;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:654.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 654; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          4 TTTTTTTTTTTTTTTGG 20


RESULT 754
ADP99302
ID   ADP99302 standard; DNA; 20 BP.
XX
AC   ADP99302;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Stem cell factor, SCF, universal PCR primer #2.
XX
KW   SCF; stem cell factor; gene therapy; haematopoietic progenitor cell;
KW   aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;
KW   myelosclerosis; osteopetrosis; metastatic carcinoma; acute leukaemia;
KW   multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;
KW   Niemann-Pick disease; Letterer-Siwe disease;
KW   refractory erythroblastic anaemia; Di Guglielmo syndrome;
KW   congestive splenomegaly; Kala awar; sarcoidosis;
KW   primary splenic pancytopaenia; miliary tuberculosis;
KW   disseminated fungus disease; Fulminating septicaemia; malaria;
KW   vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;
KW   Diamond Blackfan anaemia; hypopigmentation disorder; piebaldism;
KW   vitiligo; neurological damage; infertility; intestinal damage;
KW   irradiation; chemotherapy; AIDS; haematopoietic recovery;
KW   acute blood loss; neoplasm; cancer; ss; PCR; primer.
XX
OS   Mammalia.
XX
PN   US6759215-B1.
```

XX
PD 06-JUL-2004.
XX
PF 07-AUG-2000; 2000US-00635251.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449182.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2004-497128/47.
XX
PT Preparing a human stem cell factor (SCF) polypeptide, useful for treating
PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host
PT cells transformed or transfected with DNA encoding a human SCF.
XX
PS Example 3; SEQ ID NO 32; 210pp; English.
XX
CC The invention relates to preparing a (vertebrate) human stem cell factor
CC (SCF) polypeptide comprising growing host cells transformed or
CC transfected with DNA encoding a human SCF that stimulates growth of
CC haematopoietic progenitor cells under nutrient conditions, the DNA being
CC operatively linked to an expression control sequence, and isolating the
CC polypeptide produced. Also included is a recombinant host cell
CC transformed or transfected with an expression construct comprising a
CC vertebrate SCF polypeptide-encoding DNA operatively linked to a
CC heterologous expression regulatory sequence, permitting the expression of
CC the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat
CC and human nucleic acids encoding SCF, SCF proteins from a number of other
CC mammals and recombinantly expressed SCF protein fragments. The DNA
CC sequences are useful for effecting the large scale synthesis of SCF by a
CC variety of recombinant techniques or for generating new and useful viral
CC and circular plasmid DNA vectors, new and useful transformed and
CC transfected prokaryotic and eukaryotic host cells, and new and useful
CC methods for cultured growth of such host cells capable of expression of
CC SCF and its related products. The DNA sequences are also useful as
CC labelled probes in isolating human genomic DNA encoding SCF, in methods
CC of protein synthesis, in genetic therapy in humans and other mammals, and
CC in developing transgenic mammalian species which may serve as eukaryotic
CC hosts for production of SCF and SCF products in quantity. The SCF is
CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,
CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary
CC splenic pancytopaenia, miliary tuberculosis, disseminated fungus disease,
CC Fulminating septicaemia, malaria, vitamin B 12 and folic acid deficiency,
CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation
CC disorders such as piebaldism and vitiligo. The SCF are also useful for
CC treating neurological damage, infertility states, intestinal damage
CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful
CC for enhancing haematopoietic recovery after acute blood loss and as a
CC boost to the immune system for fighting neoplasia (cancer). The present
CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTGG 20

RESULT 755
AAQ75611
ID AAQ75611 standard; DNA; 21 BP.
XX
AC AAQ75611;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 3 TTTTTTTTTTTTTTTGG 19

RESULT 756
AAQ75622
ID AAQ75622 standard; DNA; 21 BP.
XX
AC AAQ75622;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX

```
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 757
AAQ75620
ID   AAQ75620 standard; DNA; 21 BP.
XX
AC   AAQ75620;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 758
AAQ75614
ID   AAQ75614 standard; DNA; 21 BP.
XX
AC   AAQ75614;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 759
AAQ75612
ID   AAQ75612 standard; DNA; 21 BP.
XX
AC   AAQ75612;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

```
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 760
AAQ75619
ID   AAQ75619 standard; DNA; 21 BP.
XX
AC   AAQ75619;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db          3 TTTTTTTTTTTTTTTGG 19


RESULT 761
AAV35395/c
ID   AAV35395 standard; DNA; 21 BP.
XX
AC   AAV35395;
XX
DT   13-OCT-1998  (first entry)
XX
DE   HIV-1 gag protein DNA primer #8.
XX
KW   Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW   vaccines; infection; protection; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9822596-A1.
XX
PD   28-MAY-1998.
XX
PF   19-NOV-1997;   97WO-JP004216.
XX
PR   19-NOV-1996;   96JP-00323412.
XX
PA   (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA   (JAPG ) NIPPON ZEON KK.
XX
PI   Kojima A,  Kurata T,  Yasuda A;
XX
DR   WPI; 1998-312481/27.
XX
PT   Recombinant vaccinia virus containing fusion HIB gag gene - for
PT   production in host cells of gag protein for use as vaccine.
XX
PS   Example 1; Page 66; 84pp; Japanese.
XX
CC   AAV35388-V35414 are primers used in a method which results in a
CC   recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC   such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC   region (30-300 bases in length) of a retroviral gene other than the gag
CC   gene. The gag gene may be altered so as to produce a gag protein modified
CC   from the natural sequence by the addition, deletion or substitution of at
CC   least 1 amino acid residue. The fusion gene is inserted into a region of
CC   a vaccinia virus not essential to its propagation, to give a recombinant
CC   vaccinia virus vector which is used to transform a host cell (such as
CC   HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC   culturing the host cell produces particulate structures containing the
CC   fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC   protein particles may be used in the production of vaccines for
CC   protecting against infection with retroviruses such as HIV
XX
SQ   Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
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  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTGG 1


RESULT 762
ABL57071/c
ID   ABL57071 standard; DNA; 21 BP.
XX
AC   ABL57071;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .21
FT                   /*tag= a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 1-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 62; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 21 BP; 15 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTTT 4515
              |||||||||||||||||
Db         18 AGTTTTTTTTTTTTTTT 2


RESULT 763
ABS97681/c
ID   ABS97681 standard; DNA; 21 BP.
XX
AC   ABS97681;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Histamine N-methyl transferase (HNMT) sequencing Primer #4.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; sequencing.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 13; Page 124; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
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CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   sequencing primer used to sequence the polymorphic genes of the invention
XX
SQ   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTGG 1


RESULT 764
ABS97669/c
ID   ABS97669 standard; DNA; 21 BP.
XX
AC   ABS97669;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Histamine N-methyl transferase (HNMT) PCR Primer #4.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 13; Page 123; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a PCR
CC   primer used to amplify the sequences of the invention
XX
SQ   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGG 4517
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTGG 1


RESULT 765
ADK01334
ID   ADK01334 standard; DNA; 21 BP.
XX
AC   ADK01334;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Rat DNA microarray capture oligonucleotide #54.
XX
KW   ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW   blood; nerve; germ cell; food additive; food supplement.
XX
OS   Rattus sp.
XX
PN   DE10208794-A1.
```

XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 5 TTTTTTTTTTTTTTTGG 21

RESULT 766
ADK01303
ID ADK01303 standard; DNA; 21 BP.
XX
AC ADK01303;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #23.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTGG 20

RESULT 767
ADK01301
ID ADK01301 standard; DNA; 21 BP.
XX
AC ADK01301;
XX
DT 06-MAY-2004 (first entry)
XX

DE Rat DNA microarray capture oligonucleotide #21.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGG 4517
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTGG 20

RESULT 768
AAQ75569
ID AAQ75569 standard; DNA; 20 BP.
XX
AC AAQ75569;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGTT 4520
|||||||||||||||| |||
Db 1 TTTTTTTTTTTTTTTTGTT 20

RESULT 769
AAQ75601
ID AAQ75601 standard; DNA; 20 BP.
XX
AC AAQ75601;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX

```
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTT 2143
              |||| |||| ||||||||||
Db          1 TTTTTTTTTTTTTTTTTCTT 20


RESULT 770
AAV40326
ID   AAV40326 standard; DNA; 20 BP.
XX
AC   AAV40326;
XX
DT   27-AUG-2003  (revised)
DT   14-OCT-1998  (first entry)
XX
DE   Maize oligonucleotide marker S22F.
XX
KW   Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW   polymorphic site; corn; graminae species; ss.
XX
OS   Synthetic.
OS   Zea.
XX
PN   WO9830717-A2.
XX
PD   16-JUL-1998.
XX
PF   02-DEC-1997;   97WO-EP007134.
XX
PR   02-DEC-1996;   96US-0032069P.
XX
PA   (BIOC-) BIOCEM SA.
XX
PI   Murigneux A;
XX
DR   WPI; 1998-399160/34.
XX
PT   Vegetal sequences including single nucleotide polymorphism - useful, e.g.
PT   to determine polymorphisms in plants, determine strain in plant breeding
PT   and to correlate polymorphisms with phenotypic traits.
XX
PS   Example 2; Page 9; 32pp; English.
XX
CC   The present invention describes a nucleic acid segment comprising at
CC   least 10 contiguous nucleotides from a vegetal sequence including a
CC   polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC   complement of the segment. Also described are: (1) an allele-specific
CC   oligonucleotides hybridising to segment, or their complements, and (2) a
CC   method of analysing nucleic acids from a subject, by determining if a
CC   base is occupying any one (or a set) of polymorphic sites in 261
CC   sequences derived from six maize lines (see AAV47701 to AAV47961). The
CC   segments are useful in fingerprint analysis in plants to determine which
CC   polymorphisms are present, which strain a plant belongs to and to
CC   distinguish between strains. The polymorphisms may correlate with
CC   phenotypic traits (e.g. plant growth rate or crop yield), and the
CC   segments are useful to determine the presence/absence of specific
CC   polymorphisms correlating with the existence/absence of particular
CC   traits. The segments are also useful in marker assisted back-cross
CC   techniques to select plants with a higher percentage of recurrent parent
CC   in a back-cross population. Segments incorporate SNPs which occur more
CC   frequently than other polymorphism types and are therefore more likely to
CC   be located close to genetic loci of interest; different forms of
CC   characterised SNPs are also often easier to detect than other
CC   polymorphism types. AAV40304 to AAV40369 are used in an example from the
CC   present invention as markers and PCR primers. (Updated on 27-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1021 GCTGGTGAACAGTGCTGCCC 1040
              || |||||||| ||||||||
Db          1 GCAGGTGAACAATGCTGCCC 20


RESULT 771
AAA66772
ID   AAA66772 standard; DNA; 20 BP.
XX
AC   AAA66772;
XX
DT   09-OCT-2000  (first entry)
XX
DE   Dog genomic marker oligonucleotide sequence SEQ ID NO:634.
XX
KW   Dog; genome; genomic marker; radiation hybrid map; identification;
KW   chromosome location; gene marker; polymorphic microsatellite marker;
KW   phenotype; behaviour; pedigree; ss.
XX
OS   Canis familiaris.
XX
PN   WO200029615-A2.
XX
PD   25-MAY-2000.
XX
PF   15-NOV-1999;   99WO-IB001907.
XX
PR   13-NOV-1998;   98US-0108193P.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Galibert F,  Andre C;
XX
DR   WPI; 2000-387821/33.
XX
PT   New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT   for e.g. identifying genes implicated in phenotypic and behavioral traits
PT   or in genetic diseases and for studying dog pedigrees.
XX
PS   Claim 1; Page 80; 87pp; English.
XX
CC   The present invention describes a radiation hybrid map of the dog (Canine
CC   familiaris) genome comprising the genome location of a marker selected
CC   from AAA66139 to AAA66942. The radiation hybrid map is useful for
CC   identifying and localising dog genes, since it covers approximately 80 %
CC   of the dog genome and provides a dense map integrating different types
CC   (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC   (or complementary sequences) are especially useful to identify genes
CC   responsible for phenotypic and behavioural traits in dogs, to identify
CC   morbid genes, to analyse diseases and identify implicated genes in such
CC   diseases and their alleles, and to study dog pedigrees. They may also be
CC   useful for isolating corresponding human gene sequences e.g. genes
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```
CC   involved in genetic diseases
XX
SQ   Sequence 20 BP; 0 A; 12 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              || |||||||| ||||||||
Db          1 TCCCTCTCCCTTCCTCTCTC 20


RESULT 772
ABL57565
ID   ABL57565 standard; DNA; 20 BP.
XX
AC   ABL57565;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Nucleic acid probe u.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 6; Page 23; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a nucleic acid probe of the
CC   invention that was used for investigating the effects or the numbers of
CC   G(s) in each target nucleic acid, and the number of G(s) in its
CC   corresponding invention nucleic acid probe
XX
SQ   Sequence 20 BP; 15 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db          1 AAAAAAAAAATATATATATA 20


RESULT 773
ABL95912/c
ID   ABL95912 standard; DNA; 20 BP.
XX
AC   ABL95912;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly u for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 13; Page 62; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 20 BP; 5 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATACA 2404
              ||||| |||||||||||| |
Db         20 AAAAAAAAAATATATATATA 1
```

```
RESULT 774
ACC44056/c
ID   ACC44056 standard; DNA; 20 BP.
XX
AC   ACC44056;
XX
DT   30-MAY-2003  (first entry)
XX
DE   Oligo ISIS 124647 for CD40 ligand gene expression inhibition.
XX
KW   ss; cytostatic; antiinflammatory; immunomodulator; antisense;
KW   gene therapy; human; CD40 ligand; phosphorothioate; 2'MOE wings; cancer;
KW   autoimmune disorder; inflammatory disorder; apoptosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .20
FT                   /*tag=  a
FT                   /note= "contains phosphorothioate internucleotide bonds
FT                   in the backbone replacing phosphodiester internucleotide
FT                   bonds"
FT   modified_base   1. .20
FT                   /*tag=  d
FT                   /note= "all cytidine nucleotides are 5-methylcytidine"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= 2'-O-methoxyethyl nucleotides
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= 2'-O-methoxyethyl nucleotides
XX
PN   WO2003008433-A1.
XX
PD   30-JAN-2003.
XX
PF   15-JUL-2002; 2002WO-US022635.
XX
PR   18-JUL-2001; 2001US-00909595.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Baker BF,  Wyatt JR,  Davis SE;
XX
DR   WPI; 2003-239305/23.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding a CD40
PT   ligand, useful in diagnostic and research applications, or for treating
PT   diseases associated with expression of CD40 ligand, e.g. cancer or
PT   autoimmune disorder.
XX
PS   Claim 3; Page 79; 108pp; English.
XX
CC   The invention relates to novel antisense oligonucleotide targeted to the
CC   human CD40 ligand gene. The oligonucleotides contain either
CC   phosphorothioate internucleotide bonds replacing the usual phosphodiester
CC   internucleotide bonds or have a peptide amide backbone replacing the
CC   sugar phosphate backbone. The nucleotides flanking the central 10
CC   nucleotides have 2'-methoxyethyl nucleotides (2'MOE wings) and the
CC   cytidine nucleotides are all 5-methylcytidines. The antisense compounds
CC   are useful for modulating the expression of CD40 ligand and for treating
CC   diseases or conditions associated with expression of CD40 ligand, e.g.
CC   cancer, autoimmune disorder, inflammatory disorder, or a disease or
CC   condition arising from aberrant apoptosis. The antisense compounds are
CC   also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent
CC   or delay infection, inflammation or tumor formation, as research reagents
CC   and kits, and in distinguishing between functions of various members of a
CC   biological pathway. Oligonucleotides ACC44014-ACC44091 represent the
CC   antisense oligonucleotides of the invention to inhibit expression of the
CC   human CD40 ligand gene
XX
SQ   Sequence 20 BP; 9 A; 3 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4482 AATGTATTTGATTTATAAGT 4501
              |||| |||||||||| |||
Db         20 AATGCATTTGATTTATCAGT 1


RESULT 775
ABZ59435
ID   ABZ59435 standard; DNA; 20 BP.
XX
AC   ABZ59435;
XX
DT   17-APR-2003  (first entry)
XX
DE   Human src-c chimeric phosphorothioate oligonucleotide SEQ ID NO:56.
XX
KW   Human; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;
KW   antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
KW   antisense oligonucleotide; aberrant bone remodeling; breast cancer;
KW   hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
KW   ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
KW   Kaposi's sarcoma; infection; inflammation; tumour formation;
KW   phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
XX
PN   WO200295053-A2.
XX
PD   28-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-US015684.
XX
PR   18-MAY-2001; 2001US-00860473.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett FC,  Watt AT;
XX
DR   WPI; 2003-120806/11.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding src-c,
PT   useful for diagnosing, treating or preventing diseases associated with
PT   the expression of src-c, e.g. cancer or inflammation, and in research
PT   applications.
XX
PS   Claim 3; Page 89; 137pp; English.
XX
CC   The present invention describes a compound (I) that is 8-50 nucleobases
CC   in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
CC   coding region, intron region, exon region, stop codon, intron:exon
CC   junction, exon:exon junction, or 5' mRNA variant of src-c, and which
CC   specifically hybridises with and inhibits the expression of src-c. (I)
CC   have cytostatic, antiinflammatory, osteopathic and antibacterial
CC   activities, and can be used in antisense therapy and in vaccines. The
```

CC antisense compounds (I) can be used for modulating the expression of src-
CC c and for treating diseases or conditions associated with expression of
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
CC particularly cancer, such as breast cancer, pancreatic cancer, lung
CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
CC or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation, as research reagents and kits, and in distinguishing between
CC functions of various members of a biological pathway. The present
CC sequence represents a human src-c antisense chimeric phosphorothioate
CC oligonucleotide, which is used in an example from the present invention
XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3229 TGTTGAGCCAGTGGGCCAGC 3248
|| ||||| ||||||||||
Db 1 TGCTGAGCGAGTGGGCCAGC 20

RESULT 776
ABZ89549
ID ABZ89549 standard; DNA; 20 BP.
XX
AC ABZ89549;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4791; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 2 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4079 GTATGTGTGGCTGTGGGTGT 4098
||||||||| ||||| ||||
Db 1 GTATGTGTGCCTGTGTGTGT 20

RESULT 777
ABZ88498/c
ID ABZ88498 standard; DNA; 20 BP.
XX
AC ABZ88498;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3740; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGTT 4520
|||||||||| ||||||||
Db 20 TTTTTTTTTTGGTTTGGGTT 1

RESULT 778
ABD24728/c
ID ABD24728 standard; DNA; 20 BP.
XX
AC ABD24728;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI038433-derived oligonucleotide SEQ ID 3740.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 3740; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 15 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGTT 4520
|||||||||| ||||||||
Db 20 TTTTTTTTTTGGTTTGGGTT 1

RESULT 779
ABD25779
ID ABD25779 standard; DNA; 20 BP.
XX
AC ABD25779;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI085559-derived oligonucleotide SEQ ID 4791.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4791; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 1 A; 2 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4079 GTATGTGTGGCTGTGGGTGT 4098
              ||||||||| ||||| ||||
Db          1 GTATGTGTGCCTGTGTGTGT 20
```

RESULT 780
ADH67295
ID ADH67295 standard; DNA; 20 BP.
XX
AC ADH67295;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4129.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 4129; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4495 TATAAGTTTTTTTTTTTTT 4514
              ||| || ||||||||||||||
Db          1 TATGAGCTTTTTTTTTTTT 20
```

RESULT 781
ADH66257
ID ADH66257 standard; DNA; 20 BP.
XX
AC ADH66257;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #3091.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 3091; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense

```
CC   oligonucleotides are also useful for treating diabetes, obesity,
CC   cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC   present DNA sequence represents an antisense oligonucleotide that targets
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2125 TTTCTTTTCTTTTTTTCTTT 2144
              || ||||| ||||||||||
Db          1 TTCCTTTTATTTTTTTCTTT 20


RESULT 782
ADH67152
ID   ADH67152 standard; DNA; 20 BP.
XX
AC   ADH67152;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human glucocorticoid receptor-specific antisense oligonucleotide #3986.
XX
KW   antisense oligonucleotide; glucocorticoid receptor; infection;
KW   inflammation; tumour formation; diabetes; obesity;
KW   cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW   phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS   Homo sapiens.
XX
PN   WO2003099215-A2.
XX
PD   04-DEC-2003.
XX
PF   20-MAY-2003; 2003WO-US016084.
XX
PR   20-MAY-2002; 2002US-0381857P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Crosby SD,  Nalseth AE;
XX
DR   WPI; 2004-035034/03.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT   cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS   Claim 4; SEQ ID NO 3986; 985pp; English.
XX
CC   The invention comprises an antisense oligonucleotides that are targeted
CC   to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC   antisense oligonucleotides of the invention are useful for preventing or
CC   delaying infection, inflammation or tumour formation. The antisense
CC   oligonucleotides are also useful for treating diabetes, obesity,
CC   cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC   present DNA sequence represents an antisense oligonucleotide that targets
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4496 ATAAGTTTTTTTTTTTTTTT 4515
              || || ||||||||||||||
Db          1 ATGAGCTTTTTTTTTTTTTT 20


RESULT 783
ADJ61323
ID   ADJ61323 standard; DNA; 20 BP.
XX
AC   ADJ61323;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Oligonucleotide associated to IL5R-X61176 #15.
XX
KW   interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW   airway inflammation; allergy; asthma; impeded respiration;
KW   cystic fibrosis; acute respiratory distress syndrome;
KW   pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO2004011613-A2.
XX
PD   05-FEB-2004.
XX
PF   25-JUL-2003; 2003WO-US023509.
XX
PR   29-JUL-2002; 2002US-0399076P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Tang L,  Sandrasagra A,  Aguilar D,  Miller S;
PI   Shahabuddin S,  Lu H,  Cong H;
XX
DR   WPI; 2004-203534/19.
XX
PT   Novel single or multiple target oligonucleotide anti-sense to e.g.
PT   initiation codons and introns of respiratory disease-relevant genes e.g.,
PT   CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT   disease e.g., asthma.
XX
PS   Claim 2; SEQ ID NO 2179; 85pp; English.
XX
CC   The present invention relates to an oligonucleotide anti-sense to e.g.,
CC   initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC   end of nucleic acid target comprising gene(s) chosen from e.g.
CC   interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC   oligonucleotide and optionally surfactant operatively linked to the
CC   oligonucleotide. The method is useful for preventing or treating a
CC   respiratory or lung disease, which involves administering to the airways
CC   of a subject an effective amount of an inhibitor. The oligonucleotide is
CC   useful for production of a medicament for the prevention and/or treatment
CC   of a respiratory or lung disease. The respiratory or lung disease is
CC   chosen from airway inflammation, allergy(ies), asthma, impeded
CC   respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC   (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC   (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC   obstruction. The present sequence represents an oligonucleotide of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 784
ADJ61324
ID   ADJ61324 standard; DNA; 20 BP.
```

```
XX
AC   ADJ61324;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Oligonucleotide associated to IL5R-X61176 #16.
XX
KW   interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW   airway inflammation; allergy; asthma; impeded respiration;
KW   cystic fibrosis; acute respiratory distress syndrome;
KW   pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO2004011613-A2.
XX
PD   05-FEB-2004.
XX
PF   25-JUL-2003; 2003WO-US023509.
XX
PR   29-JUL-2002; 2002US-0399076P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Tang L,  Sandrasagra A,  Aguilar D,  Miller S;
PI   Shahabuddin S,  Lu H,  Cong H;
XX
DR   WPI; 2004-203534/19.
XX
PT   Novel single or multiple target oligonucleotide anti-sense to e.g.
PT   initiation codons and introns of respiratory disease-relevant genes e.g.,
PT   CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT   disease e.g., asthma.
XX
PS   Claim 2; SEQ ID NO 2180; 85pp; English.
XX
CC   The present invention relates to an oligonucleotide anti-sense to e.g.,
CC   initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC   end of nucleic acid target comprising gene(s) chosen from e.g.
CC   interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC   oligonucleotide and optionally surfactant operatively linked to the
CC   oligonucleotide. The method is useful for preventing or treating a
CC   respiratory or lung disease, which involves administering to the airways
CC   of a subject an effective amount of an inhibitor. The oligonucleotide is
CC   useful for production of a medicament for the prevention and/or treatment
CC   of a respiratory or lung disease. The respiratory or lung disease is
CC   chosen from airway inflammation, allergy(ies), asthma, impeded
CC   respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC   (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC   (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC   obstruction. The present sequence represents an oligonucleotide of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 785
ADJ61325
ID   ADJ61325 standard; DNA; 20 BP.
XX
AC   ADJ61325;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Oligonucleotide associated to IL5R-X61176 #17.
XX
KW   interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW   airway inflammation; allergy; asthma; impeded respiration;
KW   cystic fibrosis; acute respiratory distress syndrome;
KW   pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO2004011613-A2.
XX
PD   05-FEB-2004.
XX
PF   25-JUL-2003; 2003WO-US023509.
XX
PR   29-JUL-2002; 2002US-0399076P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Tang L,  Sandrasagra A,  Aguilar D,  Miller S;
PI   Shahabuddin S,  Lu H,  Cong H;
XX
DR   WPI; 2004-203534/19.
XX
PT   Novel single or multiple target oligonucleotide anti-sense to e.g.
PT   initiation codons and introns of respiratory disease-relevant genes e.g.,
PT   CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT   disease e.g., asthma.
XX
PS   Claim 2; SEQ ID NO 2181; 85pp; English.
XX
CC   The present invention relates to an oligonucleotide anti-sense to e.g.,
CC   initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC   end of nucleic acid target comprising gene(s) chosen from e.g.
CC   interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC   oligonucleotide and optionally surfactant operatively linked to the
CC   oligonucleotide. The method is useful for preventing or treating a
CC   respiratory or lung disease, which involves administering to the airways
CC   of a subject an effective amount of an inhibitor. The oligonucleotide is
CC   useful for production of a medicament for the prevention and/or treatment
CC   of a respiratory or lung disease. The respiratory or lung disease is
CC   chosen from airway inflammation, allergy(ies), asthma, impeded
CC   respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC   (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC   (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC   obstruction. The present sequence represents an oligonucleotide of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 786
ADK61702
ID   ADK61702 standard; DNA; 20 BP.
XX
AC   ADK61702;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Base containing SSR sequence #6.
XX
KW   rice variety; amplification genetic marker; ds.
XX
OS   Oryza sp.
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XX
PN   JP2003319782-A.
XX
PD   11-NOV-2003.
XX
PF   02-MAY-2002; 2002JP-00130645.
XX
PR   02-MAY-2002; 2002JP-00130645.
XX
PA   (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
PA   (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
XX
DR   WPI; 2004-003560/01.
XX
PT   Identifying rice variety using base sequence containing SSR sequence and
PT   amplifying genetic marker.
XX
PS   Claim 22; SEQ ID NO 6; 30pp; Japanese.
XX
CC   The present invention relates to identifying a rice variety as
CC   amplification genetic marker and identifying whether test rice variety is
CC   any one of the 32 rice varieties e.g., Kasalath, breath which came or
CC   Hayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USSR22,
CC   Nihonbare. The method is useful for identifying rice variety and
CC   identifies excellent rice variety. The present sequence represents a base
CC   - containing SSR sequence of the invention.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 787
ADJ25304
ID   ADJ25304 standard; DNA; 20 BP.
XX
AC   ADJ25304;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human endothelial lipase antisense oligonucleotide, SEQ ID 3702.
XX
KW   Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW   Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW   cardiovascular disorder; metabolic syndrome X; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "This oligonucleotide has a phosphorothioate
FT                    backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                    and 3' ends, which are 4 nucleotides in length. Also all
FT                    cytidine residues are 5-methylcytidines"
XX
PN   WO2004009541-A2.
XX
PD   29-JAN-2004.
XX
PF   18-JUL-2003; 2003WO-US022410.
XX
PR   19-JUL-2002; 2002US-0397106P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Bhat BG;
XX
DR   WPI; 2004-132912/13.
XX
PT   New antisense oligonucleotide for modulating endothelial lipase
PT   expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT   high density lipoprotein or cardiovascular disorders.
XX
PS   Claim 3; SEQ ID NO 3702; 1007pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADJ21603-
CC   ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC   (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC   with and inhibits the expression of EL. The antisense oligonucleotides
CC   are useful for modulating the expression of endothelial lipase in cells
CC   or tissues to treat diseases associated with EL expression, such as
CC   dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC   disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC   used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ   Sequence 20 BP; 11 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4754 AAAATGGGGATAATAATACT 4773
              ||||| |||||||||||| |
Db          1 AAAATAGGGATAATAATAGT 20


RESULT 788
ADL58138/c
ID   ADL58138 standard; DNA; 20 BP.
XX
AC   ADL58138;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 387.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
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```
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 387; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 7 A; 5 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2220 AGCTCATGGAATTTTGAGTA 2239
              |||| |||||| ||||||||
Db         20 AGCTTATGGAAATTTGAGTA 1


RESULT 789
ADM14520
ID   ADM14520 standard; DNA; 20 BP.
XX
AC   ADM14520;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:707.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 707; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 14 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3602 TGGAAAAAAACAAAAACAGA 3621
              |||||||||| ||| |||||
Db          1 TGGAAAAAAAAAAATACAGA 20


RESULT 790
ADO46716
ID   ADO46716 standard; DNA; 20 BP.
XX
AC   ADO46716;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human oligonucleotide #2082.
XX
KW   Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW   CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW   tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW   lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW   asthma; lung allergy; inflammation; inflammatory disease;
KW   airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW   chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW   acute respiratory distress syndrome; pulmonary hypertension;
KW   lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS   Homo sapiens.
```

XX
PN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
PF 25-JUL-2003; 2003US-00627930.
XX
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-293804/27.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Claim 2; SEQ ID NO 2182; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3182 TCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 1 TCTCTCTCTCTCTCTCTCTC 20

RESULT 791
ADO46715
ID ADO46715 standard; DNA; 20 BP.
XX
AC ADO46715;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #2081.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
PN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
PF 25-JUL-2003; 2003US-00627930.
XX
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-293804/27.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Claim 2; SEQ ID NO 2181; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 792
ADO46713
ID   ADO46713 standard; DNA; 20 BP.
XX
AC   ADO46713;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human oligonucleotide #2079.
XX
KW   Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW   CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW   tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW   lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW   asthma; lung allergy; inflammation; inflammatory disease;
KW   airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW   chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW   acute respiratory distress syndrome; pulmonary hypertension;
KW   lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS   Homo sapiens.
XX
PN   US2004049022-A1.
XX
PD   11-MAR-2004.
XX
PF   25-JUL-2003; 2003US-00627930.
XX
PR   23-APR-2002; 2002WO-US013135.
PR   23-APR-2002; 2002WO-US013143.
XX
PA   (NYCE/) NYCE J W.
PA   (SAND/) SANDRASAGRA A.
PA   (TANG/) TANG L.
PA   (AGUI/) AGUILAR D.
PA   (MILL/) MILLER S.
PA   (SHAH/) SHAHABUDDIN S.
PA   (LUHH/) LU H.
PA   (CONG/) CONG H.
XX
PI   Nyce JW,  Sandrasagra A,  Tang L,  Aguilar D,  Miller S;
PI   Shahabuddin S,  Lu H,  Cong H;
XX
DR   WPI; 2004-293804/27.
XX
PT   Novel single or multiple target oligonucleotide anti-sense to e.g.
PT   initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT   RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT   asthma.
XX
PS   Claim 2; SEQ ID NO 2179; 174pp; English.
XX
CC   The invention relates to oligonucleotides anti-sense to an initiation
CC   codon, coding region, 5' or 3' intron-exon junction, intron or region
CC   with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC   chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC   -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC   tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC   also relates to a method of screening a candidate compound that binds to
CC   one or more nucleic acid target(s) or expressed product(s), for the
CC   prevention and/or treatment of a respiratory or lung disease. The
CC   oligonucleotides are useful for reducing or inhibiting expression of a
CC   gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC   CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC   tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC   useful for preventing or treating a respiratory or lung disease. The
CC   respiratory or lung disease is associated with hyper-responsiveness to
CC   and/or increased levels of, adenosine and/or levels of adenosine A
CC   receptor(s), and/or asthma and/or lung allergies associated with
CC   inflammation or an inflammatory disease. The respiratory or lung disease
CC   is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC   cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC   allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC   hypertension, lung inflammation, bronchitis, airway obstruction or
CC   bronchoconstriction. This sequence represents an oligonucleotide of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 793
ADO46714
ID   ADO46714 standard; DNA; 20 BP.
XX
AC   ADO46714;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human oligonucleotide #2080.
XX
KW   Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW   CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW   tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW   lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW   asthma; lung allergy; inflammation; inflammatory disease;
KW   airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW   chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW   acute respiratory distress syndrome; pulmonary hypertension;
KW   lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS   Homo sapiens.
XX
PN   US2004049022-A1.
XX
PD   11-MAR-2004.
XX
PF   25-JUL-2003; 2003US-00627930.
XX
PR   23-APR-2002; 2002WO-US013135.
PR   23-APR-2002; 2002WO-US013143.
XX
PA   (NYCE/) NYCE J W.
PA   (SAND/) SANDRASAGRA A.
PA   (TANG/) TANG L.
PA   (AGUI/) AGUILAR D.
PA   (MILL/) MILLER S.
PA   (SHAH/) SHAHABUDDIN S.
PA   (LUHH/) LU H.
PA   (CONG/) CONG H.
XX
PI   Nyce JW,  Sandrasagra A,  Tang L,  Aguilar D,  Miller S;
PI   Shahabuddin S,  Lu H,  Cong H;
XX
DR   WPI; 2004-293804/27.
XX
PT   Novel single or multiple target oligonucleotide anti-sense to e.g.
PT   initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT   RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT   asthma.
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XX
PS   Claim 2; SEQ ID NO 2180; 174pp; English.
XX
CC   The invention relates to oligonucleotides anti-sense to an initiation
CC   codon, coding region, 5' or 3' intron-exon junction, intron or region
CC   with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC   chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC   -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC   tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC   also relates to a method of screening a candidate compound that binds to
CC   one or more nucleic acid target(s) or expressed product(s), for the
CC   prevention and/or treatment of a respiratory or lung disease. The
CC   oligonucleotides are useful for reducing or inhibiting expression of a
CC   gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC   CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC   tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC   useful for preventing or treating a respiratory or lung disease. The
CC   respiratory or lung disease is associated with hyper-responsiveness to
CC   and/or increased levels of, adenosine and/or levels of adenosine A
CC   receptor(s), and/or asthma and/or lung allergies associated with
CC   inflammation or an inflammatory disease. The respiratory or lung disease
CC   is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC   cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC   allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC   hypertension, lung inflammation, bronchitis, airway obstruction or
CC   bronchoconstriction. This sequence represents an oligonucleotide of the
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 794
ADP69247
ID   ADP69247 standard; DNA; 20 BP.
XX
AC   ADP69247;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #141.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 141; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTTA 4521
              |||||||||||||| | |||
Db          1 TTTTTTTTTTTTTTTGTTTA 20


RESULT 795
ADP69305
ID   ADP69305 standard; DNA; 20 BP.
XX
AC   ADP69305;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #199.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 199; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
```

CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4503 TTTTTTTTTTTTTGGGTTAA 4522
||||||||||||| | ||||
Db 1 TTTTTTTTTTTTTGTTTAA 20

RESULT 796
ADP69379
ID ADP69379 standard; DNA; 20 BP.
XX
AC ADP69379;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #273.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 273; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4504 TTTTTTTTTTTTGGGTTAAA 4523
|||||||||||| | |||||
Db 1 TTTTTTTTTTTTGTTTAAA 20

RESULT 797
ADP69193
ID ADP69193 standard; DNA; 20 BP.
XX
AC ADP69193;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #87.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 87; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGTT 4520
|||||||||||||||| | ||
Db 1 TTTTTTTTTTTTTTTTGTTT 20

RESULT 798
AAQ75633
ID AAQ75633 standard; DNA; 21 BP.
XX
AC AAQ75633;

```
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| | ||
Db          2 TTTTTTTTTTTTTTTTGATT 21


RESULT 799
AAQ75778
ID   AAQ75778 standard; DNA; 21 BP.
XX
AC   AAQ75778;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTT 2143
              |||| |||| ||||||||||
Db          1 TTTTTTTTTTTTTTTTTCTT 20


RESULT 800
AAQ75650
ID   AAQ75650 standard; DNA; 21 BP.
XX
AC   AAQ75650;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||  |||
Db          1 TTTTTTTTTTTTTTTTTGTT 20
```

RESULT 801
AAQ75665
ID AAQ75665 standard; DNA; 21 BP.
XX
AC AAQ75665;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||| | ||
Db          2 TTTTTTTTTTTTTTTTGCTT 21
```

RESULT 802
AAQ75713
ID AAQ75713 standard; DNA; 21 BP.
XX
AC AAQ75713;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              ||||||||||||||  |||
Db          2 TTTTTTTTTTTTTTTTAGTT 21
```

RESULT 803
AAQ75728
ID AAQ75728 standard; DNA; 21 BP.
XX
AC AAQ75728;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of

```
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2129 TTTTCTTTTTTTCTTTAATA 2148
              |||| ||||||| |||||||
Db          2 TTTTTTTTTTTTTTTTAATA 21


RESULT 804
AAQ75649
ID   AAQ75649 standard; DNA; 21 BP.
XX
AC   AAQ75649;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||  |||
Db          1 TTTTTTTTTTTTTTTTTGTT 20


RESULT 805
AAQ75775
ID   AAQ75775 standard; DNA; 21 BP.
XX
AC   AAQ75775;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTT 2143
              |||| |||| ||||||||||
Db          1 TTTTTTTTTTTTTTTTTCTT 20


RESULT 806
AAQ75776
ID   AAQ75776 standard; DNA; 21 BP.
XX
AC   AAQ75776;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
```

```
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCTT 2143
              |||| |||| ||||||||||
Db          1 TTTTTTTTTTTTTTTTTCTT 20


RESULT 807
AAQ75745
ID   AAQ75745 standard; DNA; 21 BP.
XX
AC   AAQ75745;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||  |||
Db          2 TTTTTTTTTTTTTTTTCGTT 21


RESULT 808
AAQ75647
ID   AAQ75647 standard; DNA; 21 BP.
XX
AC   AAQ75647;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match              0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||  |||
Db          1 TTTTTTTTTTTTTTTTGTT 20


RESULT 809
AAT86582
ID   AAT86582 standard; DNA; 21 BP.
XX
AC   AAT86582;
XX
DT   25-MAR-1998  (first entry)
XX
DE   Phosphorothioate oligonucleotide #1.
XX
KW   Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;
KW   thioester; DNA synthesis; antisense oligonucleotide; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .21
```

```
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages between alternate
FT                   nucleotides (1 and 2, 3 and 4 etc.)"
XX
PN   WO9729116-A1.
XX
PD   14-AUG-1997.
XX
PF   06-FEB-1997;   97WO-GB000327.
XX
PR   06-FEB-1996;   96GB-00002326.
XX
PA   (CRUA-) CRUACHEM LTD.
XX
PI   Reese CB,  Rao MV;
XX
DR   WPI; 1997-415290/38.
XX
PT   Solid phase synthesis of phosphoro:thioate oligo:nucleotide(s) using new
PT   dimeric synthon(s) - useful as anti:sense molecules for inhibiting gene
PT   expression.
XX
PS   Example 3; Page 20; 38pp; English.
XX
CC   The present sequence represents a phosphorothioate oligonucleotide which
CC   was prepared by solid phase synthesis. The method comprises adding at
CC   least one dimeric phosphoramidite synthon, optionally having a protected
CC   thioester group in its internucleotide link, during the synthesis cycle.
CC   These novel dimeric phosphoramidite synthons are used as antisense
CC   molecules for inhibition of gene expression. The method gives increased
CC   yields of the phosphorothiate oligonucleotide (since fewer cycles are
CC   needed) and facilitates separation of impurities (greater difference in
CC   size compared with use of monomeric synthons)
XX
SQ   Sequence 21 BP; 0 A; 10 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 810
AAT86583
ID   AAT86583 standard; DNA; 21 BP.
XX
AC   AAT86583;
XX
DT   25-MAR-1998  (first entry)
XX
DE   Phosphorothioate oligonucleotide #2.
XX
KW   Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;
KW   thioester; DNA synthesis; antisense oligonucleotide; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .21
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages between alternate
FT                   nucleotides (1 and 2, 3 and 4 etc.)"
XX
PN   WO9729116-A1.
XX
PD   14-AUG-1997.
XX
PF   06-FEB-1997;   97WO-GB000327.
XX
PR   06-FEB-1996;   96GB-00002326.
XX
PA   (CRUA-) CRUACHEM LTD.
XX
PI   Reese CB,  Rao MV;
XX
DR   WPI; 1997-415290/38.
XX
PT   Solid phase synthesis of phosphoro:thioate oligo:nucleotide(s) using new
PT   dimeric synthon(s) - useful as anti:sense molecules for inhibiting gene
PT   expression.
XX
PS   Example 3; Page 25; 38pp; English.
XX
CC   The present sequence represents a phosphorothioate oligonucleotide which
CC   was prepared by solid phase synthesis. The method comprises adding at
CC   least one dimeric phosphoramidite synthon, optionally having a protected
CC   thioester group in its internucleotide link, during the synthesis cycle.
CC   These novel dimeric phosphoramidite synthons are used as antisense
CC   molecules for inhibition of gene expression. The method gives increased
CC   yields of the phosphorothiate oligonucleotide (since fewer cycles are
CC   needed) and facilitates separation of impurities (greater difference in
CC   size compared with use of monomeric synthons)
XX
SQ   Sequence 21 BP; 1 A; 10 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTCT 3200
              |||||||| ||| ||||||
Db          1 CTCTCTCTCTCTCTCTCTCT 20


RESULT 811
AAV40583
ID   AAV40583 standard; DNA; 21 BP.
XX
AC   AAV40583;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Human TSC gene exon 9 forward primer hTSCex9.
XX
KW   Thiazide-sensitive Na-Cl cotransporter; TSC; hTSC gene; human;
KW   ion transport; Gitelman's syndrome; Bartter's syndrome;
KW   hypokalaemic alkalosis; hypocalciuria; hypomagnesemia; diagnosis;
KW   therapy; SSCP; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9829431-A1.
XX
PD   09-JUL-1998.
XX
PF   19-DEC-1997;   97WO-US023553.
XX
PR   31-DEC-1996;   96US-00778052.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Lifton RP,  Simon DB;
XX
DR   WPI; 1998-388029/33.
XX
PT   Thiazide sensitive cotransporter and ATP sensitive potassium channel
PT   genes - useful for developing products for the diagnosis and treatment of
PT   ion transport disorders, e.g. Gitelman's Syndrome or Bartter's Syndrome.
XX
PS   Example 1; Page 51; 105pp; English.
XX
CC   Primers hTSCex9 forward and reverse (see AAV40583 and AAV40584,
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```
CC   respectively) are designed to amplify exon 9 of the human hTSC gene (see
CC   AAV40561) that codes for thiazide-sensitive Na-Cl cotransporter TSC (see
CC   AAW29682). Both primers are located within introns of hTSC. 27 Sets of
CC   specific primers (see AAV40565-V40618) were used for SSCP analysis of
CC   hTSC. Amplified products were analysed for molecular variants by
CC   electrophoresis, and identified variants were sequenced. Complete linkage
CC   of Gitelman's syndrome with TSC was demonstrated. Identification of the
CC   molecular basis of Gitelman's syndrome allows for the genetic diagnosis
CC   of this disorder. The invention provides products and methods useful for
CC   diagnosis and treatment of Gitelman's syndrome and other ion transport
CC   disorders
XX
SQ   Sequence 21 BP; 1 A; 12 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3183 CTCTCTCCCTCCCTCTCTCA 3202
              ||||||||||||||||  |||
Db             1 CTCTCTCCCTCCCTCCTTCA 20


RESULT 812
ABS98543/c
ID   ABS98543 standard; DNA; 21 BP.
XX
AC   ABS98543;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human acetyl choline muscarinic receptor 3 polymorphic sequence #9.
XX
KW   Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 28; Page 159; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   polymorphic DNA sequence of the invention
XX
SQ   Sequence 21 BP; 9 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
              ||||||||||| ||||| ||
Db            20 ATATATATACACATATATAT 1


RESULT 813
ACA89736/c
ID   ACA89736 standard; DNA; 21 BP.
XX
AC   ACA89736;
XX
DT   09-JUL-2003  (first entry)
XX
DE   Herbicide resistance polymorphic marker related primer #35.
XX
KW   Polymorphic marker; herbicide resistance; herbicide susceptible plant;
KW   herbicide resistant plant; Conyza canadensis; Lolium rigidum; goosegrass;
KW   glyphosate; paraquat; sulfonyl urea moiety; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003031937-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032637.
XX
PR   12-OCT-2001; 2001US-0328750P.
```

XX
PA (MORP-) MORPHOTEK INC.
XX
PI Chao Q, Grasso L, Nicolaides NC, Sass PM;
XX
DR WPI; 2003-430273/40.
XX
PT Identifying polymorphic markers of herbicide resistance in a plant, by
PT analyzing genomic DNA of herbicide resistant and susceptible plants, and
PT identifying difference that correlate with resistance or susceptibility.
XX
PS Example 6; Page 38; 168pp; English.
XX
CC The invention describes a method of identifying polymorphic markers of
CC herbicide resistance in a plant. The method involves: isolating genomic
CC DNA from an herbicide susceptible plant and an herbicide resistant plant
CC of the same species, performing genetic analysis and identifying
CC differences between their genomic DNA, identifying the difference that
CC correlate with herbicide resistance or susceptibility, thus identifying
CC polymorphic markers. The method is useful for identifying polymorphic
CC markers of herbicide resistance in a plant e.g. Conyza canadensis, Lolium
CC rigidum and goosegrass species, where the herbicides include glyphosate,
CC paraquat and sulfonyl urea moieties. This sequence represents a primer
CC associated with the identification of polymorphic markers of herbicide
CC resistance
XX
SQ Sequence 21 BP; 10 A; 0 C; 10 G; 0 T; 0 U; 1 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3182 TCTCTCTCCCTCCCTCTCTC 3201
||||||||| ||| |||||||
Db 20 TCTCTCTCTCTCTCTCTCTC 1

RESULT 814
ADK01328
ID ADK01328 standard; DNA; 21 BP.
XX
AC ADK01328;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #48.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTTCTTTTTTTCTT 2143
|||| |||| ||||||||||
Db 2 TTTTTTTTTTTTTTTTTCTT 21

RESULT 815
ADK01312
ID ADK01312 standard; DNA; 21 BP.
XX
AC ADK01312;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #32.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGGTT 4520
||||||||||||||| |||
Db 2 TTTTTTTTTTTTTTTTGTT 21

RESULT 816
ADH28008/c
ID ADH28008 standard; DNA; 21 BP.
XX
AC ADH28008;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human chromosome 1 SNP PCR primer.
XX
KW genetic alteration; diagnosis; malignant disease; tumour; metastasis;
KW single nucleotide polymorphism; SNP; cancer; PCR primer; detection;
KW human; chromosome 1; ss.
XX
OS Synthetic.
XX
PN WO2004001016-A2.
XX
PD 31-DEC-2003.
XX
PF 25-JUN-2003; 2003WO-US019926.
XX
PR 25-JUN-2002; 2002US-0391515P.
XX
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX
PI Fortina P, Maris JM, Gelfand CA;
XX
DR WPI; 2004-071731/07.
XX
PT Detecting genetic alterations associated with cancer comprises providing
PT a target nucleic acid from a patient sample having a predetermined
PT sequence in the normal population, and assessing the nucleic acid for
PT loss of heterozygosity.
XX
PS Example 1; SEQ ID NO 127; 50pp; English.
XX
CC The present invention describes a method for determining a genetic
CC alteration in a nucleic acid for the diagnosis and management of
CC malignant disease. The method comprises providing a target nucleic acid
CC from a patient sample, the target nucleic acid having a predetermined
CC sequence in the normal population; and assessing the target nucleic acid
CC for the extent of loss of heterozygosity relative to predetermined loci,
CC an increased loss of heterozygosity being correlated with enhanced tumour
CC invasiveness and metastasis. Also described is a method for determining
CC the presence or absence of at least one specific nucleotide in a target
CC nucleic acid for the diagnosis and management of malignant disease. The
CC methods are useful in detecting genetic alterations (e.g. single
CC nucleotide polymorphisms (SNPs)) in a defined polynucleotide region as a
CC means to diagnose and manage malignant diseases such as cancer. The
CC present sequence represents a PCR primer used to amplify genomic DNA
CC corresponding to known SNPs located in predetermined regions of human
CC chromosome 1, which is used in an example from the present invention.
XX
SQ Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3930 AATTCCACAGGTCATCAGAT 3949
||| |||||||||| ||||
Db 20 AATGCCACAGGTCATGAGAT 1

RESULT 817
ADH70964/c
ID ADH70964 standard; DNA; 21 BP.
XX
AC ADH70964;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta PCR primer #108.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ss; primer; PCR.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.

```
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 1158; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta PCR primer.
XX
SQ   Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3623 TTTGAGAACCTTGGACCACT 3642
              | ||||||||| ||||||||
Db         21 TCTGAGAACCTAGGACCACT 2


RESULT 818
ADH70613
ID   ADH70613 standard; DNA; 21 BP.
XX
AC   ADH70613;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #403.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 807; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 21 BP; 0 A; 10 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 5.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTCTCTC 3201
              |||||||| ||| |||||||
Db          1 TCTCTCTCTCTCTCTCTCTC 20


RESULT 819
AAQ20108
ID   AAQ20108 standard; DNA; 18 BP.
XX
AC   AAQ20108;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 942 to target human TNF Receptor mRNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW   cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  b
```

```
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 27; 42pp; English.
XX
CC   The oligomer was designed to target human TNF receptor mRNA beginning at
CC   nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC   ethanocytosine group. See also AAQ20109
XX
SQ   Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTC 2141
              ||||||||| ||||||||
Db          1 TTTTCTTTTTTTTTTTC 18


RESULT 820
AAQ30447
ID   AAQ30447 standard; DNA; 18 BP.
XX
AC   AAQ30447;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTC 2141
              ||||||||| ||||||||
Db          1 TTTTCTTTTTTTTTTTC 18


RESULT 821
AAV54170
ID   AAV54170 standard; cDNA; 18 BP.
XX
AC   AAV54170;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 7.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
```

```
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          1 GTTTTTTTTTTTTTTAG 18


RESULT 822
AAV54172
ID   AAV54172 standard; cDNA; 18 BP.
XX
AC   AAV54172;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 9.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          1 GTTTTTTTTTTTTTTCG 18


RESULT 823
AAZ90642
ID   AAZ90642 standard; DNA; 18 BP.
XX
AC   AAZ90642;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #3.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          1 GTTTTTTTTTTTTTTCG 18


RESULT 824
AAZ90640
ID   AAZ90640 standard; DNA; 18 BP.
XX
AC   AAZ90640;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #1.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
```

```
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTTGG 4517
              ||||||||||||||||| |
Db          1 GTTTTTTTTTTTTTTTAG 18


RESULT 825
ABL56900
ID   ABL56900 standard; DNA; 18 BP.
XX
AC   ABL56900;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Nucleic acid probe c.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a nucleic acid probe of the
CC   invention that was used for investigating the base selectivity of a
CC   target nucleic acid
XX
SQ   Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2384 CAAAAATAAAATATATAT 2401
              |||||| ||||||||||
Db          1 CAAAAAAAAAATATATAT 18


RESULT 826
ABX79779/c
ID   ABX79779 standard; cDNA; 18 BP.
XX
AC   ABX79779;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #104.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 385; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
```

```
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATAC 2411
              ||||||||| ||||||||
Db         18 ATATATATATATATATAC 1


RESULT 827
ADL95317/c
ID   ADL95317 standard; DNA; 18 BP.
XX
AC   ADL95317;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Anti-proliferative oligonucleotide #8.
XX
KW   ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
KW   cancer; malignant tumour.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   8
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally 32-P labelled"
XX
PN   US2004067197-A1.
XX
PD   08-APR-2004.
XX
PF   02-FEB-2001; 2001US-00775479.
XX
PR   26-NOV-1997;   97WO-CA000892.
PR   24-MAY-1999;   99US-00318106.
XX
PA   (LECL/) LECLERC G.
PA   (MART/) MARTEL R.
XX
PI   Leclerc G,  Martel R;
XX
DR   WPI; 2004-314974/29.
XX
PT   New anti-proliferative substance comprising a radiolabeled DNA carrier,
PT   useful for preventing or treating uncontrolled cellular proliferation
PT   e.g. restenosis, cancer or malignant tumors.
XX
PS   Claim 13; SEQ ID NO 8; 28pp; English.
XX
CC   The invention relates to an anti-proliferative substance for preventing
CC   uncontrolled cellular proliferation comprising a radiolabelled DNA
CC   carrier, where a radioisotope is located internally within the DNA
CC   sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier
CC   penetrates the cell membrane and is retained intracellularly for a time
CC   sufficient for the radio-isotope to effect a dose therapy. The carrier in
CC   the anti-proliferative substance is an oligonucleotide, which is linear
CC   or a plasmid, which is circular. The plasmid is of viral or bacterial
CC   origin. The oligonucleotide is a double- or a single-stranded DNA
CC   sequence, which is conjugated with an antibody for cell-specific
CC   delivery. The oligonucleotide is also conjugated to a stent surface,
CC   cholesterol, oleic acid, linoleic acid, TGFalpha, antibody, TGFbeta,
CC   cytokines or growth factors. The anti-proliferative substance is useful
CC   for preventing or treating uncontrolled cellular proliferation. The
CC   uncontrolled cell proliferation is a restenosis following angioplasty, or
CC   cancer or a malignant tumour. The present sequence represents an
CC   oligonucleotide carrier used in the invention.
XX
SQ   Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4515
              || ||||||||||||||||
Db         18 AAATTTTTTTTTTTTTT 1


RESULT 828
AAA83338
ID   AAA83338 standard; DNA; 19 BP.
XX
AC   AAA83338;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk8 ribozyme binding site #58.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 60; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 8 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 5.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1830 CACAAAGCTTCTAAAGCA 1847
              |||| |||||||||||||
Db          1 CACAGAGCTTCTAAAGCA 18


RESULT 829
AAH58500
```

ID AAH58500 standard; DNA; 19 BP.
XX
AC AAH58500;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk8 ribozyme binding site SEQ ID NO:924.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 139; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 8 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1830 CACAAAGCTTCTAAAGCA 1847
||||.||||||||||||
Db 1 CACAGAGCTTCTAAAGCA 18

RESULT 830
ADO14573/c
ID ADO14573 standard; RNA; 19 BP.
XX
AC ADO14573;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human PDGFr-targeted siNA upper strand SEQ ID NO:4.
XX
KW cytostatic; vasotropic; nephrotropic; cerebroprotective;
KW treating leukaemia; solid tumors; restenosis; polycystic kidney disease;
KW bronchiolitis; glomerulonephritis; stroke; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human;
KW platelet derived growth factor receptor; PDGFr; ss.
XX
OS Homo sapiens.
XX
PN WO2003072704-A2.
XX
PD 04-SEP-2003.
XX
PF 05-FEB-2003; 2003WO-US003473.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B;
XX
DR WPI; 2003-731605/69.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of tumors, downregulates expression of the platelet-derived
PT growth factor receptor gene.
XX
PS Example 3; SEQ ID NO 4; 148pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human platelet-derived growth factor
CC receptor (PDGFr) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA, double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siRNA; conjugates and/or
CC complexes of siRNA; and vectors that express siNA. The siNAs are used to
CC modulate expression of the PDGFr gene in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating leukaemia and solid tumours, restenosis, polycystic kidney
CC disease, bronchiolitis, glomerulonephritis and stroke. The siNAs are also
CC useful for drug screening, diagnosis, therapeutic target identification
CC and validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the upper strand of a human PDGFr-
CC targeted double-stranded siNA, which is identical to the PDGFr transcript
CC target sequence.
XX

```
SQ   Sequence 19 BP; 4 A; 8 C; 7 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 5.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1216 GGCCGCCCTCGGTCTGGC 1233
              ||||||||| ||||||||
Db         19 GGCCGCCCTGGGTCTGGC 2


RESULT 831
ADO14884
ID   ADO14884 standard; RNA; 19 BP.
XX
AC   ADO14884;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human PDGFr-targeted siNA lower strand SEQ ID NO:315.
XX
KW   cytostatic; vasotropic; nephrotropic; cerebroprotective;
KW   treating leukaemia; solid tumors; restenosis; polycystic kidney disease;
KW   bronchiolitis; glomerulonephritis; stroke; RNA interference;
KW   short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW   double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW   expression modulation; gene therapy; drug screening; diagnosis;
KW   therapeutic target identification; pharmacogenomics;
KW   gene function analysis; gene mapping; human;
KW   platelet derived growth factor receptor; PDGFr; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003072704-A2.
XX
PD   04-SEP-2003.
XX
PF   05-FEB-2003; 2003WO-US003473.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B;
XX
DR   WPI; 2003-731605/69.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of tumors, downregulates expression of the platelet-derived
PT   growth factor receptor gene.
XX
PS   Example 3; SEQ ID NO 315; 148pp; English.
XX
CC   The invention relates to short interfering nucleic acids (siNA) which
CC   downregulate expression of the human platelet-derived growth factor
CC   receptor (PDGFr) gene by RNA interference. The siNAs may or may not
CC   comprise ribonucleotides and may be double or single stranded. They
CC   further comprise sense and antisense regions, or alternatively are
CC   assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC   Specifically, the siNAs include short interfering RNA (siRNA, double-
CC   stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC   can be unmodified or chemically modified, can contain
CC   deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC   vector or enzymatically synthesised. The invention also relates to kits
CC   for the in vitro or in vivo delivery of siRNA; conjugates and/or
CC   complexes of siRNA; and vectors that express siNA. The siNAs are used to
CC   modulate expression of the PDGFr gene in cells, tissue explants or
CC   organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC   for the treatment of a variety of conditions. They may be used for
CC   treating leukaemia and solid tumours, restenosis, polycystic kidney
CC   disease, bronchiolitis, glomerulonephritis and stroke. The siNAs are also
CC   useful for drug screening, diagnosis, therapeutic target identification
CC   and validation, genetic engineering, pharmacogenomics, studying gene
CC   function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC   The present sequence represents the lower strand of a human PDGFr-
CC   targeted double-stranded siNA, which is identical to the PDGFr transcript
CC   target sequence.
XX
SQ   Sequence 19 BP; 0 A; 7 C; 8 G; 0 T; 4 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 5.6e+02;
  Matches   14;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1216 GGCCGCCCTCGGTCTGGC 1233
              |||||||: ||:|:|||
Db          1 GGCCGCCCUGGGUCUGGC 18


RESULT 832
AAQ75591
ID   AAQ75591 standard; DNA; 20 BP.
XX
AC   AAQ75591;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              |||||||||||||||| ||
Db          3 TTTTTTTTTTTTTTTCGG 20
```

RESULT 833
AAQ75563
ID AAQ75563 standard; DNA; 20 BP.
XX
AC AAQ75563;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||||||||||||||||| |
Db 3 TTTTTTTTTTTTTTTGAG 20

RESULT 834
AAQ75575
ID AAQ75575 standard; DNA; 20 BP.
XX
AC AAQ75575;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||||||||||||||||| ||
Db 3 TTTTTTTTTTTTTTTAGG 20

RESULT 835
AAQ75567
ID AAQ75567 standard; DNA; 20 BP.
XX
AC AAQ75567;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

```
SQ   Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||| |
Db          3 TTTTTTTTTTTTTTTGTG 20


RESULT 836
AAQ75571
ID   AAQ75571 standard; DNA; 20 BP.
XX
AC   AAQ75571;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGG 4518
              ||||||||||||||||| |
Db          3 TTTTTTTTTTTTTTTGCG 20


RESULT 837
ABL57552/c
ID   ABL57552 standard; DNA; 20 BP.
XX
AC   ABL57552;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly s.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 6; Page 23; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the effects of
CC   the number of G(s) in each target nucleic acid, and the number of G(S) in
CC   its corresponding invention nucleic acid probe
XX
SQ   Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1


RESULT 838
ABL57553/c
ID   ABL57553 standard; DNA; 20 BP.
XX
AC   ABL57553;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly t.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
```

KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1
```

RESULT 839
ABL57554/c
ID ABL57554 standard; DNA; 20 BP.
XX
AC ABL57554;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly u.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1
```

RESULT 840
ABL57548/c
ID ABL57548 standard; DNA; 20 BP.
XX
AC ABL57548;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribooligonucleotide poly o.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX

OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(S) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2385 AAAAATAAAATATATATA 2402
||||| ||||||||||||
Db 18 AAAAAAAAAATATATATA 1

RESULT 841
ABQ79871
ID ABQ79871 standard; DNA; 20 BP.
XX
AC ABQ79871;
XX
DT 23-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer #1.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002191369-A.
XX
PD 09-JUL-2002.
XX
PF 27-DEC-2000; 2000JP-00399573.
XX
PR 27-DEC-2000; 2000JP-00399573.
XX
PA (TOJO) TOYO KOHAN CO LTD.
PA (TAKA/) TAKAHASHI K.
XX
DR WPI; 2002-630904/68.
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT a substrate on which a DNA is immobilized used in medical, biochemical,
PT molecular biological and gene engineering fields.
XX
PS Example; Page 9; 13pp; Japanese.
XX
CC The invention relates to performing a thermal cycle of PCR by using a
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC method is useful in the medical, biochemical, molecular biological and
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC used in the method of the invention
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTTTT 4515
|| ||||||||||||||||
Db 1 AAATTTTTTTTTTTTTTT 18

RESULT 842
ABA97633/c
ID ABA97633 standard; DNA; 20 BP.
XX
AC ABA97633;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly o nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX

```
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 4 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1


RESULT 843
ABA97638/c
ID   ABA97638 standard; DNA; 20 BP.
XX
AC   ABA97638;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly t nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 4 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1


RESULT 844
ABA97639/c
ID   ABA97639 standard; DNA; 20 BP.
XX
AC   ABA97639;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly u nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 4 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1


RESULT 845
ABA97637/c
ID   ABA97637 standard; DNA; 20 BP.
XX
AC   ABA97637;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly s nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
```

```
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATATA 2402
              ||||| ||||||||||||
Db         18 AAAAAAAAAATATATATA 1


RESULT 846
AAD35095
ID   AAD35095 standard; DNA; 20 BP.
XX
AC   AAD35095;
XX
DT   25-JUL-2002  (first entry)
XX
DE   HT15-C downstream PCR primer used for identification of genes.
XX
KW   Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
KW   sex discrimination; infertility treatment; chromosomal manipulation;
KW   sperm separation; gene therapy; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   EP1195382-A2.
XX
PD   10-APR-2002.
XX
PF   02-OCT-2001; 2001EP-00123259.
XX
PR   03-OCT-2000; 2000JP-00303994.
XX
PA   (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
PA   (UYGU-) UNIV GUNMA.
XX
PI   Aizawa A,  Kawakami A,  Kondo T;
XX
DR   WPI; 2002-354153/39.
XX
PT   New X-chromosome gene expressed in haploid cells of the testis, useful
PT   for gene diagnosis, discrimination of sex, separation of sperm,
PT   infertility treatment and chromosomal manipulation.
XX
PS   Example 1; Page 4; 28pp; English.
XX
CC   The present invention relates to genes located on the X-chromosome of
CC   mammals. These genes are specifically expressed in haploid cells of the
CC   testis and encode amino acid sequences having homology with the amino
CC   acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences
CC   of the invention are used for gene diagnosis, discrimination of sex,
CC   separation of sperm, infertility treatment and chromosomal manipulation,
CC   especially in livestock. They are also used in gene therapy. The present
CC   DNA sequence is a PCR primer which is used for the identification of
CC   genes by differential display method
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4515
              ||| ||||||||||||||
Db          1 AAGCTTTTTTTTTTTTT 18


RESULT 847
ABI96151/c
ID   ABI96151 standard; DNA; 20 BP.
XX
AC   ABI96151;
XX
DT   16-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#3238 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW   oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US010958.
XX
PR   14-APR-2000; 2000US-0197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch.
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
```

```
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2527 CATGAGATGGAGAGGCTG 2544
              |||||||||| ||||||
Db         18 CATGAGATGGACAGGCTG 1


RESULT 848
AAL61371/c
ID   AAL61371 standard; DNA; 20 BP.
XX
AC   AAL61371;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Human FXR antisense oligonucleotide, ISIS 145318.
XX
KW   Human; farnesoid X receptor; FXR; cardiovascular disease; gene therapy;
KW   atherosclerosis; hypercholesterolaemia; NR1H4; bile acid receptor; BAR;
KW   retinoid X receptor-interacting protein 14; phosphorothioate backbone;
KW   RIP14; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003044167-A2.
XX
PD   30-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036691.
XX
PR   15-NOV-2001; 2001US-00002491.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Watt AT;
XX
DR   WPI; 2003-468767/44.
XX
PT   New antisense oligonucleotides for modulating human farnesoid X receptor
PT   (FXR) expression, useful for treating conditions associated with FXR in
PT   humans, e.g. cardiovascular disease, atherosclerosis or
PT   hypercholesterolemia.
XX
PS   Claim 3; Page 74; 127pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of human farnesoid X receptor (FXR). FXR is
CC   also known as NR1H4, retinoid X receptor-interacting protein 14 (RIP14)
CC   and bile acid receptor (BAR). The antisense oligonucleotide is useful for
CC   inhibiting the expression of human FXR in cells or tissues. It is
CC   particularly useful for treating or preventing a disease or condition
CC   associated with FXR in a human, e.g. cardiovascular disease,
CC   atherosclerosis or hypercholesterolaemia. The antisense compound is
CC   useful for diagnostics, therapeutics, prophylaxis, or as research
CC   reagents or kits. It is also used in gene therapy. The present sequence
CC   is an antisense oligonucleotide targetted to human FXR DNA. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5032 AACATACAGAGGATGCCT 5049
              |||| ||||||||||||||
Db         20 AACAAACAGAGGATGCCT 3


RESULT 849
ABZ89872/c
ID   ABZ89872 standard; DNA; 20 BP.
XX
AC   ABZ89872;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5114; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
```

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||||||||||||||| |
Db 18 TTTTTTTTTTTTTTTGAG 1

RESULT 850
ABZ89301/c
ID ABZ89301 standard; DNA; 20 BP.
XX
AC ABZ89301;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4543; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
||||||||||||||| |
Db 18 TTTTTTTTTTTTTTTGAG 1

RESULT 851
ABZ89719
ID ABZ89719 standard; DNA; 20 BP.
XX
AC ABZ89719;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4961; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTTT 4515
|| ||||||||||||||||
Db 1 AATTTTTTTTTTTTTTT 18

RESULT 852
ABD26102/c
ID ABD26102 standard; DNA; 20 BP.
XX
AC ABD26102;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA463249-derived oligonucleotide SEQ ID 5114.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 5114; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
|||||||||||||||| |
Db 18 TTTTTTTTTTTTTTTGAG 1

RESULT 853
ABD25949
ID ABD25949 standard; DNA; 20 BP.
XX
AC ABD25949;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA906703-derived oligonucleotide SEQ ID 4961.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX

PS Claim 15; SEQ ID NO 4961; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTTT 4515
|| ||||||||||||||||
Db 1 AATTTTTTTTTTTTTTT 18

RESULT 854
ABD25531/c
ID ABD25531 standard; DNA; 20 BP.
XX
AC ABD25531;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI125651-derived oligonucleotide SEQ ID 4543.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4543; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTGGG 4518
|||||||||||||||| |
Db 18 TTTTTTTTTTTTTTTGAG 1

RESULT 855
ADJ25197
ID ADJ25197 standard; DNA; 20 BP.
XX
AC ADJ25197;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3595.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

```
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 4 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2004009541-A2.
XX
PD   29-JAN-2004.
XX
PF   18-JUL-2003; 2003WO-US022410.
XX
PR   19-JUL-2002; 2002US-0397106P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Bhat BG;
XX
DR   WPI; 2004-132912/13.
XX
PT   New antisense oligonucleotide for modulating endothelial lipase
PT   expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT   high density lipoprotein or cardiovascular disorders.
XX
PS   Claim 3; SEQ ID NO 3595; 1007pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADJ21603-
CC   ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC   (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC   with and inhibits the expression of EL. The antisense oligonucleotides
CC   are useful for modulating the expression of endothelial lipase in cells
CC   or tissues to treat diseases associated with EL expression, such as
CC   dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC   disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC   used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ   Sequence 20 BP; 10 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4753 TAAAATGGGGATAATAAT 4770
              |||||| ||||||||||
Db          3 TAAAATAGGGATAATAAT 20


RESULT 856
ADL59739/c
ID   ADL59739 standard; DNA; 20 BP.
XX
AC   ADL59739;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1988.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate backbone. All cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1988; 555pp; English.
XX
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 5.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||| ||
Db         20 TTTTTTTTTTTTTGGCTT 3


RESULT 857
ADO52643/c
ID   ADO52643 standard; DNA; 20 BP.
XX
AC   ADO52643;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Farnesoid X receptor gene expression antisense inhibitory oligo #16.
XX
KW   ss; antidiabetic; immunosuppressive; cardiovascular; antilipemic;
KW   antiarteriosclerotic; hepatotropic; litholytic; anorectic;
KW   neuroprotective; vasotropic; antisense; gene therapy;
KW   Farnesoid X receptor; diabetes; immunological disorder;
KW   cardiovascular disorder; dyslipidemia; atherosclerosis;
KW   high density lipoprotein; low density lipoprotein; hypercholesterolemia;
KW   gallstones; hypertriglyceridemia; obesity; neurological disorder;
KW   ischemia; reperfusion; diagnostics; prophylaxis.
XX
```

OS Homo sapiens.
XX
PN WO2004030750-A1.
XX
PD 15-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030353.
XX
PR 25-SEP-2002; 2002US-0413588P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Kane CD;
XX
DR WPI; 2004-347928/32.
XX
PT New antisense oligonucleotides useful for modulating expression of
PT Farnesoid X Receptor (FXR) or for treating diseases associated with FXR,
PT e.g. diabetes, immunological disorders, cardiovascular disorders,
PT gallstones or obesity.
XX
PS Claim 4; SEQ ID NO 16; 150pp; English.
XX
CC The invention relates to an antisense compound 8-30 nucleobases in length
CC targeted to a nucleic acid molecule encoding Farnesoid X receptor (FXR),
CC where the antisense compound specifically hybridizes with and inhibits
CC the expression of FXR. The composition and methods are useful for
CC inhibiting the expression of FXR (Farnesoid X receptor) in cells or
CC tissues, or for treating diseases or conditions associated with FXR, such
CC as diabetes, immunological disorders, cardiovascular disorders, e.g.
CC dyslipidemia and its symptoms, atherosclerosis, low HDL (high density
CC lipoprotein), elevated LDL (low density lipoprotein) or
CC hypercholesterolemia, gallstones, hypertriglyceridemia, obesity,
CC neurological disorders, or ischemia/reperfusion injury. In addition, the
CC composition is used for diagnostics, prophylaxis, or as research reagents
CC or kits. This sequence corresponds to an antisense oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5032 AACATACAGAGGATGCCT 5049
|||| ||||||||||||
Db 19 AACAAACAGAGGATGCCT 2

RESULT 858
ADO52650/c
ID ADO52650 standard; DNA; 20 BP.
XX
AC ADO52650;
XX
DT 15-JUL-2004 (first entry)
XX
DE Farnesoid X receptor gene expression antisense inhibitory oligo #23.
XX
KW ss; antidiabetic; immunosuppressive; cardiovascular; antilipemic;
KW antiarteriosclerotic; hepatotropic; litholytic; anorectic;
KW neuroprotective; vasotropic; antisense; gene therapy;
KW Farnesoid X receptor; diabetes; immunological disorder;
KW cardiovascular disorder; dyslipidemia; atherosclerosis;
KW high density lipoprotein; low density lipoprotein; hypercholesterolemia;
KW gallstones; hypertriglyceridemia; obesity; neurological disorder;
KW ischemia; reperfusion; diagnostics; prophylaxis.
XX
OS Homo sapiens.
XX
PN WO2004030750-A1.
XX
PD 15-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030353.
XX
PR 25-SEP-2002; 2002US-0413588P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Kane CD;
XX
DR WPI; 2004-347928/32.
XX
PT New antisense oligonucleotides useful for modulating expression of
PT Farnesoid X Receptor (FXR) or for treating diseases associated with FXR,
PT e.g. diabetes, immunological disorders, cardiovascular disorders,
PT gallstones or obesity.
XX
PS Claim 4; SEQ ID NO 23; 150pp; English.
XX
CC The invention relates to an antisense compound 8-30 nucleobases in length
CC targeted to a nucleic acid molecule encoding Farnesoid X receptor (FXR),
CC where the antisense compound specifically hybridizes with and inhibits
CC the expression of FXR. The composition and methods are useful for
CC inhibiting the expression of FXR (Farnesoid X receptor) in cells or
CC tissues, or for treating diseases or conditions associated with FXR, such
CC as diabetes, immunological disorders, cardiovascular disorders, e.g.
CC dyslipidemia and its symptoms, atherosclerosis, low HDL (high density
CC lipoprotein), elevated LDL (low density lipoprotein) or
CC hypercholesterolemia, gallstones, hypertriglyceridemia, obesity,
CC neurological disorders, or ischemia/reperfusion injury. In addition, the
CC composition is used for diagnostics, prophylaxis, or as research reagents
CC or kits. This sequence corresponds to an antisense oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5032 AACATACAGAGGATGCCT 5049
|||| ||||||||||||
Db 20 AACAAACAGAGGATGCCT 3

RESULT 859
ADO52628/c
ID ADO52628 standard; DNA; 20 BP.
XX
AC ADO52628;
XX
DT 15-JUL-2004 (first entry)
XX
DE Farnesoid X receptor gene expression antisense inhibitory oligo #1.
XX
KW ss; antidiabetic; immunosuppressive; cardiovascular; antilipemic;
KW antiarteriosclerotic; hepatotropic; litholytic; anorectic;
KW neuroprotective; vasotropic; antisense; gene therapy;
KW Farnesoid X receptor; diabetes; immunological disorder;
KW cardiovascular disorder; dyslipidemia; atherosclerosis;
KW high density lipoprotein; low density lipoprotein; hypercholesterolemia;
KW gallstones; hypertriglyceridemia; obesity; neurological disorder;
KW ischemia; reperfusion; diagnostics; prophylaxis.
XX
OS Homo sapiens.
XX
PN WO2004030750-A1.
XX
PD 15-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030353.
XX
PR 25-SEP-2002; 2002US-0413588P.
XX

PA (PHAA) PHARMACIA CORP.
XX
PI Kane CD;
XX
DR WPI; 2004-347928/32.
XX
PT New antisense oligonucleotides useful for modulating expression of
PT Farnesoid X Receptor (FXR) or for treating diseases associated with FXR,
PT e.g. diabetes, immunological disorders, cardiovascular disorders,
PT gallstones or obesity.
XX
PS Claim 4; SEQ ID NO 1; 150pp; English.
XX
CC The invention relates to an antisense compound 8-30 nucleobases in length
CC targeted to a nucleic acid molecule encoding Farnesoid X receptor (FXR),
CC where the antisense compound specifically hybridizes with and inhibits
CC the expression of FXR. The composition and methods are useful for
CC inhibiting the expression of FXR (Farnesoid X receptor) in cells or
CC tissues, or for treating diseases or conditions associated with FXR, such
CC as diabetes, immunological disorders, cardiovascular disorders, e.g.
CC dyslipidemia and its symptoms, atherosclerosis, low HDL (high density
CC lipoprotein), elevated LDL (low density lipoprotein) or
CC hypercholesterolemia, gallstones, hypertriglyceridemia, obesity,
CC neurological disorders, or ischemia/reperfusion injury. In addition, the
CC composition is used for diagnostics, prophylaxis, or as research reagents
CC or kits. This sequence corresponds to an antisense oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5032 AACATACAGAGGATGCCT 5049
||||.|||||||||||
Db 18 AACAAACAGAGGATGCCT 1

RESULT 860
ADM11779
ID ADM11779 standard; DNA; 19 BP.
XX
AC ADM11779;
XX
DT 20-MAY-2004 (first entry)
XX
DE Environmental pollutant method-related oligo dT PCR primer.
XX
KW aromatic compound; gene expression alteration;
KW environmental pollutant analysis; ss; oligo dT; PCR; primer.
XX
OS Unidentified.
XX
PN JP2004049103-A.
XX
PD 19-FEB-2004.
XX
PF 19-JUL-2002; 2002JP-00210632.
XX
PR 19-JUL-2002; 2002JP-00210632.
XX
PA (WARI/) WARIISHI H.
PA (KUBI) KUBOTA CORP.
XX
DR WPI; 2004-232127/22.
XX
PT Novel genes of eukaryotic microorganism belonging to Phenerochate genus,
PT and exhibiting change in expression of behavior in presence of aromatic
PT compound, is useful for analyzing environmental pollutant.
XX
PS Example 1; SEQ ID NO 9; 36pp; Japanese.
XX
CC The invention comprises genes from Phanerochaete chrysosporium which
CC exhibit a change in expression in the presence of an aromatic compound.
CC The Phanerochaete chrysosporium genes of the invention are useful for
CC analysing an environmental pollutant. The present DNA sequence represents
CC an oligo dT PCR primer that was used in an example of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 2 Other;

Query Match 0.4%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTG 4516
||||||||||||||||:
Db 2 GTTTTTTTTTTTTTTTV 18

RESULT 861
ADH70350/c
ID ADH70350 standard; DNA; 16 BP.
XX
AC ADH70350;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #140.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 544; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,

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CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 16 BP; 7 A; 0 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||||||||||||
Db         16 TATATATACATATATA 1


RESULT 862
AAV37934
ID   AAV37934 standard; cDNA; 17 BP.
XX
AC   AAV37934;
XX
DT   05-OCT-1998  (first entry)
XX
DE   Primer of the specification.
XX
KW   Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9824815-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP004469.
XX
PR   05-DEC-1996;   96JP-00325752.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI   Ishiwata T,  Sakurada M,  Nishimura A,  Nakagawa S,  Kuga T,  Nishi T;
PI   Nomura N,  Nagase T,  Sawada S,  Takei M;
XX
DR   WPI; 1998-333259/29.
XX
PT   Protein from leukocytes and DNA encoding it - useful as reagents for
PT   diagnosing and treating IgA nephropathy.
XX
PS   Example 2; Page 33; 41pp; Japanese.
XX
CC   PCR primers AAV37933-39 are used in the course of the invention. The
CC   specification descibes a novel protein isolated from leukocytes of
CC   patients with IgA nephropathy. Oligonucleotides based on the DNA sequence
CC   encoding this protein are useful as reagents for diagnosing and treating
CC   IgA nephropathy
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTT 16


RESULT 863
AAV49503
ID   AAV49503 standard; cDNA to mRNA; 17 BP.
XX
AC   AAV49503;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Human eosinophil cell activator HVC002 primer #1.
XX
KW   Eosinophil cell activator; treatment; diagnosis; malignant tumour;
KW   parasitic infection; allergic inflammation; eosinophilic pneumonia;
KW   rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9824817-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP004470.
XX
PR   05-DEC-1996;   96JP-00325762.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Yoshisue H,  Saito A,  Nakagawa S,  Kuga T,  Shinkai A,  Koike M;
PI   Nishi T;
XX
DR   WPI; 1998-333261/29.
XX
PT   DNA and encoded protein which activates eosinophil cells - for treatment
PT   of cancer, parasite infection, autoimmune disease and allergic
PT   inflammation.
XX
PS   Example 1; Page 64; 92pp; Japanese.
XX
CC   AAV49503-V49507 are primers used in the isolation of a human eosinophil
CC   cell activator. This protein and antibodies generated from the protein
CC   can be used for treatment and diagnosis of malignant tumours, parasitic
CC   infections, allergic inflammation, eosinophilic pneumonia, rapid onset
CC   eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
CC   the antisense DNA in gene therapy of these disorders. The protein can be
CC   used for screening of potential agonists or antagonists of its activity
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTT 16


RESULT 864
AAA30179
ID   AAA30179 standard; DNA; 17 BP.
XX
AC   AAA30179;
XX
DT   16-AUG-2000  (first entry)
XX
DE   PCR primer GT15A used in pollenosis associated gene identification.
XX
KW   Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW   IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
```

OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 865
AAA30180
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15C used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 866
AAX82722
ID AAX82722 standard; DNA; 17 BP.
XX
AC AAX82722;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IgA nephropathy-associated cDNA primer #63.
XX
KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002855.
XX
PR 02-JUN-1998; 98JP-00152603.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
PT DNA sequences preferentially expressed in IgA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins.
XX
PS Claim 3; Page 170; 180pp; Japanese.
XX
CC This invention describes novel DNA sequences preferentially expressed in
CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IgA nephropathy
CC incorporating the antisense sequences; the treatment of IgA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IgA nephropathy containing the antibodies; and compositions
CC for the treatment of IgA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IgA nephropathy. This sequence represents a primer used in the isolation

```
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 867
AAX82720
ID   AAX82720 standard; DNA; 17 BP.
XX
AC   AAX82720;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Human IgA nephropathy-associated cDNA primer #61.
XX
KW   IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW   human; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963085-A1.
XX
PD   09-DEC-1999.
XX
PF   28-MAY-1999;   99WO-JP002855.
XX
PR   02-JUN-1998;   98JP-00152603.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Ishiwata T,  Sakurada M,  Kawabata A,  Nakagawa S,  Nishi T,  Kuga T;
PI   Sawada S,  Takei M,  Shibata K,  Furuya A;
XX
DR   WPI; 2000-097328/08.
XX
PT   DNA sequences preferentially expressed in IgA nephropathy patients,
PT   proteins encoded by them, and antibodies to those proteins.
XX
PS   Claim 3; Page 169; 180pp; Japanese.
XX
CC   This invention describes novel DNA sequences preferentially expressed in
CC   IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC   them. Independent claims cover diagnostic reagents for IgA nephropathy
CC   incorporating the antisense sequences; the treatment of IgA nephropathy
CC   using the antisense sequences for mRNA inhibition; proteins associated
CC   with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC   antibodies recognizing these proteins; the production of the proteins by
CC   culture of host cells transformed with DNA encoding them; diagnostic
CC   reagents for IgA nephropathy containing the antibodies; and compositions
CC   for the treatment of IgA nephropathy which contain the antibodies. The
CC   products of the invention can be used for the diagnosis and treatment of
CC   IgA nephropathy. This sequence represents a primer used in the isolation
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 868
AAA25449
ID   AAA25449 standard; DNA; 17 BP.
XX
AC   AAA25449;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16
```

```
RESULT 869
AAA25451
ID   AAA25451 standard; DNA; 17 BP.
XX
AC   AAA25451;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 870
AAA25452
ID   AAA25452 standard; DNA; 17 BP.
XX
AC   AAA25452;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 871
AAA25447
ID   AAA25447 standard; DNA; 17 BP.
XX
```

```
AC   AAA25447;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1945.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4514
              ||||||||||||||||
Db          2 AGTTTTTTTTTTTTTT 17


RESULT 872
AAC64202
ID   AAC64202 standard; DNA; 17 BP.
XX
AC   AAC64202;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065046-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002730.
XX
PR   27-APR-1999;   99JP-00120489.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687339/67.
XX
PT   Pollinosis-associated gene 373 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT   in diagnosis of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 69; 80pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 373 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis gene 373; expression constructs and
CC   host cells comprising pollinosis-associated gene 373 nucleic acids;
CC   pollinosis-associated gene 373 primers and probes; antibodies against the
CC   protein encoded by the gene; methods of detection of pollinosis-
CC   associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC   diseases via the detection of pollinosis-associated gene 373 nucleic
CC   acids. The invention additionally encompasses methods of screening drug
CC   candidates for the treatment of allergic disease by measuring the
CC   expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC   T-cells in the presence of a test compound relative to a control.
CC   Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC   diseases and in the screening of drug candidates for the treatment of
CC   such diseases. The present sequence represents a PCR primer used in the
CC   isolation of human pollinosis-associated gene 373 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 873
AAC64203
ID   AAC64203 standard; DNA; 17 BP.
XX
AC   AAC64203;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
```

KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065046-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002730.
XX
PR 27-APR-1999; 99JP-00120489.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687339/67.
XX
PT Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 70; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis gene 373; expression constructs and
CC host cells comprising pollinosis-associated gene 373 nucleic acids;
CC pollinosis-associated gene 373 primers and probes; antibodies against the
CC protein encoded by the gene; methods of detection of pollinosis-
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC diseases via the detection of pollinosis-associated gene 373 nucleic
CC acids. The invention additionally encompasses methods of screening drug
CC candidates for the treatment of allergic disease by measuring the
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC T-cells in the presence of a test compound relative to a control.
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC diseases and in the screening of drug candidates for the treatment of
CC such diseases. The present sequence represents a PCR primer used in the
CC isolation of human pollinosis-associated gene 373 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 874
AAC64181
ID AAC64181 standard; DNA; 17 BP.
XX
AC AAC64181;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 875
AAC64182
ID AAC64182 standard; DNA; 17 BP.
XX
AC AAC64182;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX

PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 876
AAC64171
ID AAC64171 standard; DNA; 17 BP.
XX
AC AAC64171;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 38; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 877
AAC64172
ID AAC64172 standard; DNA; 17 BP.
XX
AC AAC64172;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX

PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 38; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 878
AAC64161
ID AAC64161 standard; DNA; 17 BP.
XX
AC AAC64161;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 39; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 879
AAC64162
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;

CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 880
AAC64213
ID AAC64213 standard; DNA; 17 BP.
XX
AC AAC64213;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 41; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 881
AAC64214
ID AAC64214 standard; DNA; 17 BP.
XX
AC AAC64214;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 42; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16
```

RESULT 882
AAC64231
ID AAC64231 standard; DNA; 17 BP.
XX
AC AAC64231;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16
```

RESULT 883
AAC64230
ID AAC64230 standard; DNA; 17 BP.
XX
AC AAC64230;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16
```

```
RESULT 884
AAC92292
ID   AAC92292 standard; DNA; 17 BP.
XX
AC   AAC92292;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 43; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 885
AAC92293
ID   AAC92293 standard; DNA; 17 BP.
XX
AC   AAC92293;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 44; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 886
AAC91720
ID   AAC91720 standard; DNA; 17 BP.
XX
AC   AAC91720;
XX
DT   27-MAR-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
KW   Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW   reduced expression; detection; diagnosis; drug screening;
KW   allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200073440-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003192.
XX
PR   27-MAY-1999;   99JP-00148785.
```

XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 887
AAC91719
ID AAC91719 standard; DNA; 17 BP.
XX
AC AAC91719;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 888
AAC82875
ID AAC82875 standard; DNA; 17 BP.
XX
AC AAC82875;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #2.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in

```
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 35; 42pp; Japanese.
XX
CC   This invention describes a novel nucleic acid molecule comprising a
CC   sequence (I) which undergoes significantly low expression in subjects
CC   after pollen scattering, and is useful in diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 889
AAC82874
ID   AAC82874 standard; DNA; 17 BP.
XX
AC   AAC82874;
XX
DT   20-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 441 primer #1.
XX
KW   Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW   pollen scattering; antigen; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073435-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003190.
XX
PR   27-MAY-1999;   99JP-00148783.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2001-061526/07.
XX
PT   Pollinosis-associated gene 441 which undergoes lower expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 35; 42pp; Japanese.
XX
CC   This invention describes a novel nucleic acid molecule comprising a
CC   sequence (I) which undergoes significantly low expression in subjects
CC   after pollen scattering, and is useful in diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 890
AAH47127
ID   AAH47127 standard; DNA; 17 BP.
XX
AC   AAH47127;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15C.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 66; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 891
AAH47126
ID   AAH47126 standard; DNA; 17 BP.
XX
AC   AAH47126;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15A.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
```

PD 07-SEP-2001.
XX
PF 23-FEB-2001; 2001WO-JP001372.
XX
PR 02-MAR-2000; 2000JP-00061832.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX
DR WPI; 2001-557789/62.
XX
PT Diagnosis of allergies including atopic dermatitis.
XX
PS Example 6; Page 65; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 892
ABK49634
ID ABK49634 standard; DNA; 17 BP.
XX
AC ABK49634;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 893
ABK49635
ID ABK49635 standard; DNA; 17 BP.
XX
AC ABK49635;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases

```
CC   comprises determining the expression level of a gene containing, the
CC   human cDNA appearing as ABK49633 which has homology with
CC   acetyltransferases in the eosinophils of a patient and comparing the
CC   expression level with that in the eosinophils of a healthy individual
CC   (i.e. differential display). Also included are methods of screening for
CC   candidate compounds which affect the expression level of the gene or the
CC   activity of the protein encoded by the gene (including related proteins
CC   and mutants), the use of probes based on the gene sequence in the
CC   examination of allergic diseases, the use of reporter constructs in the
CC   screening of candidate compounds, a vector containing a the transcription
CC   -controlling region of the gene, cells transformed with the vector, an
CC   antibody against the protein and a model animal for allergic diseases
CC   which is a transgenic non-human vertebrate with lowering of expression
CC   intensity of the gene in eosinophils. The method is examining allergic
CC   diseases particularly atopic dermatitis which is also applicable in
CC   screening candidate compounds for remedies. Such method can be performed
CC   in high throughput, at low cost. The present sequence is a differential
CC   display PCR primer for the cDNA encoding the human acetyltransferase-like
CC   protein 20-90-05
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 894
ABL59038
ID   ABL59038 standard; DNA; 17 BP.
XX
AC   ABL59038;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Nucleotide sequence of PCR primer GT15A.
XX
KW   Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002095500-A.
XX
PD   02-APR-2002.
XX
PF   25-SEP-2000; 2000JP-00291316.
XX
PR   25-SEP-2000; 2000JP-00291316.
XX
PA   (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA   (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR   WPI; 2002-439993/47.
XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 895
ABL59039
ID   ABL59039 standard; DNA; 17 BP.
XX
AC   ABL59039;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Nucleotide sequence of PCR primer GT15C.
XX
KW   Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002095500-A.
XX
PD   02-APR-2002.
XX
PF   25-SEP-2000; 2000JP-00291316.
XX
PR   25-SEP-2000; 2000JP-00291316.
XX
PA   (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA   (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR   WPI; 2002-439993/47.
XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 896
ABN99829
ID   ABN99829 standard; DNA; 17 BP.
XX
AC   ABN99829;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Human allergic disease related PCR primer SEQ ID NO: 18.
XX
KW   Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW   primer; ss.
XX
```

OS Homo sapiens.
XX
PN WO200233069-A1.
XX
PD 25-APR-2002.
XX
PF 28-SEP-2001; 2001WO-JP008574.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX
DR WPI; 2002-372311/40.
XX
PT Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
PS Example 1; Page 109; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 897
ABN99830
ID ABN99830 standard; DNA; 17 BP.
XX
AC ABN99830;
XX
DT 15-AUG-2002 (first entry)
XX
DE Human allergic disease related PCR primer SEQ ID NO: 19.
XX
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX
PD 25-APR-2002.
XX
PF 28-SEP-2001; 2001WO-JP008574.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX
DR WPI; 2002-372311/40.
XX
PT Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
PS Example 1; Page 109; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 898
AAL49948
ID AAL49948 standard; DNA; 17 BP.
XX
AC AAL49948;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human B1153 expression in allergic disease related PCR primer GT15A.
XX
KW Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN WO200250269-A1.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-JP011286.
XX
PR 21-DEC-2000; 2000JP-00389476.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX
DR WPI; 2002-713252/77.
XX
PT Examination of allergic diseases comprises detecting gene B1153 over-
PT expressed in T cells of allergy patients for diagnosis treatment and
PT investigation of atopic skin inflammation and asthma.
XX
PS Example 6; Page 81; 102pp; Japanese.
XX
CC The present invention relates to a method of examining allergic diseases
CC which comprises comparing the expression level of gene B1153 in allergy
CC patients with the expression level in healthy subjects. The method is
CC useful for the treatment, prevention, diagnosis and study of allergic
CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the

```
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 899
AAL49949
ID   AAL49949 standard; DNA; 17 BP.
XX
AC   AAL49949;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human B1153 expression in allergic disease related PCR primer GT15C.
XX
KW   Human; allergy; B1153; differential expression; antiallergic; asthma;
KW   antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200250269-A1.
XX
PD   27-JUN-2002.
XX
PF   21-DEC-2001; 2001WO-JP011286.
XX
PR   21-DEC-2000; 2000JP-00389476.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Matsumoto Y,  Imai Y,  Oshida T,  Sugita Y,  Nagasu T,  Tsujimoto G;
XX
DR   WPI; 2002-713252/77.
XX
PT   Examination of allergic diseases comprises detecting gene B1153 over-
PT   expressed in T cells of allergy patients for diagnosis treatment and
PT   investigation of atopic skin inflammation and asthma.
XX
PS   Example 6; Page 82; 102pp; Japanese.
XX
CC   The present invention relates to a method of examining allergic diseases
CC   which comprises comparing the expression level of gene B1153 in allergy
CC   patients with the expression level in healthy subjects. The method is
CC   useful for the treatment, prevention, diagnosis and study of allergic
CC   diseases including atopic skin inflammation and asthma. The present
CC   sequence is a PCR primer described in the exemplification of the
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 900
AAL47234
ID   AAL47234 standard; DNA; 17 BP.
XX
AC   AAL47234;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 2.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
XX
PF   11-OCT-2001; 2001WO-JP008937.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
PI   Takahashi E;
XX
DR   WPI; 2002-372313/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   intersectin 2 gene showing different expression particularly significant
PT   increase in eosinophils in patients.
XX
PS   Example 1; Page 52; 90pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   with intersectin 2 gene or a gene with equivalent function of intersectin
CC   2 as an indicator gene, which comprises determining the expression level
CC   of the gene in the eosinophils in a patient, and comparing the expression
CC   level with that in the eosinophils of a healthy individual. The method is
CC   for examining allergic diseases, particularly atopic dermatitis, which is
CC   also applicable in screening candidate compounds for remedies. The
CC   present sequence is an anchor primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 901
AAL47235
ID   AAL47235 standard; DNA; 17 BP.
XX
AC   AAL47235;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 3.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
```

XX
PF 11-OCT-2001; 2001WO-JP008937.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX
DR WPI; 2002-372313/40.
XX
PT Method for examining allergic diseases by differential display of
PT intersectin 2 gene showing different expression particularly significant
PT increase in eosinophils in patients.
XX
PS Example 1; Page 53; 90pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC with intersectin 2 gene or a gene with equivalent function of intersectin
CC 2 as an indicator gene, which comprises determining the expression level
CC of the gene in the eosinophils in a patient, and comparing the expression
CC level with that in the eosinophils of a healthy individual. The method is
CC for examining allergic diseases, particularly atopic dermatitis, which is
CC also applicable in screening candidate compounds for remedies. The
CC present sequence is an anchor primer described in the exemplification of
CC the invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 902
ABK49757
ID ABK49757 standard; DNA; 17 BP.
XX
AC ABK49757;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15c.
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15c.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 55; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15c PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 903
ABK49756
ID ABK49756 standard; DNA; 17 BP.
XX
AC ABK49756;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15a.
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15a.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 54; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic

```
CC   diseases particularly atopic dermatitis, and may also be used to screen
CC   candidate compounds for remedies. The method of the invention can be
CC   performed in high throughput, at low cost. The present sequence
CC   represents the GT15a PCR primer used to amplify the differentially
CC   amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 904
ADB04273
ID   ADB04273 standard; DNA; 17 BP.
XX
AC   ADB04273;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5259.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5259; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 905
ADB04272
ID   ADB04272 standard; DNA; 17 BP.
XX
AC   ADB04272;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5258.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5258; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17
```

```
RESULT 906
ADB41269
ID   ADB41269 standard; DNA; 17 BP.
XX
AC   ADB41269;
XX
DT   18-DEC-2003  (revised)
DT   04-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #1592.
XX
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
PD   15-MAY-2003.
XX
PF   17-SEP-2002; 2002WO-IB004219.
XX
PR   17-SEP-2001; 2001FR-00011981.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-441574/41.
XX
PT   New nucleic acid encoding human prostate membrane-specific antigen,
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 218; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 907
ADB45964
ID   ADB45964 standard; DNA; 17 BP.
XX
AC   ADB45964;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #6287.
XX
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
PD   15-MAY-2003.
XX
PF   17-SEP-2002; 2002WO-IB004219.
XX
PR   17-SEP-2001; 2001FR-00011981.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-441574/41.
XX
PT   New nucleic acid encoding human prostate membrane-specific antigen,
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 766; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 908
ADC84469
ID   ADC84469 standard; DNA; 17 BP.
XX
AC   ADC84469;
XX
```

DT 01-JAN-2004 (first entry)
XX
DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.
XX
KW Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2003159071-A.
XX
PD 03-JUN-2003.
XX
PF 22-NOV-2001; 2001JP-00358366.
XX
PR 22-NOV-2001; 2001JP-00358366.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2003-818678/77.
XX
PT New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX
PS Example 3; SEQ ID NO 2; 43pp; Japanese.
XX
CC The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 909
ADC84468
ID ADC84468 standard; DNA; 17 BP.
XX
AC ADC84468;
XX
DT 01-JAN-2004 (first entry)
XX
DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
XX
KW Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2003159071-A.
XX
PD 03-JUN-2003.
XX
PF 22-NOV-2001; 2001JP-00358366.
XX
PR 22-NOV-2001; 2001JP-00358366.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2003-818678/77.
XX
PT New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX
PS Example 3; SEQ ID NO 1; 43pp; Japanese.
XX
CC The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 910
ADE77745
ID ADE77745 standard; DNA; 17 BP.
XX
AC ADE77745;
XX
DT 29-JAN-2004 (first entry)
XX
DE DNA oligo (SeqID 5) related to the human B1799 gene.
XX
KW ss; allergic disease; B1799; antiallergic; antiinflammatory;
KW dermatological; gene therapy; atopic dermatitis.
XX
OS Unidentified.
XX
PN WO2003083139-A1.
XX
PD 09-OCT-2003.
XX
PF 25-FEB-2003; 2003WO-JP002047.
XX
PR 03-APR-2002; 2002JP-00100908.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
XX
PI Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;
XX
DR WPI; 2003-804076/75.
XX
PT Examining allergic diseases, such as atopic dermatitis, comprises
PT comparing the expression levels of gene B1799 in T cells in a patient and
PT a healthy individual.
XX
PS Example 1; SEQ ID NO 5; 87pp; Japanese.
XX
CC This invention relates to a novel method for screening and examining
CC allergic diseases by the use of B1799 as the indicator gene.
CC Specifically, it comprises determining the expression level of this
CC indicator gene in a biological sample obtained from the patient, and
CC identifying differential expression (increased expression of B1799) in
CC comparison to that observed in a healthy individual. The present
CC invention describes the B1799 protein as antiallergic, antiinflammatory
CC and dermatological. As such, through the use of gene therapy, this method
CC can be used to treat allergic diseases particularly atopic dermatitis.
CC Furthermore, it is useful for determining a diagnosis that is convenient

```
CC   and non-invasive, and is also applicable in high throughput screening to
CC   identify candidate compounds for additional remedies. This
CC   oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human
CC   B1799 gene of the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 911
ADF47483
ID   ADF47483 standard; DNA; 17 BP.
XX
AC   ADF47483;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Gene prediction target fragment related primer, SEQ ID No 3.
XX
KW   gene prediction; database; genetic analysis; primer; ss.
XX
OS   Unidentified.
XX
PN   US2003175759-A1.
XX
PD   18-SEP-2003.
XX
PF   04-DEC-2002; 2002US-00309152.
XX
PR   25-FEB-2002; 2002JP-00047297.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Muramatsu T,  Yamamoto A;
XX
DR   WPI; 2003-852125/79.
XX
PT   Identifying novel and useful genes by searching a database utilizing size
PT   information about known nucleotide sequences to a specific sequence in a
PT   target fragment and the information about the specific sequence to
PT   extract a predicted gene.
XX
PS   Disclosure; SEQ ID NO 3; 28pp; English.
XX
CC   The invention relates to novel gene prediction methods. The novel methods
CC   comprise searching a gene database and utilising the information about
CC   the size of a known nucleotide sequence to a specific sequence in a
CC   target fragment and using the information about the specific sequence to
CC   extract a predicted gene. The methods are used for identifying novel and
CC   useful genes. The novel gene prediction methods make it possible to
CC   predict a gene contained in a DNA fragment obtained as a result of gene
CC   expression analysis effectively in a simple and easy manner. The methods
CC   make it possible to predict and identify a target fragment gene rapidly,
CC   and efficiency of genetic analysis is markedly improved. This
CC   polynucleotide sequence represents a primer used in the exemplification
CC   of the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 912
ADI48898
ID   ADI48898 standard; DNA; 17 BP.
XX
AC   ADI48898;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human tumour suppression/reversion-related DNA sequence SeqID1401.
XX
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW   primer; PCR; gene chip; antisense; viral disease; tumour;
KW   cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS   Homo sapiens.
XX
PN   WO2003025177-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004523.
XX
PR   17-SEP-2001; 2001FR-00011980.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-313354/30.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; SEQ ID NO 1401; 30pp; French.
XX
CC   This invention relates to novel isolated nucleic acid sequences involved
CC   in the phenomena of tumour suppression, tumour reversion, apoptosis
CC   and/or resistance to viruses. The invention may be useful for the
CC   development of compounds with a cytostatic, virucide, neuroprotective,
CC   nootropic or neuroleptic activity. The DNA sequences may be useful as
CC   probes and primers for detecting, indentifying, quantifying and/or
CC   amplifying nucleic acid, for example as one component of a gene chip, in
CC   vitro as antisense reagents and for production of recombinant
CC   polypeptides. The invention may therefore be useful for preparation of
CC   pharmaceuticals for prevention and/or treatment of viral diseases that
CC   are characterised by development of tumours or cell degeneration,
CC   specifically cancer but also Alzheimer's disease and schizophrenia. The
CC   present sequence is that of a nucleic acid sequence of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ   Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4832 GATCCTTCAGCACAGG 4847
              ||||||||||||||||
Db          1 GATCCTTCAGCACAGG 16


RESULT 913
ACC53203
ID   ACC53203 standard; DNA; 17 BP.
XX
AC   ACC53203;
XX
```

DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #1970.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 495; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4832 GATCCTTCAGCACAGG 4847
||||||||||||||||
Db 1 GATCCTTCAGCACAGG 16

RESULT 914
ADI13009
ID ADI13009 standard; DNA; 17 BP.
XX
AC ADI13009;
XX
DT 22-APR-2004 (first entry)
XX
DE PCR primer GT15A used to amplify human NOR-1 (MINOR) DNA SeqID 3.
XX
KW human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;
KW atopic dermatitis; antiallergic; antiinflammatory; dermatological;
KW primer.
XX
OS Homo sapiens.
XX
PN WO2004003198-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-JP008199.
XX
PR 27-JUN-2002; 2002JP-00188490.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
XX
PI Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;
XX
DR WPI; 2004-083057/08.
XX
PT Examining allergic diseases e.g. atopic dermatitis by differential
PT display based on gene expression of NOR-1 receptor protein, also
PT applicable in screening compounds for treatment of allergic diseases.
XX
PS Example 1; SEQ ID NO 3; 155pp; Japanese.
XX
CC This invention relates to a novel method for examining allergic diseases
CC that comprises comparing the expression levels of a gene encoding the NOR
CC -1 receptor protein between patients and healthy individuals.
CC Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in
CC the specialist white blood cells known as eosinophils and is involved in
CC mediating an allergic reaction. The present invention describes a
CC differential display method that can identify the expression level of
CC this gene in order to identify its usefulness in diagnosing allergic
CC diseases such as atopic dermatitis. Furthermore, compositions can also be
CC used to screen compounds for the treatment of allergic diseases.
CC Accordingly, they exhibit various activities including antiallergic,
CC antiinflammatory and dermatological. This oligonucleotide sequence is a
CC PCR primer used to amplify human NOR-1 DNA in an exemplification of the
CC invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTT 4515
|||||||||||||||
Db 1 GTTTTTTTTTTTTTT 16

RESULT 915
ADI13010
ID ADI13010 standard; DNA; 17 BP.
XX
AC ADI13010;
XX
DT 22-APR-2004 (first entry)
XX
DE PCR primer GT15C used to amplify human NOR-1 (MINOR) DNA SeqID 4.
XX
KW human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;
KW atopic dermatitis; antiallergic; antiinflammatory; dermatological;
KW primer.
XX
OS Homo sapiens.
XX
PN WO2004003198-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-JP008199.
XX
PR 27-JUN-2002; 2002JP-00188490.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
XX
PI Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;
XX
DR WPI; 2004-083057/08.
XX
PT Examining allergic diseases e.g. atopic dermatitis by differential
PT display based on gene expression of NOR-1 receptor protein, also
PT applicable in screening compounds for treatment of allergic diseases.

```
XX
PS   Example 1; SEQ ID NO 4; 155pp; Japanese.
XX
CC   This invention relates to a novel method for examining allergic diseases
CC   that comprises comparing the expression levels of a gene encoding the NOR
CC   -1 receptor protein between patients and healthy individuals.
CC   Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in
CC   the specialist white blood cells known as eosinophils and is involved in
CC   mediating an allergic reaction. The present invention describes a
CC   differential display method that can identify the expression level of
CC   this gene in order to identify its usefulness in diagnosing allergic
CC   diseases such as atopic dermatitis. Furthermore, compositions can also be
CC   used to screen compounds for the treatment of allergic diseases.
CC   Accordingly, they exhibit various activities including antiallergic,
CC   antiinflammatory and dermatological. This oligonucleotide sequence is a
CC   PCR primer used to amplify human NOR-1 DNA in an exemplification of the
CC   invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 916
ADP86141
ID   ADP86141 standard; DNA; 17 BP.
XX
AC   ADP86141;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #12.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 12; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          2 GTTTTTTTTTTTTTTT 17


RESULT 917
ADR05333
ID   ADR05333 standard; DNA; 17 BP.
XX
AC   ADR05333;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Silkworm juvenile hormone acid transmethylase cDNA PCR primer FP1.
XX
KW   ss; primer; insect repellent; insect attractant;
KW   reproductive maturation regulator; imago; diapause inducer;
KW   diapause inhibitor; larva; transformation regulator; pupa;
KW   juvenile hormone acid transmethylase; silkworm; Bombyx mori;
KW   Drosophila melanogaster; mosquito; Anopheles gambia; Spodoptera litura;
KW   Helicoverpa armigera; molting; transformation; diapause; blastogenesis;
KW   polymorphism; arthropod; cotton bollworm; PCR primer.
XX
OS   Bombyx mori.
XX
PN   WO2004065604-A1.
XX
PD   05-AUG-2004.
XX
PF   20-JAN-2003; 2003WO-JP000415.
XX
PR   20-JAN-2003; 2003WO-JP000415.
XX
PA   (NAAG-) NAT AGRIC RES ORG JAPAN.
XX
PI   Shinoda T,  Itoyama K,  Hamamura T;
XX
DR   WPI; 2004-580727/56.
XX
PT   New DNA encoding protein having juvenile-hormone acid transmethylase
PT   activity, useful for screening for a compound controlling the expression
PT   level of juvenile-hormone acid transmethylase DNA.
XX
PS   Example 1; SEQ ID NO 11; 118pp; Japanese.
XX
CC   The invention relates to a DNA (I) encoding a protein (II) having
CC   juvenile-hormone acid transmethylase activity selected from the DNA from
CC   silkworm (Bombyx mori), Drosophila melanogaster, mosquito (Anopheles
CC   gambiae), Spodoptera litura and Helicoverpa armigera, their encoded
CC   proteins (S2), DNAs (D2) that hybridize under stringent conditions with
```

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CC   the nucleic acids or an amino acid sequence (S3) comprising any one of
CC   (S2) in which one or more amino acids are substituted, deleted, inserted
CC   and/or added. (I) is useful for screening a compound that controls the
CC   expression level of (I), and as a controlling agent of molting and
CC   transformation, reproductive, diapause, blastogenesis, action,
CC   polymorphism or lifetime of arthropod. (II) is useful for screening a
CC   compound having binding affinity with respect to (II), which involves
CC   contacting test compound with (II), detecting the binding of (II) with
CC   test compound, and selecting the compound that binds with (II). (II) is
CC   useful for screening a compound that controls the activity of (II), which
CC   involves contacting test compound with (II), measuring the activity of
CC   (II), and selecting the compound that decreases or increases the activity
CC   of (II), based on comparison of the activity of (II) in absence of test
CC   compound. (II) is useful for manufacturing activated juvenile hormone.
CC   This sequence corresponds to a PCR primer used to amplify and isolate the
CC   transmethylase cDNA from the silkworm Bombyx mori.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 918
AAN30173/c
ID   AAN30173 standard; DNA; 18 BP.
XX
AC   AAN30173;
XX
DT   09-SEP-2004  (revised)
DT   05-APR-1992  (first entry)
XX
DE   L1 region of the bovine papillomavirus type 1a genome, fragment.
XX
KW   Diagnostioc reagent; vaccine; medicine; wart; tumour; ss.
XX
OS   Bovine papillomavirus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .18
FT                   /*tag=  a
XX
PN   EP92456-A.
XX
PD   26-OCT-1983.
XX
PF   01-APR-1983;   83EP-00901081.
XX
PR   05-APR-1982;   82FR-00005887.
XX
PA   (INSP ) INST PASTEUR.
PA   (DANO/) DANOS O.
XX
PI   Danos O,  Katinka M,  Yaniv M;
XX
DR   WPI; 1983-802979/44.
DR   P-PSDB; AAP30313.
XX
PT   DNA fragment coding for Papillomavirus antigenic proteins - and derived
PT   immunogen, vaccine and antibody.
XX
PS   Claim 6; Page 16; 25pp; French.
XX
CC   The inventors claim DNA fragments capable of expressing, in a host, a
CC   prod. contg. at least one antigenic determinant of papillomavirus (PV),
CC   (see AAN30170-N30173). Also claimed are immunogens consisting of at least
CC   one peptide sequence coded for by the DNA fragments (see AAP30310-
CC   P30313), vaccines contg. the immunogens and antibodies raised from them.
CC   The vaccines are useful in human and veterinary medicine and the
CC   antibodies are useful as diagnostic reagents. The DNA fragments are most
CC   esp. derived from the L1 region of human PV type 1a
CC
CC   Revised record issued on 09-SEP-2004 : Correction of feature table key
XX
SQ   Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         17 TTTTTTTTTTTTTTTG 2


RESULT 919
AAT94669
ID   AAT94669 standard; DNA; 18 BP.
XX
AC   AAT94669;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchG.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18
```

RESULT 920
AAV54175
ID AAV54175 standard; cDNA; 18 BP.
XX
AC AAV54175;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 12.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 51; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 921
AAV54173
ID AAV54173 standard; cDNA; 18 BP.
XX
AC AAV54173;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 10.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 50; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 GTTTTTTTTTTTTTTT 16

RESULT 922
AAV54164
ID AAV54164 standard; cDNA; 18 BP.
XX
AC AAV54164;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 1.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 47; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 923
AAV54166
ID   AAV54166 standard; cDNA; 18 BP.
XX
AC   AAV54166;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 3.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 924
AAV54169
ID   AAV54169 standard; cDNA; 18 BP.
XX
AC   AAV54169;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 6.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 925
AAV54167
ID   AAV54167 standard; cDNA; 18 BP.
XX
AC   AAV54167;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 4.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
```

```
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 926
AAZ90649
ID   AAZ90649 standard; DNA; 18 BP.
XX
AC   AAZ90649;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #10.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 927
AAZ90648
ID   AAZ90648 standard; DNA; 18 BP.
XX
AC   AAZ90648;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #9.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 928
AAZ90646
ID   AAZ90646 standard; DNA; 18 BP.
XX
AC   AAZ90646;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #7.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
```

```
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 929
AAZ90645
ID   AAZ90645 standard; DNA; 18 BP.
XX
AC   AAZ90645;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #6.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 930
AAZ90643
ID   AAZ90643 standard; DNA; 18 BP.
XX
AC   AAZ90643;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #4.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 931
AAZ90651
ID   AAZ90651 standard; DNA; 18 BP.
XX
AC   AAZ90651;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #12.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
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```
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          1 GTTTTTTTTTTTTTTT 16


RESULT 932
AAA58386
ID   AAA58386 standard; DNA; 18 BP.
XX
AC   AAA58386;
XX
DT   01-NOV-2000  (first entry)
XX
DE   Polynucleotide # 2 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999;   99WO-US026612.
XX
PR   10-NOV-1998;   98US-0107828P.
PR   09-NOV-1999;   99US-00437076.
XX
PA   (BIOC-) BIOCRYSTAL LTD.
XX
PI   Barbera-Guillem E,  Nelson MB,  Castro S;
XX
DR   WPI; 2000-376593/32.
XX
PT   Functionalized nanocrystal carrying polynucleotide, used for detecting
PT   target analyte, forms dendrimers with complementary nanocrystals to
PT   amplify the fluorescent signal.
XX
PS   Example 3; Page 69; 72pp; English.
XX
CC   The present invention relates to functionalised nanocrystals for use in
CC   nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC   proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC   attached to their surfaces with one end of the polynucleotide extending
CC   outwardly from the nanocrystal. The present sequence is one such
CC   polynucleotide. These nanocrystals are used with a second series of
CC   nanocrystals, which have polynucleotides complementary to the first
CC   polynucleotides, so that the respective complementary strands hybridise
CC   to each other and form a dendrimer. This dendrimer produces a signal
CC   which can then be detected e.g. fluorescence. The present sequence is
CC   composed mainly of Thymine bases. This sequence may therefore be used
CC   with a polynucleotide composed mainly of Adenine bases (AAA58385)
XX
SQ   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
             ||||||||||||||||
Db          3 GTTTTTTTTTTTTTTT 18


RESULT 933
AAF75596
ID   AAF75596 standard; DNA; 18 BP.
XX
AC   AAF75596;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #1.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 100; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
             ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 934
AAF75597
ID   AAF75597 standard; DNA; 18 BP.
```

```
XX
AC   AAF75597;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #2.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 100; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 935
AAD16463
ID   AAD16463 standard; DNA; 18 BP.
XX
AC   AAD16463;
XX
DT   19-NOV-2001  (first entry)
XX
DE   K. singaporensis isomaltulose synthase sucrose resposive region DNA.
XX
KW   Isomaltulose synthase; KIS protein; sucrose responsive region;
KW   transgenic plant; ds.
XX
OS   Klebsiella singaporensis.
XX
PN   WO200160993-A1.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2000; 2000WO-SG000023.
XX
PR   15-FEB-2000; 2000WO-SG000023.
XX
PA   (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
PI   Zhang LH,  Li X,  Zhang D;
XX
DR   WPI; 2001-536568/59.
XX
PT   New KIS protein, an isomaltulose synthase for conversion of sucrose into
PT   isomaltulose.
XX
PS   Example 3; Fig 7; 82pp; English.
XX
CC   The present invention relates to the KIS protein, a novel isomaltulose (6
CC   -o-alpha-D-glucopyranosyl-D-fructofuranose) synthase. The KIS enzyme
CC   converts sucrose into isomaltulose. It is useful for transformation into
CC   transgenic plants to produce plants which are capable of converting
CC   sucrose into isomaltulose. Isomaltulose is a reducing sugar with physical
CC   properties and taste very similar to sucrose. The present sequence is
CC   Klebsiella singaporensis isomaltulose synthase (KIS) protein AT-rich
CC   sucrose responsive region DNA
XX
SQ   Sequence 18 BP; 6 A; 2 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2137 TTTTCTTTAATAACAA 2152
              ||||||||||||||||
Db          1 TTTTCTTTAATAACAA 16


RESULT 936
AAQ75549
ID   AAQ75549 standard; DNA; 19 BP.
XX
AC   AAQ75549;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
```

```
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 937
AAQ75548
ID   AAQ75548 standard; DNA; 19 BP.
XX
AC   AAQ75548;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 938
AAQ75550
ID   AAQ75550 standard; DNA; 19 BP.
XX
AC   AAQ75550;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 939
ACA98771/c
ID   ACA98771 standard; DNA; 19 BP.
XX
AC   ACA98771;
XX
DT   28-JUL-2003  (first entry)
XX
DE   Human CYP2C8 SNP detection PCR primer #211.
XX
KW   Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
KW   cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
KW   single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200299099-A2.
XX
PD   12-DEC-2002.
XX
PF   31-MAY-2002; 2002WO-EP006000.
XX
PR   01-JUN-2001; 2001EP-00112899.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Penger A,  Sprenger R,  Brinkmann U;
XX
DR   WPI; 2003-167344/16.
```

```
XX
PT   New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT   2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT   arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
PS   Example 2; Page 52; 178pp; English.
XX
CC   The invention describes a new polynucleotide comprises a polynucleotide:
CC   (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC   in the specification; (b) encoding any of seven polypeptides having 7
CC   amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC   hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC   encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC   polynucleotide, gene, vector, polypeptide or antibody is useful for
CC   diagnosing or treating a disease, for preparing a diagnostic composition
CC   for diagnosing a disease, or for preparing a pharmaceutical composition
CC   for treating a disease. This disease includes arachidonic acid
CC   metabolism, cancer or cardiovascular diseases. This sequence represents a
CC   primer used to isolate regions of the human cytochrome P450 polypetide
CC   2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
CC   (SNP) in that region of different individuals useful in disease diagnosis
XX
SQ   Sequence 19 BP; 10 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||||||||||||||
Db         18 TATACATATATACATT 3


RESULT 940
ACA98774
ID   ACA98774 standard; DNA; 19 BP.
XX
AC   ACA98774;
XX
DT   28-JUL-2003  (first entry)
XX
DE   Human CYP2C8 SNP detection PCR primer #214.
XX
KW   Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
KW   cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
KW   single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200299099-A2.
XX
PD   12-DEC-2002.
XX
PF   31-MAY-2002; 2002WO-EP006000.
XX
PR   01-JUN-2001; 2001EP-00112899.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Penger A,  Sprenger R,  Brinkmann U;
XX
DR   WPI; 2003-167344/16.
XX
PT   New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT   2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT   arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
PS   Example 2; Page 52; 178pp; English.
XX
CC   The invention describes a new polynucleotide comprises a polynucleotide:
CC   (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC   in the specification; (b) encoding any of seven polypeptides having 7
CC   amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC   hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC   encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC   polynucleotide, gene, vector, polypeptide or antibody is useful for
CC   diagnosing or treating a disease, for preparing a diagnostic composition
CC   for diagnosing a disease, or for preparing a pharmaceutical composition
CC   for treating a disease. This disease includes arachidonic acid
CC   metabolism, cancer or cardiovascular diseases. This sequence represents a
CC   primer used to isolate regions of the human cytochrome P450 polypetide
CC   2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
CC   (SNP) in that region of different individuals useful in disease diagnosis
XX
SQ   Sequence 19 BP; 7 A; 2 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2399 TATACATATATACATT 2414
              ||||||||||||||||
Db          2 TATACATATATACATT 17


RESULT 941
ADE29541/c
ID   ADE29541 standard; RNA; 19 BP.
XX
AC   ADE29541;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition;
KW   mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW   cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW   immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW   antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW   inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW   psoriasis; inflammatory bowel disease; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003072590-A1.
XX
PD   04-SEP-2003.
XX
PF   28-JAN-2003; 2003WO-US002510.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Usman N,  Haeberli P,  Chowrira B;
XX
DR   WPI; 2003-689980/65.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer, downregulates expression of mitogen-activated
PT   protein kinase genes.
XX
PS   Example 3; SEQ ID NO 163; 164pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of a mitogen-activated protein kinase
CC   (MAPK) genes by RNA interference. Also described: (1) a method for
CC   modulating expression of MAPK genes in cells, tissue explants or
```

CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 18 TTTTTTTTTTTTTTTG 3

RESULT 942
ADE29704
ID ADE29704 standard; RNA; 19 BP.
XX
AC ADE29704;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:326.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003072590-A1.
XX
PD 04-SEP-2003.
XX
PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;
XX
DR WPI; 2003-689980/65.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
PS Example 3; SEQ ID NO 326; 164pp; English.

XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 0 C; 1 G; 0 T; 16 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 6.2%; Pred. No. 6.5e+02;
Matches 1; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
:::::::::::::::|
Db 2 UUUUUUUUUUUUUUUG 17

RESULT 943
ADR81681
ID ADR81681 standard; DNA; 19 BP.
XX
AC ADR81681;
XX
DT 16-DEC-2004 (first entry)
XX
DE Hepatitis C virus (HCV) oligonucleotide seqid 6180.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.
XX
OS Hepatitis C virus.
XX
PN WO2004080406-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US007070.
XX
PR 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.

PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Bumcrot D;
XX
DR WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
PS Example 5; SEQ ID NO 6180; 378pp; English.
XX
CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or disregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholestorolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can
CC be used to control HCV gene expression.
XX
SQ Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4500 GTTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 3 GTTTTTTTTTTTTTTT 18

RESULT 944
AAQ75566
ID AAQ75566 standard; DNA; 20 BP.
XX
AC AAQ75566;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 3 TTTTTTTTTTTTTTTG 18

RESULT 945
AAQ75574
ID AAQ75574 standard; DNA; 20 BP.
XX
AC AAQ75574;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The

```
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 946
AAQ75568
ID   AAQ75568 standard; DNA; 20 BP.
XX
AC   AAQ75568;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 947
AAQ75570
ID   AAQ75570 standard; DNA; 20 BP.
XX
AC   AAQ75570;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 948
AAQ75572
ID   AAQ75572 standard; DNA; 20 BP.
XX
AC   AAQ75572;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
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XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 949
AAQ75564
ID   AAQ75564 standard; DNA; 20 BP.
XX
AC   AAQ75564;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 950
AAQ75565
ID   AAQ75565 standard; DNA; 20 BP.
XX
AC   AAQ75565;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 951
AAQ75573
ID   AAQ75573 standard; DNA; 20 BP.
XX
AC   AAQ75573;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
```

```
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 952
AAX38448/c
ID   AAX38448 standard; DNA; 20 BP.
XX
AC   AAX38448;
XX
DT   16-JUN-1999  (first entry)
XX
DE   E. coli SecA antisense oligonucleotide 4.
XX
KW   Microorganism inhibitor; antisense; nuclease resistant; treatment;
KW   ribonucleotide reductase; secA gene; pathological condition; R1 subunit;
KW   antimicrobial agent; crop protection; primer; R2 subunit; ss.
XX
OS   Synthetic.
OS   Escherichia coli.
XX
PN   WO9902673-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-CA000666.
XX
PR   10-JUL-1997;   97US-0052160P.
XX
PA   (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI   Wright JA,  Young AH,  Dugourd D;
XX
DR   WPI; 1999-120874/10.
XX
PT   New oligonucleotides complementary to RR or SecA genes - useful to
PT   inhibit growth of microorganisms.
XX
PS   Disclosure; Page 22; 103pp; English.
XX
CC   This invention describes novel antisense oligonucleotides (AAX38301-
CC   X38552) which are nuclease resistant, and comprises about 3-50
CC   nucleotides complementary to the ribonucleotide reductase gene or the
CC   secA gene of a microorganism. The antisense oligonucleotides are used to
CC   treat mammalian pathological conditions mediated by microorganisms. The
CC   oligonucleotides are particularly useful as antimicrobial agents in crop
CC   protection
XX
SQ   Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1284 GAACCGGAGATGGAAA 1299
              ||||||||||||||||
Db         18 GAACCGGAGATGGAAA 3


RESULT 953
AAF83959
ID   AAF83959 standard; DNA; 20 BP.
XX
AC   AAF83959;
XX
DT   06-AUG-2001  (first entry)
XX
DE   BAP28 gene fragment amplifying primer BAP28polyTcourt.
XX
KW   BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100669-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-IB001183.
XX
PR   25-JUN-1999;   99US-0141323P.
PR   18-JAN-2000; 2000US-0176880P.
XX
PA   (GEST ) GENSET.
XX
PI   Barry C,  Bougueleret L,  Chumakov I,  Cohen-Akenine A;
XX
DR   WPI; 2001-367032/38.
XX
PT   New BAP28 polynucleotides and polypeptides overexpressed in prostate
PT   cancer cells for diagnosing prostate tumors, e.g. by hybridization or
PT   polymerase chain reaction assays.
XX
PS   Example; Page 347; 349pp; English.
XX
CC   The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
CC   sequences and regulatory region located at the 3' and 5' ends of the
CC   BAP28 coding region. The BAP28 polypeptides can be expressed by standard
CC   recombinant methodology. BAP28 polynucleotides and polypeptides have been
CC   found to be over expressed in prostate tumour cells, therefore levels of
CC   BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
CC   reaction (PCR)) to diagnose patient suffering from or susceptible to
CC   prostate cancer. Antibodies specific for the BAP28 polypeptides are
CC   useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
CC   useful in genetic analysis. Sequences AAF83934-963 represent primers for
CC   the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on
CC   the opposite of the coding strand of BAP28)
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16
```

```
RESULT 954
AAD12369
ID   AAD12369 standard; DNA; 20 BP.
XX
AC   AAD12369;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human caspase 8 mRNA antisense compound ISIS 107647.
XX
KW   Caspase 8; infection; inflammation; tumour; research reagent; cytostatic;
KW   gene therapy; antisense; human; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    2
FT                    /*tag=  d
FT                    /mod_base= m5c
FT   modified_base    12
FT                    /*tag=  e
FT                    /mod_base= m5c
FT   modified_base    15
FT                    /*tag=  f
FT                    /mod_base= m5c
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    18
FT                    /*tag=  g
FT                    /mod_base= m5c
XX
PN   US6258600-B1.
XX
PD   10-JUL-2001.
XX
PF   19-JAN-2000; 2000US-00487445.
XX
PR   19-JAN-2000; 2000US-00487445.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Zhang H,  Cowsert LM;
XX
DR   WPI; 2001-432165/46.
XX
PT   New antisense compounds capable of modulating expression of caspase 8 for
PT   the diagnoses, prophylaxis and treatment of diseases associated with
PT   expression of caspase 8, e.g. inflammation and tumor formation.
XX
PS   Example 15; Col 43-44; 56pp; English.
XX
CC   The invention relates to antisense compounds which inhibit the expression
CC   of human caspase 8. The antisense compound is useful for diagnosing and
CC   treating diseases associated with the expression of caspase 8 and for
CC   prophylaxis e.g. to prevent or delay infection, inflammation or tumour
CC   formation, and as a research reagent. The present sequence is an
CC   antisense compound targetted to human caspase 8 mRNA
XX
SQ   Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1772 GTTGATTATCTTCAGC 1787
              ||||||||||||||||
Db          3 GTTGATTATCTTCAGC 18


RESULT 955
ABA05915
ID   ABA05915 standard; DNA; 20 BP.
XX
AC   ABA05915;
XX
DT   05-MAR-2002  (first entry)
XX
DE   Hepatitis B virus diagnostic PCR primer SEQ ID NO 5.
XX
KW   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW   PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
PN   EP1152063-A1.
XX
PD   07-NOV-2001.
XX
PF   03-MAY-2000; 2000EP-00109436.
XX
PR   03-MAY-2000; 2000EP-00109436.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Schroeder KH,  Koike K;
XX
DR   WPI; 2002-068256/10.
XX
PT   Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT   risk for hepatocellular carcinoma, comprises identifying full length HBV
PT   transcripts and truncated HBV transcripts in a serum sample.
XX
PS   Example 1; Page 6; 25pp; English.
XX
CC   The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC   stages comprising identification of full length HBV transcripts (I) and
CC   truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC   is indicative of a particular infection stage. The method is useful for
CC   diagnosing HBV infection stages and determining the risk for developing
CC   hepatocellular carcinoma. The present sequence is that of a HBV
CC   diagnostic PCR primer, useful for the invention
XX
SQ   Sequence 20 BP; 0 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 956
ABA05916
ID   ABA05916 standard; DNA; 20 BP.
XX
AC   ABA05916;
XX
DT   05-MAR-2002  (first entry)
XX
DE   Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
XX
```

```
KW   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW   PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
PN   EP1152063-A1.
XX
PD   07-NOV-2001.
XX
PF   03-MAY-2000; 2000EP-00109436.
XX
PR   03-MAY-2000; 2000EP-00109436.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Schroeder KH,  Koike K;
XX
DR   WPI; 2002-068256/10.
XX
PT   Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT   risk for hepatocellular carcinoma, comprises identifying full length HBV
PT   transcripts and truncated HBV transcripts in a serum sample.
XX
PS   Example 1; Page 6; 25pp; English.
XX
CC   The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC   stages comprising identification of full length HBV transcripts (I) and
CC   truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC   is indicative of a particular infection stage. The method is useful for
CC   diagnosing HBV infection stages and determining the risk for developing
CC   hepatocellular carcinoma. The present sequence is that of a HBV
CC   diagnostic PCR primer, useful for the invention
XX
SQ   Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 957
AAD55499/c
ID   AAD55499 standard; DNA; 20 BP.
XX
AC   AAD55499;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human FGFR-3 antisense oligonucleotide, ISIS #125205.
XX
KW   Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
KW   developmental disorder; hyperproliferative disorder; antisense therapy;
KW   FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidine residues
FT                   are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2 -methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2003023004-A2.
XX
PD   20-MAR-2003.
XX
PF   06-SEP-2002; 2002WO-US028549.
XX
PR   10-SEP-2001; 2001US-00953047.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Wyatt JR;
XX
DR   WPI; 2003-313244/30.
XX
PT   Novel compound targeted to a nucleic acid molecule encoding fibroblast
PT   growth factor receptor 3, useful for inhibiting the expression of the
PT   receptor and for treating an animal having cancer or developmental
PT   disorder.
XX
PS   Example 15; Page 79; 120pp; English.
XX
CC   The invention relates to antisense compounds targetted to a nucleic acid
CC   molecule encoding fibroblast growth factor (FGF) receptor 3 (also known
CC   as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense
CC   compounds of the invention are useful for treating diseases or conditions
CC   associated with FGFR-3 such as developmental disorders or
CC   hyperproliferative disorders, especially cancer of colorectal, bladder,
CC   bone, lung, cervical, breast or skin. They are useful as research
CC   reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools
CC   in differential and/or combinatorial analyses to elucidate expression
CC   patterns of a portion of the genes expressed within cells and tissues.
CC   They are also useful in antisense therapy. The present sequence is an
CC   antisense oligonucleotide targetted to human FGFR-3
XX
SQ   Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATATA 2410
              ||||||||||||||||
Db         17 TATATATACATATATA 2


RESULT 958
ADD24998
ID   ADD24998 standard; DNA; 20 BP.
XX
AC   ADD24998;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human caspase-8 antisense oligonucleotide ISIS 107647.
XX
KW   Caspase-8; cytostatic; immunosuppressant; anti-HIV; ss;
KW   antisense gene therapy; apoptosis; hyperproliferative disorder;
KW   haematopoietic disorder; autoimmune disorder; viral infection; AIDS;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   amyotrophic lateral sclerosis; retinitis pigmentosa; blood cell disorder;
KW   cancer; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone and all cytidines are 5
FT                   -methycytidines"
```

```
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residues"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residues"
XX
PN   US2003083296-A1.
XX
PD   01-MAY-2003.
XX
PF   12-JUL-2002; 2002US-00181177.
XX
PR   19-JAN-2000; 2000US-00487445.
PR   11-JAN-2001; 2001WO-US000955.
XX
PA   (ZHAN/) ZHANG H.
PA   (COWS/) COWSERT L M.
XX
PI   Zhang H,  Cowsert LM;
XX
DR   WPI; 2003-810793/76.
XX
PT   New compounds, particularly antisense oligonucleotides targeted to a
PT   nucleic acid encoding caspase 8, useful for treating a disease/condition
PT   associated with caspase 8, such as hyperproliferative or autoimmune
PT   disorders.
XX
PS   Example 15; SEQ ID NO 55; 59pp; English.
XX
CC   The invention relates to a compound 8-30 nucleobases in length targeted
CC   to, and which specifically hybridises with a nucleic acid molecule
CC   encoding caspase 8 (a protein involved in apoptosis), and inhibits the
CC   expression of caspase 8, i.e. an antisense oligonucleotide. Also included
CC   are a compound 8-30 nucleobases in length that specifically hybridises
CC   with at least an 8-nucleobase portion of an active site on a nucleic acid
CC   molecule encoding caspase 8, a composition comprising the compound and a
CC   carrier or diluent, inhibiting the expression of caspase 8 in cells or
CC   tissues (by contacting the cells or tissues with the compound so that
CC   expression of caspase 8 is inhibited) and treating an animal having a
CC   disease or condition associated with caspase 8 by administering to the
CC   animal a therapeutic or prophylactic amount of the compound so that
CC   expression of caspase 8 is inhibited. The compound, composition and
CC   methods are useful for treating a disease or condition associated with
CC   caspase 8, such as hyperproliferative, haematopoietic or autoimmune
CC   disorder, viral infection such as AIDS, neurological disorders (e.g.
CC   Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC   retinitis pigmentosa), blood cell disorders and cancer. They are also
CC   useful in research and diagnostics for modulating the expression of
CC   interleukin 8. The present sequence is a caspase-8 targeting antisense
CC   oligonucleotide of the invention.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1772 GTTGATTATCTTCAGC 1787
              ||||||||||||||||
Db          3 GTTGATTATCTTCAGC 18


RESULT 959
ABZ89676/c
ID   ABZ89676 standard; DNA; 20 BP.
XX
AC   ABZ89676;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4918; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         20 TTTTTTTTTTTTTTTG 5


RESULT 960
ABZ88938/c
ID   ABZ88938 standard; DNA; 20 BP.
XX
AC   ABZ88938;
XX
DT   17-OCT-2003  (first entry)
XX
```

DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4180; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 18 TTTTTTTTTTTTTTTG 3

RESULT 961
ABZ88618/c
ID ABZ88618 standard; DNA; 20 BP.
XX
AC ABZ88618;
XX
DT 17-OCT-2003 (first entry)
XX

DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3860; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 16 TTTTTTTTTTTTTTTG 1

RESULT 962
ABD24848/c
ID ABD24848 standard; DNA; 20 BP.
XX
AC ABD24848;
XX
DT 29-JUL-2004 (first entry)
XX

DE AI092623-derived oligonucleotide SEQ ID 3860.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 3860; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
|||||||||||||||||
Db 16 TTTTTTTTTTTTTTTG 1

RESULT 963
ABD25168/c
ID ABD25168 standard; DNA; 20 BP.
XX
AC ABD25168;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI041482-derived oligonucleotide SEQ ID 4180.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4180; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to

```
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         18 TTTTTTTTTTTTTTTG 3


RESULT 964
ADH67348
ID   ADH67348 standard; DNA; 20 BP.
XX
AC   ADH67348;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human glucocorticoid receptor-specific antisense oligonucleotide #4182.
XX
KW   antisense oligonucleotide; glucocorticoid receptor; infection;
KW   inflammation; tumour formation; diabetes; obesity;
KW   cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW   phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS   Homo sapiens.
XX
PN   WO2003099215-A2.
XX
PD   04-DEC-2003.
XX
PF   20-MAY-2003; 2003WO-US016084.
XX
PR   20-MAY-2002; 2002US-0381857P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Crosby SD,  Nalseth AE;
XX
DR   WPI; 2004-035034/03.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT   cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS   Claim 4; SEQ ID NO 4182; 985pp; English.
XX
CC   The invention comprises an antisense oligonucleotides that are targeted
CC   to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC   antisense oligonucleotides of the invention are useful for preventing or
CC   delaying infection, inflammation or tumour formation. The antisense
CC   oligonucleotides are also useful for treating diabetes, obesity,
CC   cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC   present DNA sequence represents an antisense oligonucleotide that targets
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          5 TTTTTTTTTTTTTTTG 20


RESULT 965
ADH66659
ID   ADH66659 standard; DNA; 20 BP.
XX
AC   ADH66659;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human glucocorticoid receptor-specific antisense oligonucleotide #3493.
XX
KW   antisense oligonucleotide; glucocorticoid receptor; infection;
KW   inflammation; tumour formation; diabetes; obesity;
KW   cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW   phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS   Homo sapiens.
XX
PN   WO2003099215-A2.
XX
PD   04-DEC-2003.
XX
PF   20-MAY-2003; 2003WO-US016084.
XX
PR   20-MAY-2002; 2002US-0381857P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Crosby SD,  Nalseth AE;
XX
DR   WPI; 2004-035034/03.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT   cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS   Claim 4; SEQ ID NO 3493; 985pp; English.
XX
CC   The invention comprises an antisense oligonucleotides that are targeted
CC   to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC   antisense oligonucleotides of the invention are useful for preventing or
CC   delaying infection, inflammation or tumour formation. The antisense
CC   oligonucleotides are also useful for treating diabetes, obesity,
CC   cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC   present DNA sequence represents an antisense oligonucleotide that targets
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          3 TTTTTTTTTTTTTTTG 18


RESULT 966
ADH66380
ID   ADH66380 standard; DNA; 20 BP.
XX
AC   ADH66380;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human glucocorticoid receptor-specific antisense oligonucleotide #3214.
XX
KW   antisense oligonucleotide; glucocorticoid receptor; infection;
KW   inflammation; tumour formation; diabetes; obesity;
KW   cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW   phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
```

XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 3214; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTG 17

RESULT 967
ADH66379
ID ADH66379 standard; DNA; 20 BP.
XX
AC ADH66379;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #3213.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 3213; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 TTTTTTTTTTTTTTTG 16

RESULT 968
ADH67400
ID ADH67400 standard; DNA; 20 BP.
XX
AC ADH67400;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4234.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 4234; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets

```
CC   the human glucocorticoid receptor gene. NOTE: The present sequence
CC   contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          4 TTTTTTTTTTTTTTTG 19


RESULT 969
ADK94634
ID   ADK94634 standard; DNA; 20 BP.
XX
AC   ADK94634;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Primer of the invention #354.
XX
KW   human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS   Synthetic.
XX
PN   JP2003259875-A.
XX
PD   16-SEP-2003.
XX
PF   08-MAR-2002; 2002JP-00064373.
XX
PR   08-MAR-2002; 2002JP-00064373.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2004-093977/10.
XX
PT   Novel polynucleotide useful for PCR amplification along with two DNA
PT   fragment from another set of sequences, or for detecting single
PT   nucleotide polymorphism in human gene.
XX
PS   Claim 2; SEQ ID NO 3663; 2627pp; Japanese.
XX
CC   The present invention relates to a polynucleotide isolated from a human
CC   gene and is useful for detecting a single nucleotide polymorphism in a
CC   human gene or for diagnosing of disease. The invention enables the
CC   detection of a single nucleotide polymorphism in a human gene. The
CC   present sequence represents a primer of the invention.
XX
SQ   Sequence 20 BP; 0 A; 11 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3182 TCTCTCTCCCTCCCTC 3197
              ||||||||||||||||
Db          4 TCTCTCTCCCTCCCTC 19


RESULT 970
ADK74647
ID   ADK74647 standard; DNA; 20 BP.
XX
AC   ADK74647;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1981.
XX
KW   Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW   diabetic neuropathy; arthritic pain; migraine headache;
KW   infantile epilepsy; ataxia; ss.
XX
OS   Synthetic.
XX
PN   WO2004016754-A2.
XX
PD   26-FEB-2004.
XX
PF   14-AUG-2003; 2003WO-US025465.
XX
PR   14-AUG-2002; 2002US-0403416P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Roberds SL;
XX
DR   WPI; 2004-203785/19.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   Nav1.3, useful for useful for treating a disease or condition associated
PT   with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT   disorder, or ataxia.
XX
PS   Claim 4; SEQ ID NO 1981; 417pp; English.
XX
CC   The present invention relates to an antisense compound targeted to a
CC   nucleic acid molecule encoding Nav1.3, where the antisense compound
CC   specifically hybridizes with and inhibits the expression of Nav1.3. The
CC   compound and composition are useful for treating a disease or condition
CC   associated with Nav1.3, e.g. pain including but not limited to
CC   neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC   diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC   pain from burns, migraine headache, cluster headache, mild-to-moderate
CC   headache; seizure disorder such as childhood seizure disorder, including
CC   but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC   sequence represents a chimeric phosphorothioate oligonucleotide with
CC   2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC   human Nav1.3 expression, the oligonucleotides are designed to target
CC   different regions of the human Nav1.3 RNA.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          5 TTTTTTTTTTTTTTTG 20


RESULT 971
ADK73558
ID   ADK73558 standard; DNA; 20 BP.
XX
AC   ADK73558;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide to target Nav1.3 #892.
XX
KW   Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW   diabetic neuropathy; arthritic pain; migraine headache;
KW   infantile epilepsy; ataxia; ss.
XX
OS   Synthetic.
XX
PN   WO2004016754-A2.
XX
PD   26-FEB-2004.
XX
```

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PF   14-AUG-2003; 2003WO-US025465.
XX
PR   14-AUG-2002; 2002US-0403416P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Roberds SL;
XX
DR   WPI; 2004-203785/19.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   Nav1.3, useful for useful for treating a disease or condition associated
PT   with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT   disorder, or ataxia.
XX
PS   Claim 4; SEQ ID NO 892; 417pp; English.
XX
CC   The present invention relates to an antisense compound targeted to a
CC   nucleic acid molecule encoding Nav1.3, where the antisense compound
CC   specifically hybridizes with and inhibits the expression of Nav1.3. The
CC   compound and composition are useful for treating a disease or condition
CC   associated with Nav1.3, e.g. pain including but not limited to
CC   neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC   diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC   pain from burns, migraine headache, cluster headache, mild-to-moderate
CC   headache; seizure disorder such as childhood seizure disorder, including
CC   but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC   sequence represents a chimeric phosphorothioate oligonucleotide with
CC   2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC   human Nav1.3 expression, the oligonucleotides are designed to target
CC   different regions of the human Nav1.3 RNA.
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTG 16


RESULT 972
ADK73725
ID   ADK73725 standard; DNA; 20 BP.
XX
AC   ADK73725;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1059.
XX
KW   Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW   diabetic neuropathy; arthritic pain; migraine headache;
KW   infantile epilepsy; ataxia; ss.
XX
OS   Synthetic.
XX
PN   WO2004016754-A2.
XX
PD   26-FEB-2004.
XX
PF   14-AUG-2003; 2003WO-US025465.
XX
PR   14-AUG-2002; 2002US-0403416P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Roberds SL;
XX
DR   WPI; 2004-203785/19.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   Nav1.3, useful for useful for treating a disease or condition associated
PT   with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT   disorder, or ataxia.
XX
PS   Claim 4; SEQ ID NO 1059; 417pp; English.
XX
CC   The present invention relates to an antisense compound targeted to a
CC   nucleic acid molecule encoding Nav1.3, where the antisense compound
CC   specifically hybridizes with and inhibits the expression of Nav1.3. The
CC   compound and composition are useful for treating a disease or condition
CC   associated with Nav1.3, e.g. pain including but not limited to
CC   neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC   diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC   pain from burns, migraine headache, cluster headache, mild-to-moderate
CC   headache; seizure disorder such as childhood seizure disorder, including
CC   but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC   sequence represents a chimeric phosphorothioate oligonucleotide with
CC   2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC   human Nav1.3 expression, the oligonucleotides are designed to target
CC   different regions of the human Nav1.3 RNA.
XX
SQ   Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTG 17


RESULT 973
ADK74442
ID   ADK74442 standard; DNA; 20 BP.
XX
AC   ADK74442;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1776.
XX
KW   Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW   diabetic neuropathy; arthritic pain; migraine headache;
KW   infantile epilepsy; ataxia; ss.
XX
OS   Synthetic.
XX
PN   WO2004016754-A2.
XX
PD   26-FEB-2004.
XX
PF   14-AUG-2003; 2003WO-US025465.
XX
PR   14-AUG-2002; 2002US-0403416P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Roberds SL;
XX
DR   WPI; 2004-203785/19.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   Nav1.3, useful for useful for treating a disease or condition associated
PT   with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT   disorder, or ataxia.
XX
PS   Claim 4; SEQ ID NO 1776; 417pp; English.
XX
CC   The present invention relates to an antisense compound targeted to a
CC   nucleic acid molecule encoding Nav1.3, where the antisense compound
CC   specifically hybridizes with and inhibits the expression of Nav1.3. The
```

CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 4 TTTTTTTTTTTTTTTG 19

RESULT 974
ADK74413
ID ADK74413 standard; DNA; 20 BP.
XX
AC ADK74413;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1747.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1747; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 3 TTTTTTTTTTTTTTTG 18

RESULT 975
ADK19329
ID ADK19329 standard; DNA; 20 BP.
XX
AC ADK19329;
XX
DT 20-MAY-2004 (first entry)
XX
DE Immunostimulatory nucleic acid #374.
XX
KW immunostimulatory nucleic acid; asthma; allergy; cancer;
KW infectious disease; autoimmune disease; airway remodeling;
KW chronic obstructive pulmonary disease; asthma; IL-6; interleukin-6;
KW TNFalpha; tumour necrosis factor alpha; IFNalpha; interferon-alpha;
KW IFNgamma; interferon-gamma; IP-10; interferon inducible protein;
KW viral infection; bacteria infection; parasitic infection; ss.
XX
OS Synthetic.
XX
PN WO2004016805-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025935.
XX
PR 19-AUG-2002; 2002US-0404479P.
PR 19-AUG-2002; 2002US-0404820P.
PR 27-NOV-2002; 2002US-0429701P.
PR 14-FEB-2003; 2003US-0447377P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Samulowitz U, Vollmer J, Uhlmann E, Jurk M, Lipford G;
PI Rankin R;
XX
DR WPI; 2004-257200/24.
XX
PT New immunostimulatory nucleic acid molecule having pyrimidine-purine
PT dinucleotide and a chimeric backbone, useful in treating and preventing
PT asthma, allergy, cancer, infectious disease, autoimmune disease or airway
PT remodeling.
XX
PS Example 28; SEQ ID NO 376; 276pp; English.
XX
CC The invention relates to an immunostimulatory nucleic acid molecule
CC comprising an internal pyrimidine-purine (YZ) dinucleotide and chimeric
CC backbone, where one internal YZ dinucleotide has a phosphodiester(-like)
CC internucleotide linkage, where optionally each additional internal YZ
CC dinucleotide has a phosphodiester(-like) or stabilised internucleotide
CC linkage, where other internucleotide linkages are stabilised. The
CC oligonucleotide is useful in stimulating or modulating an immune
CC response. The medicament shifts the immune response to a Th1 biased
CC response from a Th2 biased response. The oligonucleotide is also useful
CC in the manufacture of a medicament for treating asthma, allergy, cancer,
CC infectious disease, autoimmune disease, airway remodeling or chronic
CC obstructive pulmonary disease or in treating a subject who is a smoker or
CC who is free of symptoms of asthma. The oligonucleotide is useful in
CC inducing cytokine expression, e.g. IL-6 (interleukin-6), TNFalpha (tumour
CC necrosis factor alpha), IFNalpha (interferon-alpha), IFNgamma (interferon

```
CC   -gamma) and IP-10 (interferon inducible protein). The oligonucleotide is
CC   also useful in treating and preventing infections caused by viruses,
CC   bacteria and parasites. The present sequence represents an
CC   immunostimulatory nucleic acid.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          5 GTTTTTTTTTTTTTTT 20


RESULT 976
ADK19330
ID   ADK19330 standard; DNA; 20 BP.
XX
AC   ADK19330;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Immunostimulatory nucleic acid #375.
XX
KW   immunostimulatory nucleic acid; asthma; allergy; cancer;
KW   infectious disease; autoimmune disease; airway remodeling;
KW   chronic obstructive pulmonary disease; asthma; IL-6; interleukin-6;
KW   TNFalpha; tumour necrosis factor alpha; IFNalpha; interferon-alpha;
KW   IFNgamma; interferon-gamma; IP-10; interferon inducible protein;
KW   viral infection; bacteria infection; parasitic infection; ss.
XX
OS   Synthetic.
XX
PN   WO2004016805-A2.
XX
PD   26-FEB-2004.
XX
PF   19-AUG-2003; 2003WO-US025935.
XX
PR   19-AUG-2002; 2002US-0404479P.
PR   19-AUG-2002; 2002US-0404820P.
PR   27-NOV-2002; 2002US-0429701P.
PR   14-FEB-2003; 2003US-0447377P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Samulowitz U,  Vollmer J,  Uhlmann E,  Jurk M,  Lipford G;
PI   Rankin R;
XX
DR   WPI; 2004-257200/24.
XX
PT   New immunostimulatory nucleic acid molecule having pyrimidine-purine
PT   dinucleotide and a chimeric backbone, useful in treating and preventing
PT   asthma, allergy, cancer, infectious disease, autoimmune disease or airway
PT   remodeling.
XX
PS   Example 28; SEQ ID NO 377; 276pp; English.
XX
CC   The invention relates to an immunostimulatory nucleic acid molecule
CC   comprising an internal pyrimidine-purine (YZ) dinucleotide and chimeric
CC   backbone, where one internal YZ dinucleotide has a phosphodiester(-like)
CC   internucleotide linkage, where optionally each additional internal YZ
CC   dinucleotide has a phosphodiester(-like) or stabilised internucleotide
CC   linkage, where other internucleotide linkages are stabilised. The
CC   oligonucleotide is useful in stimulating or modulating an immune
CC   response. The medicament shifts the immune response to a Th1 biased
CC   response from a Th2 biased response. The oligonucleotide is also useful
CC   in the manufacture of a medicament for treating asthma, allergy, cancer,
CC   infectious disease, autoimmune disease, airway remodeling or chronic
CC   obstructive pulmonary disease or in treating a subject who is a smoker or
CC   who is free of symptoms of asthma. The oligonucleotide is useful in
CC   inducing cytokine expression, e.g. IL-6 (interleukin-6), TNFalpha (tumour
CC   necrosis factor alpha), IFNalpha (interferon-alpha), IFNgamma (interferon
CC   -gamma) and IP-10 (interferon inducible protein). The oligonucleotide is
CC   also useful in treating and preventing infections caused by viruses,
CC   bacteria and parasites. The present sequence represents an
CC   immunostimulatory nucleic acid.
XX
SQ   Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          5 GTTTTTTTTTTTTTTT 20


RESULT 977
ADL59743/c
ID   ADL59743 standard; DNA; 20 BP.
XX
AC   ADL59743;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human ESM-1 antisense oligonucleotide seqid 1992.
XX
KW   cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW   gene therapy; endothelial specific molecule-1; ESM-1;
KW   ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW   angiogenic disorder; immunological disorder; cardiovascular disorder;
KW   neurological disorder; antisense technology; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= phosphorothioate backbone. All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2004021978-A2.
XX
PD   18-MAR-2004.
XX
PF   19-AUG-2003; 2003WO-US025833.
XX
PR   19-AUG-2002; 2002US-0404495P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Weinstein EJ,  Griggs DW;
XX
DR   WPI; 2004-248358/23.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
PT   composition for treating e.g., diabetes, cancer or cardiovascular
PT   disorder.
XX
PS   Claim 3; SEQ ID NO 1992; 555pp; English.
XX
```

```
CC   The invention describes a new antisense compound, having a sequence
CC   comprising 8-30 bp targeted to a nucleic acid encoding endothelial
CC   specific molecule-1 (ESM-1), that specifically hybridises with the
CC   nucleic acid ESM-1 and inhibits its expression. Also described are: a
CC   composition; inhibiting the expression of ESM-1 in cells or tissues; and
CC   treating an animal having a disease or condition associated with ESM-1.
CC   The compound is useful for preparing a composition for treating diabetes,
CC   cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
CC   cardiovascular or neurological disorder. This sequence represents an
CC   antisense oligonucleotide that can be used to modulate expression of
CC   endothelial specific molecule-1 (ESM-1).
XX
SQ   Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTG 1


RESULT 978
ADM14246
ID   ADM14246 standard; DNA; 20 BP.
XX
AC   ADM14246;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:433.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 433; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||||
Db          5 TTTTTTTTTTTTTTTG 20


RESULT 979
ADM14751
ID   ADM14751 standard; DNA; 20 BP.
XX
AC   ADM14751;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:938.
XX
KW   chimeric; antisense oligonucleotide; phosphorothioate; human;
KW   microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW   microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW   immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW   neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW   immunomodulatory; cardiovascular; gene therapy; inflammation;
KW   Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW   reperfusion injury; ophthalmic disorder; immunological disorder;
KW   cardiovascular disorder; neurological disorder; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages and all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methocyethyls"
FT   modified_base   16. .20
```

```
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls"
XX
PN   WO2004028458-A2.
XX
PD   08-APR-2004.
XX
PF   25-SEP-2003; 2003WO-US030374.
XX
PR   25-SEP-2002; 2002US-0413549P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Gierse JK;
XX
DR   WPI; 2004-305094/28.
XX
PT   New antisense compound, having a sequence targeted to a nucleic acid
PT   encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT   inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT   ischemia.
XX
PS   Claim 4; SEQ ID NO 938; 132pp; English.
XX
CC   The present sequence represents a chimeric antisense oligonucleotide
CC   targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC   human mPGES-1 gene is located on chromosome 9, more specifically to
CC   9q34.3. The present invention also describes: (1) antisense compounds,
CC   having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC   mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC   inhibits its expression; (2) a method of inhibiting the expression of
CC   mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with mPGES-1. MPGES-1 chimeric
CC   antisense oligonucleotides and antisense compounds have cytostatic,
CC   antidiabetic, immunomodulator, cardiant, neuroprotective,
CC   antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC   ophthalmological, immunomodulatory and cardiovascular activities, and can
CC   be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC   can be used for preparing a composition for treating a disease or
CC   condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC   disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC   ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ   Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTGG 16


RESULT 980
ADE27324/c
ID   ADE27324 standard; RNA; 19 BP.
XX
AC   ADE27324;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:268.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 268; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4808 AATGCTTTTTAGAAAGCAT 4826
              |||||||| || |||||||
Db         19 AATGCTTTCTAAAAAGCAT 1


RESULT 981
ADE27614
ID   ADE27614 standard; RNA; 19 BP.
XX
AC   ADE27614;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:558.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
```

```
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 558; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 3 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   57.9%;  Pred. No. 7e+02;
  Matches   11;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4808 AATGCTTTTTAGAAAGCAT 4826
              ||:||::: :| ||||||:
Db          1 AAUGCUUUCUAAAAAGCAU 19


RESULT 982
AAQ75557
ID   AAQ75557 standard; DNA; 19 BP.
XX
AC   AAQ75557;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCT 2142
              |||| |||| |||||||||
Db          1 TTTTTTTTTTTTTTTTTCT 19


RESULT 983
AAV28402/c
ID   AAV28402 standard; DNA; 19 BP.
XX
AC   AAV28402;
XX
DT   24-JUL-1998  (first entry)
XX
DE   Wild type transposon 5 (Tn5) inside end (IE) sequence.
XX
KW   Tn5 transposase; modified; enzyme; in vitro transposition; mutant;
KW   target; marker; transposon 5; plasmid pRZTL1; ds.
XX
OS   Escherichia coli.
XX
PN   WO9810077-A1.
XX
PD   12-MAR-1998.
XX
PF   09-SEP-1997;   97WO-US015941.
XX
PR   09-SEP-1996;   96US-00814877.
PR   02-MAY-1997;   97US-00850880.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Reznikoff WS,  Goryshin IY,  Zhou H;
XX
DR   WPI; 1998-193627/17.
XX
PT   Modified Tn5 transposase construct used in novel system for in vitro
PT   transposition - used to, e.g. create absolute defective mutants, provide
PT   selective markers and to facilitate insertion of specialised DNA
PT   sequences into target DNA.
XX
PS   Example; Page 21; 73pp; English.
XX
CC   This is the transposon 5 (Tn5) wild type inside end (IE) sequence. The
CC   invention provides a genetic construct that contains a nucleotide
CC   sequence encoding a modified Tn5 transposase enzyme that has both greater
CC   avidity for Tn5 OE repeats and is less likely to assume an inactive
```

CC multimeric form than a wild type Tn5 transposase and a transposable DNA
CC sequence flanked at its 5' and 3' ends by an 18 or 19 base pair flanking
CC DNA sequence comprising nucleotide A at position 10, T at 11 and A at 12.
CC The modified Tn5 transposase and the transposable DNA which is a DNA
CC donor molecule are used in a system for in vitro transposition. The
CC system and method can be used to create absolute defective mutants, to
CC provide selective markers to target DNA, to provide portable regions of
CC homology to a target DNA, to facilitate insertion of specialised DNA
CC sequences into target DNA, to provide primer binding sites or tags for
CC DNA sequencing , to facilitate production of genetic fusion for gene
CC expression studies and protein domain mapping, as well as to bring
CC together other desired combinations of DNA sequences (combinatorial
CC genetics). The modified Tn5 transposase facilitates in vitro
CC transposition reaction rates of at least about 100-fold higher than can
CC be achieved using wild type transposase (as measure in vivo). In vitro
CC transposition using this system can also use donor DNA and target DNA
CC that is circular or linear. The system also requires no outside high
CC energy source and no other protein other than the modified transposase
XX
SQ Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4182 AGATCTGATCAAGAGTCCG 4200
||||||||||||||| | |
Db 19 AGATCTGATCAAGAGACAG 1

RESULT 984
AAZ06438/c
ID AAZ06438 standard; DNA; 19 BP.
XX
AC AAZ06438;
XX
DT 09-NOV-1999 (first entry)
XX
DE Wildtype Inside End (OE) termini.
XX
KW transposase; modified form; wildtype; multimeric; OE termini; IE termini;
KW outside end termini; inside end termini; plasmid; repeat sequence;
KW mutation; ds.
XX
OS Transposon Tn5.
XX
PN US5948622-A.
XX
PD 07-SEP-1999.
XX
PF 06-OCT-1997; 97US-00944916.
XX
PR 09-SEP-1996; 96US-00814877.
PR 02-MAY-1997; 97US-00850880.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Zhou H, York DL, Goryshin IY, Reznikoff WS;
XX
DR WPI; 1999-517947/43.
XX
PT In vitro transposition using a Tn5 based genetic construct.
XX
PS Example 1; Col 16; 48pp; English.
XX
CC Wildtype Outside End (OE, AAZ06435) and Inside End (IE, AAZ06438) were
CC compared and an effort made to randomize the nucleotides at each of the
CC seven positions of difference. A population of oligonucleotides
CC degenerate at each position of difference was created. This resulted in
CC individual oligonucleotides in the population randomly included either
CC the nucleotide of the wildtype OE or the wildtype IE. 128 distinct
CC oligonucleotides were generated, which had the sequence characteristics
CC of both OE and IE and so can be referred to as OE/IE-like sequences. Two
CC of these OE/IE-like sequences are the mutant OE sequences AAZ06436 and
CC AAZ06437
XX
SQ Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4182 AGATCTGATCAAGAGTCCG 4200
||||||||||||||| | |
Db 19 AGATCTGATCAAGAGACAG 1

RESULT 985
AAA11741/c
ID AAA11741 standard; DNA; 19 BP.
XX
AC AAA11741;
XX
DT 21-JUL-2000 (first entry)
XX
DE Transposon Tn5 inside end DNA fragment.
XX
KW Transposon; transposase; insertion mutation; synaptic complex; ss.
XX
OS Transposon Tn5.
XX
PN WO200017343-A1.
XX
PD 30-MAR-2000.
XX
PF 21-SEP-1999; 99WO-US021960.
XX
PR 23-SEP-1998; 98US-00159363.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Reznikoff WS, Goryshin IY;
XX
DR WPI; 2000-283573/24.
XX
PT Making insertional mutations at random or quasi-random positions in
PT cellular nucleic acids in target cells, useful for identifying
PT chromosomal regions involved in expressing or regulating expression of
PT proteins.
XX
PS Example; Fig 3; 25pp; English.
XX
CC This invention describes a novel method (I) for making an insertional
CC mutation at a random or quasi-random position in cellular nucleic acid in
CC a target cell. The invention describes a method (II) for forming a
CC synaptic complex between a Tn5 transposase protein (X) and a
CC polynucleotide (Y) that comprises a pair of nucleotide sequences adapted
CC for operably interacting with the Tn5 transposase to form a synaptic
CC complex and a transposable nucleotide sequence between them, comprising
CC combining (X) and (Y) in vitro under conditions that disfavor
CC polynucleotide strand transfer to form the synaptic complex. Methods for
CC the insertion of exogenous nucleic acids into the nucleic acids of target
CC cells are used to identify chromosomal regions involved in expressing or
CC regulating expression of proteins. The same methods may be used in the
CC development of new therapeutic agents. The transposable polynucleotides
CC used to form synaptic complexes can consist of transposon apart from any
CC flanking sequences. This is advantageous in that it reduces the
CC likelihood of intramolecular transposition and increases the likelihood
CC of transposition into a target genome. Eliminating donor backbone
CC sequences from the polynucleotide simplifies preparation of the
CC transposon sequences to be used in (I). Additionally, the synaptic
CC complex can form under conditions that disfavor non-productive
CC intramolecular transposition events. This is advantageous because all of
CC the synaptic complexes can undergo transposition when combined with
CC cellular DNA. Little, if any, of the nucleic acid in the synaptic
CC complexes is inactive. This sequence represents a novel transposon Tn5

```
CC   inside end DNA fragment described in the method of the invention
XX
SQ   Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 986
AAA86321
ID   AAA86321 standard; DNA; 19 BP.
XX
AC   AAA86321;
XX
DT   04-DEC-2000  (first entry)
XX
DE   PCBA HH ribozyme binding site #53.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 106; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1117 TGAGGGCTTCCACAACTAC 1135
              |||||||||| ||| ||||
Db          1 TGAGGGCTTCGACACCTAC 19


RESULT 987
AAD21281/c
ID   AAD21281 standard; DNA; 19 BP.
XX
AC   AAD21281;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Inside end (IE) terminal sequence of wild-type Tn5 transposon.
XX
KW   Insertional mutation; synaptic complex; transposon; screening;
KW   inside end; IE; ds.
XX
OS   Unidentified.
XX
PN   US6294385-B1.
XX
PD   25-SEP-2001.
XX
PF   10-AUG-2000; 2000US-00635969.
XX
PR   23-SEP-1998;   98US-00159363.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Goryshin IY,  Reznikoff WS;
XX
DR   WPI; 2001-656171/75.
XX
PT   Making an insertional mutations, especially useful for efficiently
PT   inserting a transposable polynucleotide in a target cell, comprises
PT   introducing into the target cell a synaptic complex.
XX
PS   Disclosure; Fig 3; 11pp; English.
XX
CC   The present invention relates to a method for making an insertional
CC   mutation at a random or quasi-random position in cellular nucleic acid in
CC   a target cell comprising introducing into the target cell a synaptic
CC   complex. The method is particularly useful for efficiently inserting a
CC   transposable polynucleotide at random or quasi-random locations in the
CC   chromosomal or extra-chromosomal nucleic acid of a target cell. The
CC   method may also be used for screening the genome of cells that comprise
CC   an insertional mutation that induces a phenotypic or genotypic change
CC   relative to the cells that are not subject to insertional mutagenesis.
CC   The present sequence is the inside end (IE) terminal sequence of wild-
CC   type Tn5 transposon, used in the exemplification of the invention
XX
SQ   Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 988
AAC85194/c
ID   AAC85194 standard; DNA; 19 BP.
XX
AC   AAC85194;
XX
DT   14-MAY-2001  (first entry)
XX
DE   Tn5 transposase inside end (IE) nucleotide sequence.
XX
KW   Tn5 transposon; transposase; mutant; transposition; enzyme; catalyse; ds.
XX
OS   Transposon Tn5.
XX
PN   WO200109363-A1.
XX
PD   08-FEB-2001.
XX
PF   02-AUG-2000; 2000WO-US021052.
XX
PR   02-AUG-1999;   99US-0146686P.
```

```
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Reznikoff WS,  Naumann TA;
XX
DR   WPI; 2001-182968/18.
XX
PT   Mutant Tn5 transposase enzymes which have preference for Tn5 inside ends
PT   over Tn5 outside ends useful for in vitro transpositions and in systems
PT   for transposing a transposable DNA sequence in vitro.
XX
PS   Disclosure; Fig 1; 37pp; English.
XX
CC   The invention relates to a mutant Tn5 transposase protein (I) modified
CC   relative to wild-type Tn5 transposase protein, which differs from the
CC   wild-type protein at amino acid positions 58 or 372 and which has a
CC   preference for Tn5 inside ends (IEs) over Tn5 outside ends (OEs). (I) is
CC   useful in a system for transposing a transposable DNA sequence in vitro.
CC   The system comprises (I), a donor DNA molecule comprising a transposable
CC   DNA sequence which is flanked at its 5' and 3' ends by a wild-type
CC   methylated IE sequence and a target DNA molecule into which the
CC   transposable element can transpose. It is also useful in a in vitro
CC   transposition method which involves combining a donor DNA molecule that
CC   comprises a transposable DNA sequence of interest being flanked at its 5'
CC   and 3' ends by a wild-type Tn5 IE sequence with a target DNA molecule and
CC   (I), in a reaction buffer at a temperature below physiological
CC   temperature until the modified transposase binds to the IE sequences and
CC   then raising the temperature enzyme to catalyse in vitro transposition.
CC   The present sequence represents the nucleotide sequence of Tn5
CC   transposase IE
XX
SQ   Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 989
AAC91689/c
ID   AAC91689 standard; DNA; 19 BP.
XX
AC   AAC91689;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Transposon Tn5 IS50R I end (5' insertion end).
XX
KW   Transposable element; MHC epitope; major histocompatibility complex;
KW   intracellular bacterial pathogen; loxP site; Cre recombinase;
KW   insertion end; in-frame fusion; detection; antigen;
KW   disseminated insertions of class-I epitopes; DICE-I; transposon Tn5;
KW   I end; ds.
XX
OS   Escherichia coli.
XX
PN   WO200071158-A1.
XX
PD   30-NOV-2000.
XX
PF   26-MAY-2000; 2000WO-US014687.
XX
PR   26-MAY-1999;   99US-0136210P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Heffron FL,  Parker DC,  Ellefson DD;
XX
DR   WPI; 2001-031967/04.
XX
PT   Transposable element for detecting an antigenic epitope of a pathogen,
PT   comprising 5' and 3' recombining sites, nucleic acid sequences encoding a
PT   selectable marker and major histocompatibility complex (MHC) epitope, and
PT   an insertion end.
XX
PS   Claim 17; Fig 11; 63pp; English.
XX
CC   The invention relates to a novel transposable element comprising DNA
CC   encoding a selectable marker (e.g., antibiotic resistance) located
CC   between a 5' recombining site and a 3' recombining site (e.g., loxP
CC   sites); DNA encoding an MHC (major histocompatibility complex) epitope
CC   either 5' of the 5' recombining site or 3' of the 3' recombining site;
CC   and insertion ends comprising an inverted repeat sequence at the 5' and
CC   3' ends of the transposable element sufficient for integration of the
CC   transposable element. The transposable elements of the invention are able
CC   to introduce in-frame insertions throughout the chromosome of an
CC   intracellular bacterial pathogen. This system "tags" the bacterial gene
CC   and resulting protein, allowing the identification of proteins secreted
CC   across the membranes of the eukaryotic cell infected by the bacterium. In
CC   one embodiment, the transposable elements contain an antibiotic
CC   resistance cassette, two minimal loxP recombination sites, an MHC class I
CC   or class II epitope, and flanking insertion ends. A transposase, such as
CC   the Cre recombinase protein, is expressed in trans from a plasmid, or can
CC   be included in the transposable element. The Cre recombinase loops out
CC   the intervening sequences containing the antibiotic resistance cassette.
CC   When the transposable element inserts within a gene, the resolved
CC   insertion places the MHC class I or class II epitope in frame with the
CC   gene. The transposable elements of the invention are useful for detecting
CC   an antigenic epitope of an intracellular bacterial pathogen, such as
CC   Salmonella sp., Mycobacterium tuberculosis and Listeria monocytogenes.
CC   Certain embodiments of the technology, termed "disseminated insertions of
CC   class-I epitopes" (DICE-I; DICE-II for class II epitopes) allow the rapid
CC   and accurate identification of proteins involved in bacterial
CC   pathogenesis so that such proteins can be used as vaccine and drug
CC   targets. Carrier vaccines may be generated by infecting bacteria with a
CC   transposable element of the invention which additionally comprises an
CC   antigen associated with a disease, preferably cancer or a viral or
CC   bacterial disease, operably linked to the MHC epitope DNA of the
CC   transposable element. The present sequence represents a transposon Tn5
CC   IS50R I end (5' insertion end) claimed for use in a transposable element
CC   of the invention
XX
SQ   Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 990
AAH61483
ID   AAH61483 standard; DNA; 19 BP.
XX
AC   AAH61483;
XX
DT   10-SEP-2001  (first entry)
XX
DE   PCNA HH ribozyme binding site SEQ ID NO:3907.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
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KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 356; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1117 TGAGGGCTTCCACAACTAC 1135
              ||||||||||  ||| ||||
Db          1 TGAGGGCTTCGACACCTAC 19


RESULT 991
ACA90054/c
ID   ACA90054 standard; DNA; 19 BP.
XX
AC   ACA90054;
XX
DT   10-JUL-2003  (first entry)
XX
DE   Cardiovascular disease differential gene expression related primer #101.
XX
KW   Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
KW   myocardial infarction; cardiant; antiarteriosclerotic; antianginal;
KW   gene therapy; differential gene expression; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031650-A2.
XX
PD   17-APR-2003.
XX
PF   02-OCT-2002; 2002WO-EP011034.
XX
PR   08-OCT-2001; 2001GB-00024145.
XX
PA   (FARB ) BAYER AG.
XX
PI   Munnes M,  Gehrmann M,  Wick M,  Schmitz G;
XX
DR   WPI; 2003-403108/38.
XX
PT   Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
PT   angina, ischemia, myocardial infarction or arteriosclerosis by detection
PT   of a polynucleotide in a biological sample comprises detecting a
PT   hybridization complex.
XX
PS   Example 3; Page 105; 454pp; English.
XX
CC   The invention describes a method of predicting, diagnosing or prognosing
CC   a cardiovascular disease by detection of a polynucleotide in a biological
CC   sample comprises hybridising at least one of the polynucleotide to a
CC   nucleic acid material of a biological sample, thus forming a
CC   hybridisation complex, and detecting the hybridisation complex. The
CC   polynucleotides, polypeptides, antisense molecule, antibody and reagent
CC   are useful for preparing compositions for preventing, predicting or
CC   diagnosing, or a medicament for treating a cardiovascular disease, e.g.
CC   arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
CC   This sequence represents a primer used to identify genes differentially
CC   regulated in individuals with cardiovascular disease
XX
SQ   Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1320 GGGGTCCCTCAGGTTTCCT 1338
              ||||||||||||||| | |
Db         19 GGGGTCCCTCAGGTTCCTT 1

RESULT 992
ABZ22886/c
ID   ABZ22886 standard; DNA; 19 BP.
XX
AC   ABZ22886;
XX
DT   07-APR-2003  (first entry)
XX
DE   Oligonucleotide kh2.
XX
KW   Phosphorothioate; locked nucleic acid; LNA; immunostimulatory;
KW   cytostatic; antimicrobial; gene therapy; pathogenic infection; cancer;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "5'-terminally modified by fluorescein"
XX
PN   WO2002102825-A2.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-GB002728.
XX
PR   15-JUN-2001; 2001GB-00014719.
XX
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PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Catchpole IR;
XX
DR   WPI; 2003-157022/15.
XX
PT   Novel locked nucleic acid conjugate useful in manufacturing a medicament
PT   for treating or preventing pathogenic infections or cancer, has an
PT   oligonucleotide having locked nucleic acid based on a functional moiety.
XX
PS   Example 5; Page 36; 101pp; English.
XX
CC   The present invention describes a locked nucleic acid (LNA) conjugate (I)
CC   comprising an oligonucleotide having at least one locked nucleic acid
CC   based on a functional moiety. Also described: (1) a complex (II)
CC   comprising (I) and a DNA sequence having a complementary sequence to the
CC   oligonucleotide, and encoding a gene under the control of a promoter; (2)
CC   a pharmaceutical composition (III) comprising (II) and a carrier or
CC   diluent; (3) a device loaded with (III); and (4) an oligonucleotide (IV)
CC   comprising a first region comprising an oligonucleotide sequence having
CC   at least one LNA, and a second region comprising an immunostimulatory
CC   oligonucleotide region containing at least one unmethylated CG di-
CC   nucleotide motif. (I) has cytostatic and antimicrobial activities, and
CC   can be used in gene therapy. (I) and (II) can be used in medicine, and in
CC   the manufacture of a medicament for the treatment or the prevention of
CC   pathogenic infections or cancer. (I) is useful for the preparation of
CC   (III), by hybridising (I) with a plasmid capable of expressing a gene
CC   encoding an antigen or therapeutic protein, and formulating the resulting
CC   complex with a pharmaceutical carrier. The present sequence represents an
CC   oligonucleotide, which is used in an example from the present invention
XX
SQ   Sequence 19 BP; 9 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3181 CTCTCTCTCCCTCCCTCTC 3199
              ||||||||| ||| |||||
Db         19 CTCTCTCTCTCTCTCTCTC 1


RESULT 993
AAD58808/c
ID   AAD58808 standard; DNA; 19 BP.
XX
AC   AAD58808;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Tn5 transposon element DNA #2.
XX
KW   Therapeutic protein; gene therapy; transposon; ds.
XX
OS   Unidentified.
XX
PN   US2003143740-A1.
XX
PD   31-JUL-2003.
XX
PF   15-OCT-2002; 2002US-00272552.
XX
PR   15-OCT-2001; 2001US-0329474P.
PR   08-NOV-2001; 2001US-0344865P.
XX
PA   (WOOD/) WOODDELL C.
PA   (HERW/) HERWEIJER H.
PA   (WOLF/) WOLFF J A.
XX
PI   Wooddell C,  Herweijer H,  Wolff JA;
XX
DR   WPI; 2003-645713/61.
XX
PT   Integrating nucleic acid into mammalian genome, useful for gene therapy,
PT   comprises delivering a complex between nucleic acid containing a
PT   transposon and a transposase specific for the transposon.
XX
PS   Disclosure; Page 3; 20pp; English.
XX
CC   The invention relates to a method of integrating nucleic acid into the
CC   genome of mammalian cells. The method involves forming an integrator
CC   complex between the nucleic acid containing a transposon and a
CC   transposase specific for the transposon and delivering the integrator
CC   complex to a mammalian cell. The method and composition is useful for
CC   integrating nucleic acid into the genome of mammalian cells, especially
CC   nucleic acids encoding therapeutic proteins for gene therapy. The
CC   transposon may be used to integrate large DNA molecules, up to 10 kb or
CC   larger, into the genome of a mammalian cell. The present sequence is Tn5
CC   transposon element DNA (end binding sequence). This sequence is used to
CC   illustrate the method of the invention
XX
SQ   Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4182 AGATCTGATCAAGAGTCCG 4200
              ||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1


RESULT 994
ADF36101
ID   ADF36101 standard; RNA; 19 BP.
XX
AC   ADF36101;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human VEGFR1 short interfering nucleic acid (siNA) SEQ ID NO:390.
XX
KW   double-stranded short interfering nucleic acid;
KW   short interfering nucleic acid; siNA; downregulation;
KW   vascular endothelial growth factor receptor; VEGFR; antiangiogenic;
KW   cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
KW   nephrotropic; gynaecological; angiogenesis-associated condition; cancer;
KW   diabetic retinopathy; macular degeneration; neovascular glaucoma;
KW   arthritis; psoriasis; endometriosis; angiofibroma;
KW   polycystic kidney disease; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003070910-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005022.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   29-MAY-2002; 2002WO-US017674.
PR   06-JUN-2002; 2002US-0386782P.
PR   03-JUL-2002; 2002US-0393796P.
PR   29-JUL-2002; 2002US-0399348P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   04-NOV-2002; 2002US-00287949.
PR   27-NOV-2002; 2002US-00306747.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Pavco P;
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XX
DR   WPI; 2003-679876/64.
XX
PT   New double-stranded interfering nucleic acid, useful e.g. for treatment
PT   and diagnosis of cancer, downregulates the vascular endothelial growth
PT   factor receptor gene.
XX
PS   Example 3; SEQ ID NO 390; 207pp; English.
XX
CC   The present invention describes a double-stranded short interfering
CC   nucleic acid (siNA) that downregulates expression of the vascular
CC   endothelial growth factor receptor (VEGFR) gene. Also described: (1) a
CC   siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
CC   delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors
CC   that express siNA; and (5) single-stranded siNA with similar properties.
CC   The siNAs have antiangiogenic, cytostatic, antidiabetic,
CC   ophthalmological, antiarthritic, antipsoriatic, nephrotropic and
CC   gynaecological activities. The siNA are useful for modulating
CC   (downregulating) the expression of VEGFR genes. The siNA are potentially
CC   useful for treating a wide range of angiogenesis-associated conditions,
CC   particularly cancers, diabetic retinopathy, macular degeneration,
CC   neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma,
CC   and polycystic kidney disease. The siNA may also be useful for diagnosis,
CC   drug screening, target identification and validation, genetic
CC   engineering, studying gene function, and also for gene mapping (e.g. of
CC   single-nucleotide polymorphisms). The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 19 BP; 0 A; 0 C; 11 G; 0 T; 8 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   52.6%;  Pred. No. 7e+02;
  Matches   10;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              :|:|:|  :|:|||:|:||
Db          1 UGUGUGUGUGUGGGUGUGG 19


RESULT 995
ADF36528/c
ID   ADF36528 standard; RNA; 19 BP.
XX
AC   ADF36528;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human VEGFR1 short interfering nucleic acid (siNA) SEQ ID NO:817.
XX
KW   double-stranded short interfering nucleic acid;
KW   short interfering nucleic acid; siNA; downregulation;
KW   vascular endothelial growth factor receptor; VEGFR; antiangiogenic;
KW   cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
KW   nephrotropic; gynaecological; angiogenesis-associated condition; cancer;
KW   diabetic retinopathy; macular degeneration; neovascular glaucoma;
KW   arthritis; psoriasis; endometriosis; angiofibroma;
KW   polycystic kidney disease; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003070910-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005022.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   29-MAY-2002; 2002WO-US017674.
PR   06-JUN-2002; 2002US-0386782P.
PR   03-JUL-2002; 2002US-0393796P.
PR   29-JUL-2002; 2002US-0399348P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   04-NOV-2002; 2002US-00287949.
PR   27-NOV-2002; 2002US-00306747.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Pavco P;
XX
DR   WPI; 2003-679876/64.
XX
PT   New double-stranded interfering nucleic acid, useful e.g. for treatment
PT   and diagnosis of cancer, downregulates the vascular endothelial growth
PT   factor receptor gene.
XX
PS   Example 3; SEQ ID NO 817; 207pp; English.
XX
CC   The present invention describes a double-stranded short interfering
CC   nucleic acid (siNA) that downregulates expression of the vascular
CC   endothelial growth factor receptor (VEGFR) gene. Also described: (1) a
CC   siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
CC   delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors
CC   that express siNA; and (5) single-stranded siNA with similar properties.
CC   The siNAs have antiangiogenic, cytostatic, antidiabetic,
CC   ophthalmological, antiarthritic, antipsoriatic, nephrotropic and
CC   gynaecological activities. The siNA are useful for modulating
CC   (downregulating) the expression of VEGFR genes. The siNA are potentially
CC   useful for treating a wide range of angiogenesis-associated conditions,
CC   particularly cancers, diabetic retinopathy, macular degeneration,
CC   neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma,
CC   and polycystic kidney disease. The siNA may also be useful for diagnosis,
CC   drug screening, target identification and validation, genetic
CC   engineering, studying gene function, and also for gene mapping (e.g. of
CC   single-nucleotide polymorphisms). The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 19 BP; 8 A; 11 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4082 TGTGTGGCTGTGGGTGTGG 4100
              ||||||  ||||||||||||
Db         19 TGTGTGTGTGTGGGTGTGG 1


RESULT 996
ADH16535/c
ID   ADH16535 standard; RNA; 19 BP.
XX
AC   ADH16535;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human BACE transcript target sequence/siNA upper strand, SEQ ID NO:325.
XX
KW   RNA interference; short interfering nucleic acid; siNA;
KW   short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW   short hairpin RNA; shRNA; expression modulation; gene therapy;
KW   drug screening; diagnosis; therapeutic target identification;
KW   pharmacogenomics; gene function analysis; gene mapping;
KW   Alzheimer's disease; dementia; stroke; cardiovascular accident;
KW   beta-secretase; BACE; human; target sequence; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003070895-A2.
XX
PD   28-AUG-2003.
XX
```

```
PF   18-FEB-2003; 2003WO-US004710.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   25-JUL-2002; 2002US-00205309.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-697608/66.
XX
PT   New short interfering nucleic acids, useful e.g. for treatment and
PT   diagnosis of Alzheimer's disease, which down regulates expression of the
PT   beta-secretase gene.
XX
PS   Example 3; SEQ ID NO 325; 144pp; English.
XX
CC   The invention relates to short interfering nucleic acids (siNA) which
CC   downregulate expression of the human beta-secretase (BACE) gene by RNA
CC   interference. The siNAs may or may not comprise ribonucleotides and may
CC   be double or single stranded. They further comprise sense and antisense
CC   regions, or alternatively are assembled from a sense oligonucleotide and
CC   an antisense oligonucleotide. Specifically, the siNAs include short
CC   interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC   hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC   can contain deoxyribonucleotides, and can be chemically synthesised,
CC   expressed from a vector or enzymatically synthesised. The invention also
CC   relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC   and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC   used to modulate expression of the BACE gene in cells, tissue explants or
CC   organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC   for the treatment of a variety of conditions. They may be used for
CC   treating Alzheimer's disease or other degenerative conditions such as
CC   dementia and stroke/cardiovascular accident. The siNAs are also useful
CC   for drug screening, diagnosis, therapeutic target identification and
CC   validation, genetic engineering, pharmacogenomics, studying gene
CC   function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC   The present sequence represents the upper strand of a human BACE-targeted
CC   double-stranded siNA, which is identical to the BACE transcript target
CC   sequence.
XX
SQ   Sequence 19 BP; 16 A; 1 C; 1 G; 0 T; 1 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              |||||||||||||||  ||
Db         19 TTTTTTTTTTTTTTGACTT 1


RESULT 997
ADH16860
ID   ADH16860 standard; RNA; 19 BP.
XX
AC   ADH16860;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human BACE siNA lower strand, SEQ ID NO:650.
XX
KW   RNA interference; short interfering nucleic acid; siNA;
KW   short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW   short hairpin RNA; shRNA; expression modulation; gene therapy;
KW   drug screening; diagnosis; therapeutic target identification;
KW   pharmacogenomics; gene function analysis; gene mapping;
KW   Alzheimer's disease; dementia; stroke; cardiovascular accident;
KW   beta-secretase; BACE; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003070895-A2.
XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US004710.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   25-JUL-2002; 2002US-00205309.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-697608/66.
XX
PT   New short interfering nucleic acids, useful e.g. for treatment and
PT   diagnosis of Alzheimer's disease, which down regulates expression of the
PT   beta-secretase gene.
XX
PS   Example 3; SEQ ID NO 650; 144pp; English.
XX
CC   The invention relates to short interfering nucleic acids (siNA) which
CC   downregulate expression of the human beta-secretase (BACE) gene by RNA
CC   interference. The siNAs may or may not comprise ribonucleotides and may
CC   be double or single stranded. They further comprise sense and antisense
CC   regions, or alternatively are assembled from a sense oligonucleotide and
CC   an antisense oligonucleotide. Specifically, the siNAs include short
CC   interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC   hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC   can contain deoxyribonucleotides, and can be chemically synthesised,
CC   expressed from a vector or enzymatically synthesised. The invention also
CC   relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC   and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC   used to modulate expression of the BACE gene in cells, tissue explants or
CC   organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC   for the treatment of a variety of conditions. They may be used for
CC   treating Alzheimer's disease or other degenerative conditions such as
CC   dementia and stroke/cardiovascular accident. The siNAs are also useful
CC   for drug screening, diagnosis, therapeutic target identification and
CC   validation, genetic engineering, pharmacogenomics, studying gene
CC   function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC   The present sequence represents the lower strand of a human BACE-targeted
CC   double-stranded siNA.
XX
SQ   Sequence 19 BP; 1 A; 1 C; 1 G; 0 T; 16 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   5.3%;  Pred. No. 7e+02;
  Matches    1;  Conservative   16;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGGTT 4520
              :::::::::::::::|  ::
Db          1 UUUUUUUUUUUUUUGACUU 19


RESULT 998
ADH70642
ID   ADH70642 standard; DNA; 19 BP.
XX
AC   ADH70642;
XX
DT   25-MAR-2004  (first entry)
```

XX
DE Human Vbeta gene repeat sequence #432.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 836; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2395 TATATATACATATATACAT 2413
||||||||| ||||||| ||
Db 1 TATATATAAATATATATAT 19

RESULT 999
ADH70567/c
ID ADH70567 standard; DNA; 19 BP.
XX
AC ADH70567;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #357.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosome;
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
OS Homo sapiens.
XX
PN US2002150891-A1.
XX
PD 17-OCT-2002.
XX
PF 05-MAR-1999; 99US-00263959.
XX
PR 19-SEP-1994; 94US-00309335.
PR 19-SEP-1995; 95US-00531241.
XX
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
XX
PI Hood LE, Rowen L;
XX
DR WPI; 2004-059052/06.
XX
PT Kit for diagnozing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
PS Disclosure; SEQ ID NO 761; 164pp; English.
XX
CC The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, Type II hypersensitivities such as those present in
CC Goodpasture's syndrome and Type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ Sequence 19 BP; 16 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7e+02;

```
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCT 2142
              ||||||||||||||| || |
Db         19 TTTTCTTTTCTTTTCTTTT 1


RESULT 1000
ADH70449
ID   ADH70449 standard; DNA; 19 BP.
XX
AC   ADH70449;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #239.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 643; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 19 BP; 0 A; 3 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTTCT 2142
              ||||||||||||||| || |
Db          1 TTTTCTTTTCTTTTCTTTT 19


RESULT 1001
ADM97645
ID   ADM97645 standard; DNA; 19 BP.
XX
AC   ADM97645;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human MIA-2 coding sequence PCR primer SEQ ID NO: 30.
XX
KW   ss; PCR; human; MIA-2; cytostatic; hepatotropic;
KW   melanoma-inhibiting activity-2; liver cirrhosis; liver fibrosis;
KW   liver damage; primer.
XX
OS   Homo sapiens.
XX
PN   EP1410803-A1.
XX
PD   21-APR-2004.
XX
PF   16-OCT-2003; 2003EP-00023591.
XX
PR   16-OCT-2002; 2002DE-01048248.
PR   07-FEB-2003; 2003DE-01005082.
XX
PA   (SCIL-) SCIL PROTEINS GMBH.
XX
PI   Bosserhoff A,  Hellerbrand C,  Buettner R;
XX
DR   WPI; 2004-319027/30.
XX
PT   New mammalian melanoma-inhibitory activity-2 proteins and encoding
PT   nucleic acids, are useful for treating cancer, fibrosis and cirrhosis of
PT   the liver.
XX
PS   Claim 18; Page 30; 54pp; German.
XX
CC   The present invention provides the protein and coding sequences of human
CC   and murine MIA-2 (melanoma-inhibiting activity-2) proteins. The sequences
CC   are useful in antifibrotic therapy, also for treating cirrhosis and
CC   fibrosis of the liver. The same material, also antibodies and aptamers
CC   directed against an epitope of the proteins and probes that hybridize to
CC   the coding sequences, can be used to treat liver tumours and metastases.
CC   The antibodies, aptamers and probes are also useful for diagnosis,
CC   particularly of liver damage and the acute phase of an inflammatory or
CC   infective disease (e.g. Crohn's disease, gastroenteritis, rheumatoid
CC   arthritis, spondylitis, mycocarditis). The sequences are also used to
CC   prepare organ cultures from hepatocytes, and these cultures are useful
CC   for purifying blood from patients with inadequate liver function. The
CC   present sequence is a PCR primer used to isolate the human coding
CC   sequence of the invention.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2317 AATAAGATGGCTGTGGCAT 2335
```

```
                    || |||||||| |||||||
Db          1 AAGAAGATGGCGGTGGCAT 19
```

RESULT 1002
ADQ16517/c
ID ADQ16517 standard; DNA; 19 BP.
XX
AC ADQ16517;
XX
DT 23-SEP-2004 (first entry)
XX
DE Transposon Tn5 inner element.
XX
KW Transposon Tn5; ss; transposase mediated integration; transposon;
KW transposase; Tn5 inner element; random insertional mutagenesis;
KW RNA polymerase III promoter; U1 snRNA gene.
XX
OS Transposon Tn5.
XX
PN US2004126887-A1.
XX
PD 01-JUL-2004.
XX
PF 08-NOV-2002; 2002US-00291342.
XX
PR 08-NOV-2001; 2001US-0344865P.
XX
PA (WOOD/) WOODDELL C.
PA (HERW/) HERWEIJER H.
PA (WOLF/) WOLFF J A.
XX
PI Wooddell C, Herweijer H, Wolff JA;
XX
DR WPI; 2004-542387/52.
XX
PT Composition useful for enhancing transposase mediated integration of
PT transposon into target nucleic acid, comprising integrator complex, and
PT enhancing reagent.
XX
PS Disclosure; SEQ ID NO 2; 14pp; English.
XX
CC The invention relates to a composition for enhancing transposase mediated
CC integration of a transposon into a target nucleic acid, comprising an
CC integrator complex and an enhancing reagent. The invention also relates
CC to a method of integrating a nucleic acid into a target nucleic acid,
CC involving making a transposon, forming an integrator complex, combining
CC the integrator complex and a cationic enhancing reagent together in
CC solution, and incubating the composition with a target nucleic acid,
CC where the transposase integrates the transposon into the target nucleic
CC acid. The transposase is a hyperactive mutant Tn5 transposase. The Tn5
CC transposase is flanked by elements chosen from Tn5 outer elements, Tn5
CC inner elements and Tn5 mosaic elements. The enhancing reagent is chosen
CC from transfection reagents, polycations, cationic polymers and cationic
CC lipids. The enhancing reagent comprises both cationic proteins and
CC cationic lipids. The composition and the method are useful for providing
CC random insertional mutagenesis, in which integration of a transposon into
CC a target nucleic acid inserts a molecular tag or disrupts a target
CC sequence, where the integration of a molecular tag facilitates cloning,
CC sequencing or identification by providing a detectable marker, and the
CC integration into a coding region disrupts gene function and facilitates
CC study of a gene. The composition is useful for identifying enhancer
CC elements, for sequencing DNA and for integrating large DNA fragments with
CC known ends into a target nucleic acid such as a plasmid, an artificial
CC chromosome or a viral vector. The composition is also useful for
CC integrating e.g. therapeutic genes, siRNA genes, reporter genes, marker
CC or tag sequences, genes containing RNA polymerase III promoters or
CC modified U1 snRNA genes. This sequence represents a transposon Tn5 inner
CC element used in the scope of the invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match 0.4%; Score 15.8; DB 1; Length 19;
  Best Local Similarity 89.5%; Pred. No. 7e+02;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4182 AGATCTGATCAAGAGTCCG 4200
              |||||||||||||||| | |
Db         19 AGATCTGATCAAGAGACAG 1
```

RESULT 1003
AAV19118
ID AAV19118 standard; DNA; 17 BP.
XX
AC AAV19118;
XX
DT 28-AUG-1998 (first entry)
XX
DE Anchored oligo(T) primer.
XX
KW Secreted apoptosis-related protein; SARP; mSARP1; mouse; prostate cancer;
KW breast cancer; diagnosis; gene therapy; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9813493-A2.
XX
PD 02-APR-1998.
XX
PF 24-SEP-1997; 97WO-US017154.
XX
PR 24-SEP-1996; 96US-0026603P.
PR 11-OCT-1996; 96US-0028363P.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Umansky S, Melkonyan H;
XX
DR WPI; 1998-230704/20.
XX
PT New secreted apoptosis-related proteins - useful for modulating
PT apoptosis, particularly for treatment of prostatic or breast cancer, also
PT for diagnosis and monitoring of disease.
XX
PS Example 1; Page 30; 101pp; English.
XX
CC This oligo(T) synthetic oligonucleotide was used for first strand cDNA
CC synthesis from total RNA isolated from either logarithmically growing or
CC quiescent 10T1/2 mouse fibroblast cells. It was also used with an
CC arbitarary d(N10) primer in PCR. The PCR products were used in a
CC differential display to identify the mSARP1 gene (see AAV19112) that
CC codes for novel murine secreted apoposis-related protein mSARP1 (see
CC AAW37814). The invention relates to SARP polynucleotides (see also
CC AAV19113-15) and polypeptides (see also AAW37815-17), antibodies specific
CC for SARP, and use of such polynucleotides and antibodies in diagnostic
CC and therapeutic methods, and methods for treating diseases related to the
CC regulation of SARP expression in tissue and body fluid samples, including
CC cancers
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match 0.4%; Score 15.6; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 6.8e+02;
  Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  :
Db          1 TTTTTTTTTTTTTTNS 17
```

RESULT 1004
ABK98126
ID ABK98126 standard; DNA; 18 BP.
XX
AC ABK98126;

XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #15.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Col 41; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 18 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 2 Other;

Query Match 0.4%; Score 15.6; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2125 TTTCTTTTCTTTTTTTCT 2142
||| |||||:|||||||
Db 1 TTTDTTTTCTDTTTTTCT 18

RESULT 1005
ACA98775
ID ACA98775 standard; DNA; 19 BP.
XX
AC ACA98775;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human CYP2C8 SNP detection PCR primer #215.
XX
KW Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
KW cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
KW single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200299099-A2.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-EP006000.
XX
PR 01-JUN-2001; 2001EP-00112899.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Penger A, Sprenger R, Brinkmann U;
XX
DR WPI; 2003-167344/16.
XX
PT New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
PS Example 2; Page 52; 178pp; English.
XX
CC The invention describes a new polynucleotide comprises a polynucleotide:
CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC in the specification; (b) encoding any of seven polypeptides having 7
CC amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC polynucleotide, gene, vector, polypeptide or antibody is useful for
CC diagnosing or treating a disease, for preparing a diagnostic composition
CC for diagnosing a disease, or for preparing a pharmaceutical composition
CC for treating a disease. This disease includes arachidonic acid
CC metabolism, cancer or cardiovascular diseases. This sequence represents a
CC primer used to isolate regions of the human cytochrome P450 polypetide
CC 2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
CC (SNP) in that region of different individuals useful in disease diagnosis
XX
SQ Sequence 19 BP; 7 A; 2 C; 0 G; 9 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.6; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 7.5e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2399 TATACATATATACATT 2414
||||||||:|||||||
Db 2 TATACATAYATACATT 17

RESULT 1006
ACA98772/c
ID ACA98772 standard; DNA; 19 BP.
XX
AC ACA98772;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human CYP2C8 SNP detection PCR primer #212.
XX
KW Cytochrome P450 polypeptide 2C8; CYP2C8; arachidonic acid metabolism;
KW cancer; cardiovascular disease; cytostatic; cardiovascular; gene therapy;
KW single nucleotide polymorphism detection; SNP detection; PCR; primer; ss.
XX
OS Homo sapiens.

XX
PN WO200299099-A2.
XX
PD 12-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-EP006000.
XX
PR 01-JUN-2001; 2001EP-00112899.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Penger A, Sprenger R, Brinkmann U;
XX
DR WPI; 2003-167344/16.
XX
PT New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
PS Example 2; Page 52; 178pp; English.
XX
CC The invention describes a new polynucleotide comprises a polynucleotide:
CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC in the specification; (b) encoding any of seven polypeptides having 7
CC amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC polynucleotide, gene, vector, polypeptide or antibody is useful for
CC diagnosing or treating a disease, for preparing a diagnostic composition
CC for diagnosing a disease, or for preparing a pharmaceutical composition
CC for treating a disease. This disease includes arachidonic acid
CC metabolism, cancer or cardiovascular diseases. This sequence represents a
CC primer used to isolate regions of the human cytochrome P450 polypetide
CC 2C8 gene (CYP2C8) in order to identify the single nucleotide polymorphism
CC (SNP) in that region of different individuals useful in disease diagnosis
XX
SQ Sequence 19 BP; 9 A; 0 C; 2 G; 7 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.6; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 7.5e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2399 TATACATATATACATT 2414
||||||||:|||||||
Db 18 TATACATAYATACATT 3

RESULT 1007
AAT12451
ID AAT12451 standard; DNA; 17 BP.
XX
AC AAT12451;
XX
DT 17-SEP-1996 (first entry)
XX
DE Antiviral phosphorothioate oligonucleotide #34.
XX
KW Antiviral; phosphorothioate; mRNA 4; mRNA 5; herpes simplex virus 1; HSV;
KW viral infection; HIV; varicella zoster virus; VZV; therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .17
FT /*tag= a
FT /note= "phosphorothioate oligonucleotides"
XX
PN WO9603500-A1.
XX
PD 08-FEB-1996.
XX
PF 25-JUL-1995; 95WO-JP001472.
XX
PR 26-JUL-1994; 94JP-00173862.
PR 01-NOV-1994; 94JP-00268603.
XX
PA (LTTL-) LTT INST CO LTD.
PA (KAKE) KAKEN PHARM CO LTD.
XX
PI Shoji Y, Shimada J, Mizushima Y, Iwatani W, Tamura N;
XX
DR WPI; 1996-117045/12.
XX
PT Antiviral phosphoro:thioate oligo:nucleotide(s) - active against e.g.
PT herpes simplex virus 1, HIV and varicella zoster virus.
XX
PS Claim 6; Page 151; 163pp; Japanese.
XX
CC AAT12435-T12454 represent phosphorothioate oligonucleotides with
CC antiviral activity. These sequences, and the phosphorothioate
CC oligonucleotides represented by AAT12418-T12434 (which are complementary
CC to regions of the mRNA 4 or 5 of herpes simplex virus 1 (HSV)), are
CC effective in the prevention and treatment of viral infection. The
CC sequences are especially effective against infection by HSV, HIV or
CC varicella zoster virus (VZV)
XX
SQ Sequence 17 BP; 0 A; 0 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4085 GTGGCTGTGGGTGTGGG 4101
|||| ||||||||||||
Db 1 GTGGGTGTGGGTGTGGG 17

RESULT 1008
AAX69799
ID AAX69799 standard; RNA; 17 BP.
XX
AC AAX69799;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.

```
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 7.3e+02;
  Matches    1;  Conservative    15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4515
              | ::::::::::::::
Db          1 ACUUUUUUUUUUUUUU 17


RESULT 1009
AAA25446
ID   AAA25446 standard; DNA; 17 BP.
XX
AC   AAA25446;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1944.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4497 TAAGTTTTTTTTTTTT 4513
              | ||||||||||||||||
Db          1 TTAGTTTTTTTTTTTT 17


RESULT 1010
ABT35107/c
ID   ABT35107 standard; DNA; 17 BP.
XX
AC   ABT35107;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Tumour suppression related human fukutin oligo SEQ ID No 744.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW   antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; protein chip; gene therapy; tumour suppression;
KW   human fukutin; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003025175-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004208.
XX
PR   17-SEP-2001; 2001FR-00011978.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-313353/30.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; Page 121; 720pp; French.
XX
CC   The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC   given in the specification, a sequence containing at least 15 consecutive
CC   nucleotides from the 17 mer sequence, a sequence with, after optimal
CC   alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC   hybridizes to them under highly stringent conditions, or the complement
CC   of any of them, or the corresponding RNA. The novel isolated nucleic
CC   acids of the invention are useful as probes and primers for detecting,
CC   identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC   component of a gene chip, in vitro as (anti)sense reagents, and for
CC   production of recombinant polypeptides. Any of the nucleic acids,
CC   polypeptides, vectors containing the nucleic acids, cells containing the
CC   vector or antibodies directed against the polypeptides are useful for
CC   preparation of pharmaceuticals for prevention and/or treatment of viral
CC   diseases that are characterised by development of tumours or cell
CC   degeneration, specifically cancer but also Alzheimer's disease and
```

```
CC   schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC   patient samples is useful for diagnosis and/or prognosis of these
CC   diseases. The polypeptides can also be used to generate antibodies, and
CC   both the polypeptide and antibodies are useful as components of protein
CC   chips. The nucleic acid sequences of the invention can be used in gene
CC   therapy. This polynucleotide sequence represents a tumour suppression
CC   related human fukutin oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 3 A; 2 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4170 AATGATAAACTCAGATC 4186
              ||||||||||  ||||||
Db         17 AATGATAAACACAGATC 1


RESULT 1011
ADB04274
ID   ADB04274 standard; DNA; 17 BP.
XX
AC   ADB04274;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5260.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5260; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTGGG 4518
              |||||||||||||||| |
Db          1 TTTTTTTTTTTTTTGAG 17


RESULT 1012
ABZ61148
ID   ABZ61148 standard; RNA; 17 BP.
XX
AC   ABZ61148;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human K-Ras DNAzyme substrate #1260.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 109; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 5 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   58.8%;  Pred. No. 7.3e+02;
  Matches   10;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1475 ACAACTCTGCCTTTATG 1491
              |||| :|:|||:::|:|
Db          1 ACAAAUCUGCCUUUAUG 17
```

```
RESULT 1013
ACC52668/c
ID   ACC52668 standard; DNA; 17 BP.
XX
AC   ACC52668;
XX
DT   27-JUN-2003  (first entry)
XX
DE   Human tumour suppressor sequence #1435.
XX
KW   ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW   tumour regression; apoptosis; virus resistance; diagnosis;
KW   cellular degeneration.
XX
OS   Homo sapiens.
XX
PN   FR2826373-A1.
XX
PD   27-DEC-2002.
XX
PF   20-JUN-2001; 2001FR-00008139.
XX
PR   20-JUN-2001; 2001FR-00008139.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Tuijnder M,  Telerman A,  Amson R;
XX
DR   WPI; 2003-250498/25.
XX
PT   New nucleic acid sequences associated with tumor suppression, regression,
PT   apoptosis or virus resistance are useful to diagnose and treat viral
PT   disease, development of tumor cells and cell degeneration.
XX
PS   Claim 1; Page 371; 798pp; French.
XX
CC   This sequence represents an isolated nucleic acid sequence associated
CC   with tumour suppression or regression, apoptosis or virus resistance. The
CC   invention relates to these sequences or sequences having at least 80%
CC   identity to them, and polypeptides encoded by the sequences or
CC   polypeptides having 80% identity to the polypeptide sequences. The
CC   invention is used to diagnose or treat viral disease or disease
CC   characterized by development of tumour cells or cellular degeneration
XX
SQ   Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2582 TCACATAGGAAGGGATC 2598
              ||||||||| ||||||
Db         17 TCACATAGGATGGGATC 1


RESULT 1014
ADP86140
ID   ADP86140 standard; DNA; 17 BP.
XX
AC   ADP86140;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #11.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 11; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  |
Db          1 TTTTTTTTTTTTTTCG 17


RESULT 1015
ADP86143
ID   ADP86143 standard; DNA; 17 BP.
XX
AC   ADP86143;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #14.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
```

```
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 14; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTTT 4514
              | ||||||||||||||||
Db          1 ACGTTTTTTTTTTTTTT 17


RESULT 1016
AAQ30446
ID   AAQ30446 standard; DNA; 18 BP.
XX
AC   AAQ30446;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR941 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base    18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTT 2140
              ||||||||| |||||||
Db          1 TTTTCTTTTTTTTTTTT 17


RESULT 1017
AAQ25501/c
ID   AAQ25501 standard; DNA; 18 BP.
XX
AC   AAQ25501;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Purine rich HUMNFR target duplex sequence.
XX
KW   Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV;
KW   hepatitis; malignancy; inflammation; ds.
XX
OS   Synthetic.
XX
PN   WO9209705-A1.
XX
```

PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91WO-US008811.
XX
PR 23-NOV-1990; 90US-00617907.
PR 18-JAN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00686544.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
PT New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX
PS Claim 11; Page 64; 77pp; English.
XX
CC The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
CC sequence beginning at nucleotide 2354. The sequence is a viral duplex
CC sequence contg. a purine-rich region concentrated on one chain of the
CC duplex. The sequence may be prepd. by standard DNA synthesis. The HUMNFR
CC duplex sequence is used as a target for novel oligomers which are capable
CC of forming a triplex at physiological pH by coupling into the major
CC groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of
CC forming a triplex with this sequence. The oligomers are used in the
CC treatment of inflammation. Similar oligomers may be used to target viral
CC DNA duplexes specific for HIV, herpes and other viruses. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. The oligomer is able to
CC inhibit gene expression, as verified by in vitro systems. See also
CC AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 18 BP; 16 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2128 CTTTTCTTTTTTTCTTT 2144
||||| |||||||||||
Db 18 CTTTTTTTTTTTTCTTT 2

RESULT 1018
AAV35391
ID AAV35391 standard; DNA; 18 BP.
XX
AC AAV35391;
XX
DT 13-OCT-1998 (first entry)
XX
DE HIV-1 gag protein DNA primer #4.
XX
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX
OS Synthetic.
XX
PN WO9822596-A1.
XX
PD 28-MAY-1998.
XX
PF 19-NOV-1997; 97WO-JP004216.
XX
PR 19-NOV-1996; 96JP-00323412.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (JAPG) NIPPON ZEON KK.
XX
PI Kojima A, Kurata T, Yasuda A;
XX
DR WPI; 1998-312481/27.
XX
PT Recombinant vaccinia virus containing fusion HIB gag gene - for
PT production in host cells of gag protein for use as vaccine.
XX
PS Example 1; Page 64; 84pp; Japanese.
XX
CC AAV35388-V35414 are primers used in a method which results in a
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC region (30-300 bases in length) of a retroviral gene other than the gag
CC gene. The gag gene may be altered so as to produce a gag protein modified
CC from the natural sequence by the addition, deletion or substitution of at
CC least 1 amino acid residue. The fusion gene is inserted into a region of
CC a vaccinia virus not essential to its propagation, to give a recombinant
CC vaccinia virus vector which is used to transform a host cell (such as
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC culturing the host cell produces particulate structures containing the
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC protein particles may be used in the production of vaccines for
CC protecting against infection with retroviruses such as HIV
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTT 4515
|| |||||||||||||
Db 1 AGCTTTTTTTTTTTTT 17

RESULT 1019
AAV07750/c
ID AAV07750 standard; DNA; 18 BP.
XX
AC AAV07750;
XX
DT 02-DEC-1998 (first entry)
XX
DE Phosphorothioate oligodeoxynucleotide.
XX
KW phosphorothioate; electrospray ionisation-Fourier transform;
KW mass spectrometry; off-resonance excitation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1. .18
FT /*tag= a
FT /note= "phosphorothioate internucleotide linkages"
XX
PN WO9840520-A1.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US004919.
XX
PR 14-MAR-1997; 97US-0040717P.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Wang BH;
XX
DR WPI; 1998-520830/44.
XX

```
PT   Determining the nucleotide sequence of a nucleic acid analyte - using
PT   electro-spray ionisation.
XX
PS   Example 1; Fig 3A; 25pp; English.
XX
CC   The invention relates to an analytical method for determining the
CC   nucleotide sequence of nucleic acid analytes, including chemically
CC   modified oligonucleotides. This new method utilises electrospray
CC   ionisation-Fourier transform mass spectrometry. The ions are excited by
CC   sustained off-resonance excitation with single shot excitation, and the
CC   target fragmented by collisionally activated dissociation by a neutral
CC   gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
CC   can be nozzle skimmer dissociation. The method is used in molecular
CC   biology and biomedical applications. The method, utilising electrospray
CC   ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
CC   is extremely rapid and acts directly on the oligonucleotide. The method
CC   is effective for a variety of nucleic acid analytes, particularly
CC   chemically modified oligonucleotides which have not previously been
CC   successfully sequenced. The present sequence represents a
CC   phosphorothioate oligodeoxynucleotide
XX
SQ   Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4499 AGTTTTTTTTTTTTTT 4515
              | ||||||||||||||
Db         18 ATTTTTTTTTTTTTTT 2


RESULT 1020
AAV21967
ID   AAV21967 standard; DNA; 18 BP.
XX
AC   AAV21967;
XX
DT   14-JUL-1998  (first entry)
XX
DE   Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
XX
KW   Nuclease resistant; bacterial infection; antibiotic; target;
KW   veterinary medicine; treatment; human; industrial process;
KW   bacterial control; ss.
XX
OS   Synthetic.
XX
PN   WO9803533-A1.
XX
PD   29-JAN-1998.
XX
PF   23-JUL-1997;   97WO-US012961.
XX
PR   24-JUL-1996;   96US-00685575.
XX
PA   (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI   Arrow A,  Dale RMK,  Thompson TL;
XX
DR   WPI; 1998-120687/11.
XX
PT   Treating bacterial infections in humans or animals with
PT   oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT   nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT   with antibiotics.
XX
PS   Claim 49; Page 87; 163pp; English.
XX
CC   This antisense oligonucleotide is nuclease resistant and can be used in
CC   the treatment of animals, including humans, having a bacterial infection.
CC   The treatment comprises administration of such nuclease resistant
CC   oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC   and formulated with a carrier. A compound comprising this nuclease
CC   resistant oligonucleotide can be covalently linked to an antibiotic. The
CC   method is used to treat infections by a wide variety of Gram-positive and
CC   Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC   The methods are particularly used in immuno-compromised individuals (e.g.
CC   patients with acquired immunodeficiency syndrome or those receiving
CC   chemotherapy or radiation therapy), optionally in combination with, or
CC   fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC   therapeutic use, the oligonucleotides can be used to control bacteria in
CC   laboratory cultures, foods, beverages and industrial processes. The
CC   oligonucleotides are specific for bacteria, without affecting metabolism
CC   in mammalian cells. They may also activate RNase H and have a general,
CC   non-specific immune-stimulating effect. The oligonucleotides can be
CC   administered orally, intranasally, rectally, topically or by injection,
CC   optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC   enhances cellular uptake
XX
SQ   Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          1 ATATATATATATATATA 17


RESULT 1021
AAV21967/c
ID   AAV21967 standard; DNA; 18 BP.
XX
AC   AAV21967;
XX
DT   14-JUL-1998  (first entry)
XX
DE   Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
XX
KW   Nuclease resistant; bacterial infection; antibiotic; target;
KW   veterinary medicine; treatment; human; industrial process;
KW   bacterial control; ss.
XX
OS   Synthetic.
XX
PN   WO9803533-A1.
XX
PD   29-JAN-1998.
XX
PF   23-JUL-1997;   97WO-US012961.
XX
PR   24-JUL-1996;   96US-00685575.
XX
PA   (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI   Arrow A,  Dale RMK,  Thompson TL;
XX
DR   WPI; 1998-120687/11.
XX
PT   Treating bacterial infections in humans or animals with
PT   oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT   nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT   with antibiotics.
XX
PS   Claim 49; Page 87; 163pp; English.
XX
CC   This antisense oligonucleotide is nuclease resistant and can be used in
CC   the treatment of animals, including humans, having a bacterial infection.
CC   The treatment comprises administration of such nuclease resistant
CC   oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC   and formulated with a carrier. A compound comprising this nuclease
CC   resistant oligonucleotide can be covalently linked to an antibiotic. The
CC   method is used to treat infections by a wide variety of Gram-positive and
CC   Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
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```
CC   The methods are particularly used in immuno-compromised individuals (e.g.
CC   patients with acquired immunodeficiency syndrome or those receiving
CC   chemotherapy or radiation therapy), optionally in combination with, or
CC   fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC   therapeutic use, the oligonucleotides can be used to control bacteria in
CC   laboratory cultures, foods, beverages and industrial processes. The
CC   oligonucleotides are specific for bacteria, without affecting metabolism
CC   in mammalian cells. They may also activate RNase H and have a general,
CC   non-specific immune-stimulating effect. The oligonucleotides can be
CC   administered orally, intranasally, rectally, topically or by injection,
CC   optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC   enhances cellular uptake
XX
SQ   Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         18 ATATATATATATATATA 2


RESULT 1022
AAX19941
ID   AAX19941 standard; DNA; 18 BP.
XX
AC   AAX19941;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:1 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          2 ATATATATATATATATA 18


RESULT 1023
AAX19941/c
ID   AAX19941 standard; DNA; 18 BP.
XX
AC   AAX19941;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Primer SEQ ID NO:1 from JP11075880.
XX
KW   Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP11075880-A.
XX
PD   23-MAR-1999.
XX
PF   10-JUL-1998;   98JP-00195719.
XX
PR   14-JUL-1997;   97JP-00205378.
XX
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR   WPI; 1999-257710/22.
XX
PT   Labelling of an oligonucleotide - useful for detecting genes.
XX
PS   Example 1; Page 7; 10pp; Japanese.
XX
CC   A method has been developed for labelling an oligonucleotide having a
CC   repeated sequence of (XY)n (where X and Y consists of a combination of
CC   adenine and thymine or uracil or guanine and cytosine, and n is an
CC   integer of 1 or more ) at the 3'-terminal side in which the repeated
CC   sequence is added and extended using a labelled body of the nucleotide
CC   constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC   3' exonuclease activity. The method can be used for detecting a gene. The
CC   method can detect a gene in a sensitivity up to ten times higher than
CC   prior art methods. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         17 ATATATATATATATATA 1


RESULT 1024
AAX87332
ID   AAX87332 standard; DNA; 18 BP.
XX
AC   AAX87332;
XX
DT   27-SEP-1999  (first entry)
XX
DE   Reverse transcription primer P1.
XX
KW   SAG gene; sensitive to apoptosis; mouse; cancer; tumour;
KW   neurodegenerative disease; muscular dystrophy; wound healing; vulnerary;
KW   therapy; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9932514-A2.
XX
```

PD 01-JUL-1999.
XX
PF 15-DEC-1998; 98WO-US026705.
XX
PR 19-DEC-1997; 97US-0068179P.
PR 11-SEP-1998; 98US-0099840P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Sun Y;
XX
DR WPI; 1999-430152/36.
XX
PT SAG: Sensitive to Apoptosis Gene and related proteins, useful for
PT promoting cell growth and protecting cells against apoptosis.
XX
PS Example 1; Page 14; 84pp; English.
XX
CC This primer was used for reverse transcription of RNA isolated from mouse
CC tumour lines L-RT101 (epidermal tumour cell line) and H-Tx (spontaneously
CC transformed liver line). It was also used as the reverse primer in PCR
CC amplification of the resulting cDNA. Primers P1 and P2 (see AAX87333)
CC reproducibly detected differential expression of a gene between 1,10-
CC phenanthroline (OP)-treated and OP-nontreated L-RT101 and H-Tx cells. An
CC OP-inducible clone was used as a probe to isolate a full-length clone
CC (see AAX87313) corresponding to the mouse sensitive to apoptosis gene
CC (SAG). SAG is a redox-sensitive, haem-binding protein domain that
CC promotes cell growth, protects cells from apoptosis, scavenges oxygen
CC radicals and can be used for the reversion of a tumour phenotype
XX
SQ Sequence 18 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTT 4514
||| ||||||||||||
Db 1 AAGCTTTTTTTTTTTT 17

RESULT 1025
AAX89278/c
ID AAX89278 standard; DNA; 18 BP.
XX
AC AAX89278;
XX
DT 20-SEP-1999 (first entry)
XX
DE PDE8A specific primer 8A specific-outer.
XX
KW Human; cyclic nucleotide phosphodiesterase; PDE8; diagnosis; cancer;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5932423-A.
XX
PD 03-AUG-1999.
XX
PF 19-NOV-1997; 97US-00974565.
XX
PR 25-MAR-1996; 96US-00624663.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Coleman R, Seilhamer JJ, Fisher DA, Au-Young J, Cocks BG;
XX
DR WPI; 1999-443593/37.
XX
PT New polynucleotides encoding cyclic nucleotide phosphodiesterases which
PT modulate signal transduction.
XX
PS Example 1; Col 36; 66pp; English.
XX
CC The invention provides human cyclic nucleotide phosphodiesterases (PDE8)
CC (AAY27193-196) and polynucleotides (AAX89274-277) which encode PDE8.
CC Polynucleotide sequences encoding PDE8 are useful: (1) for diagnosing
CC conditions or disorders associated with PDE8 expression, and (2) in
CC assays detect activation or induction of various cancers. Sequences
CC AAX89278-283 represent PCR primers for amplifying PDE8 encoding
CC polynucleotides
XX
SQ Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 900 TGCTGCTGATGTGCTTC 916
| |||||||||||||||
Db 17 TTCTGCTGATGTGCTTC 1

RESULT 1026
AAA72005/c
ID AAA72005 standard; DNA; 18 BP.
XX
AC AAA72005;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human PDE8A specific outer PCR primer, SEQ ID NO:10.
XX
KW Cyclic nucleotide phosphodiesterase; human; PDE8A; PDE8A(E); promonocyte;
KW expressed sequence tag; EST; PDE4A homologue;
KW signal transduction regulation; drug screening; cancer; tumour;
KW immune disorder; neuronal disorder; PDE8 antagonist; antisense therapy;
KW antibody; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6080548-A.
XX
PD 27-JUN-2000.
XX
PF 23-FEB-1999; 99US-00255748.
XX
PR 19-NOV-1997; 97US-00974565.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Seilhamer JJ, Fisher DA, Au-Young J, Cocks BG, Coleman R;
XX
DR WPI; 2000-441515/38.
XX
PT Novel cyclic nucleotide phosphodiesterase polypeptide and polynucleotide
PT for diagnosis, prevention, and treatment of cancer, immune and neuronal
PT disorders.
XX
PS Example V; Col 36; 65pp; English.
XX
CC The invention relates to proteins (AAB11935-B11938) which are members of
CC a novel family of human cyclic nucleotide phosphodiesterases, and to
CC cDNAs encoding them (AAA72001-A72004). ESTs (expressed sequence tags)
CC encoding fragments of PDE8A/PDE8A(E) (AAB11935, AAB11937) and
CC PDE8B/PDE8B(E) (AAB11936, AAB11938) were isolated from promonocyte and
CC atrial tissue cDNA libraries respectively, and extended via PCR using
CC lambda-gt10 human testis or stomach cDNA libraries. Members of the PDE8
CC family have chemical and structural to rat PDE4A (GI1705952). Cyclic
CC nucleotide phosphodiesterases degrade cyclic nucleotides to their
CC corresponding monophosphates, thereby regulating the intracellular
CC concentrations of cyclic nucleotides and their effects on signal
CC transduction. PDE8 proteins (AAB11935-B11938) and nucleotides (AAA72001-
CC A72004) may be used in the diagnosis, prevention and treatment of cancers

```
CC   (such as those of the bone marrow, brain or breast), immune disorders
CC   (e.g., allergies, systemic lupus erythematosus, rheumatoid arthritis) and
CC   neuronal disorders (e.g., Alzheimer's disease, Parkinson's disease and
CC   Huntington's disease). Such conditions may be treated using a PDE8
CC   antagonist which should have the effect of increasing intracellular
CC   levels of cAMP, which in turn inhibits some immune and inflammatory
CC   responses. The PDE8 proteins can be used to raise antibodies which may be
CC   used therapeutically and in diagnosis. The proteins can also be used to
CC   screen potential modulators of PDE8 activity. PDE8 nucleic acids may be
CC   used in antisense therapy, and as a source of probes and primers for use
CC   in diagnostic techniques. Sequences AAA72005-A72010 represent PCR primers
CC   used in an exemplification to extend ESTs encoding PDE8A and PDE8A(E)
XX
SQ   Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              | ||||||||||||||||
Db         17 TTCTGCTGATGTGCTTC 1


RESULT 1027
ABL57540
ID   ABL57540 standard; DNA; 18 BP.
XX
AC   ABL57540;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Nucleic acid probe d.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a nucleic acid probe of the
CC   invention that was used for investigating the base selectivity of a
CC   target nucleic acid
XX
SQ   Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 1028
ABL57543
ID   ABL57543 standard; DNA; 18 BP.
XX
AC   ABL57543;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Nucleic acid probe h.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
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```
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a nucleic acid probe of the
CC   invention that was used for investigating the base selectivity of a
CC   target nucleic acid
XX
SQ   Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2385 AAAAATAAAATATATAT 2401
              ||||| ||||||||||
Db          2 AAAAAAAAAATATATAT 18


RESULT 1029
AAC87202
ID   AAC87202 standard; DNA; 18 BP.
XX
AC   AAC87202;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Escherichia coli fruR PCR primer, SEQ ID NO:2.
XX
KW   Amplification and sequencing by interlaced nesting; ASIN PCR;
KW   nucleic acid amplification; primer walking; genome sequencing; fruR gene;
KW   PCR primer; ss.
XX
OS   Escherichia coli.
XX
PN   WO200066768-A1.
XX
PD   09-NOV-2000.
XX
PF   01-MAY-2000; 2000WO-AU000391.
XX
PR   30-APR-1999;   99AU-00000087.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
PI   Tillett D;
XX
DR   WPI; 2001-007232/01.
XX
PT   Amplifying a nucleotide sequence for genome sequences and genetic
PT   analysis, involves utilizing interlaced nesting primers.
XX
PS   Example 1; Page 17; 50pp; English.
XX
CC   The invention relates to a novel method of amplification of a nucleotide
CC   sequence using interlaced nesting primers. The method may be used for
CC   sequencing, particularly for genome sequencing, and is referred to as
CC   "amplification and sequencing by interlaced nesting" (ASIN). The method
CC   involves amplifying a nucleotide sequence having at least one region of
CC   known sequence comprising two adjacent known regions (R1 and R2). A first
CC   primer comprising, in the 5' to 3' direction, a 5' tag sequence, a
CC   degenerate sequence corresponding to R1 and a sequence complementary to
CC   R2 is used in a first amplification reaction. The amplification product
CC   is then used as a template in a second amplification reaction with a
CC   second primer comprising, in the 5' to 3' direction, a sequence which
CC   hybridises to the complementary strand of the 5' tag sequence and a
CC   sequence complementary to R1 of the nucleotide sequence of interest, to
CC   generate a second amplification product. The second amplification product
CC   may then be sequenced. The method of amplification used in the method is
CC   preferably PCR. The invention also relates to primers, primer sets,
CC   primer libraries and kits for use in the method of the invention, and
CC   products of the method of the invention. The method, primers, and kits
CC   are useful for primer walking, and are useful for amplifying and
CC   sequencing nucleotide sequences of interest, particularly genomes. The
CC   present sequence represents an Escherichia coli fruR PCR primer used in
CC   an exemplification of the invention
XX
SQ   Sequence 18 BP; 6 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1423 TTAACCCATTCCAGTAC 1439
              ||||||||| |||||||
Db          2 TTAACCCATACCAGTAC 18


RESULT 1030
ABK13935
ID   ABK13935 standard; DNA; 18 BP.
XX
AC   ABK13935;
XX
DT   21-MAY-2002  (first entry)
XX
DE   5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW   Identification of transcribed gene; mRNA profile; gene expression;
KW   cellular process; fingerprinting; susceptibility to external factor;
KW   development; disease; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200208461-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-IB001539.
XX
PR   21-JUL-2000; 2000GB-00018016.
PR   21-JUL-2000; 2000US-0219925P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G;
XX
DR   WPI; 2002-217065/27.
XX
PT   Providing mRNA profile, by generating two independent patterns
PT   characteristic of sample mRNA population, analyzing patterns, comparing
PT   gene expression by cell types under varied conditions, and identifying
PT   genes.
XX
PS   Disclosure; Fig 1; 67pp; English.
XX
CC   The present invention relates to a method for providing a profile of mRNA
CC   molecules present in a sample. The method comprises generating two
CC   independent patterns characteristic of the population of mRNA molecules
CC   expressed in the sample and analysing the patterns using a combinatorial
CC   algorithm, comparing gene expression by different or same cell types
CC   under different conditions, and identifying genes having a role in
CC   various cellular processes. The method is useful for the analysis and
CC   identification of transcribed genes, and fingerprinting. The method can
CC   be used to identify genes which play a role in determining various
CC   cellular processes, including susceptibility to external factors,
CC   development, and disease. The present sequence for a PCR primer is used
CC   in the production of a single pattern characteristic of a sample,
CC   employing a Type II restriction enzyme (i.e. HaeII) in the methods of the
CC   present invention
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
```

```
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 1031
ABL38718
ID   ABL38718 standard; DNA; 18 BP.
XX
AC   ABL38718;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 85.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 116; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          1 ATATATATATATATATA 17


RESULT 1032
ABL38718/c
ID   ABL38718 standard; DNA; 18 BP.
XX
AC   ABL38718;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 85.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 116; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         18 ATATATATATATATATA 2


RESULT 1033
ABL31389/c
ID   ABL31389 standard; DNA; 18 BP.
```

```
XX
AC   ABL31389;
XX
DT   21-MAR-2002  (first entry)
XX
DE   Human HLA genotyping oligonucleotide SEQ ID NO 878.
XX
KW   Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW   immunogenetic; transplantation; genetic disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192572-A1.
XX
PD   06-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-JP004662.
XX
PR   01-JUN-2000; 2000JP-00164798.
XX
PA   (NISN ) NISSHINBO IND INC.
PA   (SYST-) SYSTEM RES INC.
XX
PI   Inoko H,  Kagiya T,  Ichihara T,  Matsumura Y,  Moriya S,  Nishida M;
XX
DR   WPI; 2002-122074/16.
XX
PT   Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT   individuals e.g. by determining immunogenetic differences when
PT   transplanting between them.
XX
PS   Claim 10; Page 259; 345pp; Japanese.
XX
CC   The invention relates to a typing kit for judging human leukocyte antigen
CC   (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC   oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC   genes e.g. belonging to HLA class I antigens on human genome and
CC   containing gene polymorphisms as alloantigens have been immobilised as
CC   primers for amplification of cleaved nucleic acids relating to gene
CC   polymorphisms. The method is useful for judging HLA genotypes of
CC   individuals by determining immunogenetic differences before transplanting
CC   between them, providing genetic information to decide compatibility of
CC   organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC   pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC   diagnosis of genetic diseases and identifying individuals
XX
SQ   Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4390 TGCAGGATTCCCTTCTG 4406
              | ||||||||||||||||
Db         17 TCCAGGATTCCCTTCTG 1


RESULT 1034
ACF36339
ID   ACF36339 standard; DNA; 18 BP.
XX
AC   ACF36339;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA fragment.
XX
KW   Gene variant identification; restriction enzyme; HaeII; ds.
XX
OS   Synthetic.
XX
PN   WO2003064689-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000255.
XX
PR   29-JAN-2002; 2002US-0352245P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Lonnerberg P,  Oldin M,  Linnarsson S,  Ernfors P;
XX
DR   WPI; 2003-627619/59.
XX
PT   Determining polyadenylation sites within transcribed gene sequences
PT   present in a sample comprises assigning to gene fragments gene candidates
PT   within a database by comparing signals in the dataset with the database.
XX
PS   Example; Fig 2; 81pp; English.
XX
CC   The invention relates to determining the presence of and/or identifying a
CC   polyadenylation site within a sequence of a transcribed gene or variants
CC   present in a sample. The method involves assigning to gene fragments gene
CC   candidates within a database by comparing signals in the dataset with the
CC   database, the database comprising data representing mRNAs with known
CC   polyA sites and/or 'virtual genes' representing a possible
CC   polyadenylation site within an actual gene. The method is useful for
CC   determining the presence of and/or identifying a polyadenylation site or
CC   alternative polyadenylation sites within a sequence of a transcribed gene
CC   or sequences of transcribed gene variants present or potentially present
CC   in a sample, in identifying gene features, particularly in identifying
CC   differences between sequence variants that occur in a population of
CC   nucleic acid molecules, especially in identifying or discovering polyA
CC   site usage or determining polyA site usage in a nucleic acid sample, and
CC   gene variants arising from alternative polyA sites. The present sequence
CC   represents a double stranded product DNA fragment
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 1035
ACF36364
ID   ACF36364 standard; DNA; 18 BP.
XX
AC   ACF36364;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA.
XX
KW   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW   electrophoresis; type II restriction enzyme; HaeII; ds.
XX
OS   Synthetic.
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G,  Metsis A,  Pihlak A;
PI   Montelius A;
```

```
XX
DR   WPI; 2003-618365/58.
XX
PT   Producing a population of double-stranded product DNA molecules, useful
PT   for mRNA profiling, comprises amplification by nested polymerase chain
PT   reaction.
XX
PS   Example; Fig 1; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   double stranded product DNA, which aids in outlining an approach to
CC   production of a single pattern characteristic of a sample, employing a
CC   type II restriction enzyme (HaeII)
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCG 18


RESULT 1036
ADC64943
ID   ADC64943 standard; DNA; 18 BP.
XX
AC   ADC64943;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Camellia sinensis L. (O.) Kuntze related PCR primer T11G.
XX
KW   Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
OS   Synthetic.
OS   Camellia sinensis.
XX
PN   CN1377966-A.
XX
PD   06-NOV-2002.
XX
PF   30-MAR-2001; 2001CN-00112459.
XX
PR   30-MAR-2001; 2001CN-00112459.
XX
PA   (SCIN-) SCI & IND RES COMMISSION.
XX
DR   WPI; 2003-230959/23.
XX
PT   Cloning of a new gene sequence expressed and inhibited during winter
PT   dormancy of a tea tree top plumelet, comprises identification, cloning
PT   and analysis of a new primer in the gene sequence.
XX
PS   Example 3; Page 32; 66pp; Chinese.
XX
CC   The present invention describes the cloning of a new gene sequence
CC   expressed and inhibited during hibernation of the top plumelet of a
CC   Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC   identification, cloning and analysis of a primer terminal in the gene
CC   sequence expressed and inhibited during hibernation of the top plumelet
CC   of the tea tree. The present sequence represents a PCR primer which is
CC   used in an example from the present invention.
XX
SQ   Sequence 18 BP; 2 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| |||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 1037
ADC64942
ID   ADC64942 standard; DNA; 18 BP.
XX
AC   ADC64942;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Camellia sinensis L. (O.) Kuntze related PCR primer T11C.
XX
KW   Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
OS   Synthetic.
OS   Camellia sinensis.
XX
PN   CN1377966-A.
XX
PD   06-NOV-2002.
XX
PF   30-MAR-2001; 2001CN-00112459.
XX
PR   30-MAR-2001; 2001CN-00112459.
XX
PA   (SCIN-) SCI & IND RES COMMISSION.
XX
DR   WPI; 2003-230959/23.
XX
PT   Cloning of a new gene sequence expressed and inhibited during winter
PT   dormancy of a tea tree top plumelet, comprises identification, cloning
PT   and analysis of a new primer in the gene sequence.
XX
PS   Example 3; Page 32; 66pp; Chinese.
XX
CC   The present invention describes the cloning of a new gene sequence
CC   expressed and inhibited during hibernation of the top plumelet of a
CC   Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC   identification, cloning and analysis of a primer terminal in the gene
CC   sequence expressed and inhibited during hibernation of the top plumelet
CC   of the tea tree. The present sequence represents a PCR primer which is
CC   used in an example from the present invention.
XX
SQ   Sequence 18 BP; 2 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| |||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 1038
ADC64941
ID   ADC64941 standard; DNA; 18 BP.
XX
AC   ADC64941;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Camellia sinensis L. (O.) Kuntze related PCR primer T11A.
XX
KW   Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
```

OS Synthetic.
OS Camellia sinensis.
XX
PN CN1377966-A.
XX
PD 06-NOV-2002.
XX
PF 30-MAR-2001; 2001CN-00112459.
XX
PR 30-MAR-2001; 2001CN-00112459.
XX
PA (SCIN-) SCI & IND RES COMMISSION.
XX
DR WPI; 2003-230959/23.
XX
PT Cloning of a new gene sequence expressed and inhibited during winter
PT dormancy of a tea tree top plumelet, comprises identification, cloning
PT and analysis of a new primer in the gene sequence.
XX
PS Example 3; Page 32; 66pp; Chinese.
XX
CC The present invention describes the cloning of a new gene sequence
CC expressed and inhibited during hibernation of the top plumelet of a
CC Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC identification, cloning and analysis of a primer terminal in the gene
CC sequence expressed and inhibited during hibernation of the top plumelet
CC of the tea tree. The present sequence represents a PCR primer which is
CC used in an example from the present invention.
XX
SQ Sequence 18 BP; 3 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17
```

RESULT 1039
AAD63454
ID AAD63454 standard; DNA; 18 BP.
XX
AC AAD63454;
XX
DT 12-FEB-2004 (first entry)
XX
DE Tea non-dormant (ND) and dormant (D) buds amplifying primer, T11G.
XX
KW Tea; gene regulation; transgene; winter dormancy; PCR; primer; ss.
XX
OS Camellia sinensis.
XX
PN US2003180723-A1.
XX
PD 25-SEP-2003.
XX
PF 31-MAR-2001; 2001US-00823887.
XX
PR 31-MAR-2001; 2001US-00823887.
XX
PA (KUMA/) KUMAR S.
PA (LALL/) LAL L.
PA (AHUJ/) AHUJA P S.
XX
PI Kumar S, Lal L, Ahuja PS;
XX
DR WPI; 2003-852228/79.
XX
PT Novel DNA sequences expressed and repressed during winter dormancy in the
PT apical buds of tea bushes, useful for obtaining important information on
PT gene regulation, and for synthesizing unique proteins for raising
PT antibodies.
XX
PS Example 3; Page 12; 0pp; English.
XX
CC The invention relates to a method for cloning novel DNA sequences
CC expressed and repressed during winter dormancy in the apical buds of
CC Camellia sinensis L. (O.) Kuntze (tea) bushes or a tree species. The
CC novel DNA sequences are useful for obtaining important information on
CC gene regulation, for modulating winter dormancy in plants after
CC transferring these genes using Agrobacterium-mediated transformation and
CC Biallistic-mediated transformation. They are also useful in modulating
CC winter dormancy in plants such as tea, plums, cherries, peaches, Taxus,
CC apples, pears, vines, grapes, olives, Kiwi fruit, figs, morus,
CC strawberries, raspberries, loganberries, almonds, cranberries,
CC blackberries, walnuts and chestnuts after transferring these genes suing
CC the transformation methods cited. The obtained important information on
CC gene regulation can be exploited to regulate gene expression in
CC transgene. The novel cDNAs and genomic DNAs are useful for synthesising
CC unique proteins for raising antibodies. The antibodies can be used as
CC probes to look for similar proteins in other plants, animal and/or
CC microbial systems or the like. These are also useful as probes to look
CC for expression of these sequences of nucleotides in other plants, animal
CC and/or microbial systems. The present sequence is a PCR primer used for
CC amplifying non-dormant (ND) and dormant (D) apical buds of tea. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 18 BP; 2 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17
```

RESULT 1040
AAD63452
ID AAD63452 standard; DNA; 18 BP.
XX
AC AAD63452;
XX
DT 12-FEB-2004 (first entry)
XX
DE Tea non-dormant (ND) and dormant (D) buds amplifying primer, T11A.
XX
KW Tea; gene regulation; transgene; winter dormancy; PCR; primer; ss.
XX
OS Camellia sinensis.
XX
PN US2003180723-A1.
XX
PD 25-SEP-2003.
XX
PF 31-MAR-2001; 2001US-00823887.
XX
PR 31-MAR-2001; 2001US-00823887.
XX
PA (KUMA/) KUMAR S.
PA (LALL/) LAL L.
PA (AHUJ/) AHUJA P S.
XX
PI Kumar S, Lal L, Ahuja PS;
XX
DR WPI; 2003-852228/79.
XX
PT Novel DNA sequences expressed and repressed during winter dormancy in the
PT apical buds of tea bushes, useful for obtaining important information on
PT gene regulation, and for synthesizing unique proteins for raising
PT antibodies.
XX
PS Example 3; Page 12; 0pp; English.

XX
CC The invention relates to a method for cloning novel DNA sequences
CC expressed and repressed during winter dormancy in the apical buds of
CC Camellia sinensis L. (O.) Kuntze (tea) bushes or a tree species. The
CC novel DNA sequences are useful for obtaining important information on
CC gene regulation, for modulating winter dormancy in plants after
CC transferring these genes using Agrobacterium-mediated transformation and
CC Biallistic-mediated transformation. They are also useful in modulating
CC winter dormancy in plants such as tea, plums, cherries, peaches, Taxus,
CC apples, pears, vines, grapes, olives, Kiwi fruit, figs, morus,
CC strawberries, raspberries, loganberries, almonds, cranberries,
CC blackberries, walnuts and chestnuts after transferring these genes suing
CC the transformation methods cited. The obtained important information on
CC gene regulation can be exploited to regulate gene expression in
CC transgene. The novel cDNAs and genomic DNAs are useful for synthesising
CC unique proteins for raising antibodies. The antibodies can be used as
CC probes to look for similar proteins in other plants, animal and/or
CC microbial systems or the like. These are also useful as probes to look
CC for expression of these sequences of nucleotides in other plants, animal
CC and/or microbial systems. The present sequence is a PCR primer used for
CC amplifying non-dormant (ND) and dormant (D) apical buds of tea. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 18 BP; 3 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTT 4514
||| ||||||||||||
Db 1 AAGCTTTTTTTTTTTT 17

RESULT 1041
AAD63453
ID AAD63453 standard; DNA; 18 BP.
XX
AC AAD63453;
XX
DT 12-FEB-2004 (first entry)
XX
DE Tea non-dormant (ND) and dormant (D) buds amplifying primer, T11C.
XX
KW Tea; gene regulation; transgene; winter dormancy; PCR; primer; ss.
XX
OS Camellia sinensis.
XX
PN US2003180723-A1.
XX
PD 25-SEP-2003.
XX
PF 31-MAR-2001; 2001US-00823887.
XX
PR 31-MAR-2001; 2001US-00823887.
XX
PA (KUMA/) KUMAR S.
PA (LALL/) LAL L.
PA (AHUJ/) AHUJA P S.
XX
PI Kumar S, Lal L, Ahuja PS;
XX
DR WPI; 2003-852228/79.
XX
PT Novel DNA sequences expressed and repressed during winter dormancy in the
PT apical buds of tea bushes, useful for obtaining important information on
PT gene regulation, and for synthesizing unique proteins for raising
PT antibodies.
XX
PS Example 3; Page 12; 0pp; English.
XX
CC The invention relates to a method for cloning novel DNA sequences
CC expressed and repressed during winter dormancy in the apical buds of
CC Camellia sinensis L. (O.) Kuntze (tea) bushes or a tree species. The
CC novel DNA sequences are useful for obtaining important information on
CC gene regulation, for modulating winter dormancy in plants after
CC transferring these genes using Agrobacterium-mediated transformation and
CC Biallistic-mediated transformation. They are also useful in modulating
CC winter dormancy in plants such as tea, plums, cherries, peaches, Taxus,
CC apples, pears, vines, grapes, olives, Kiwi fruit, figs, morus,
CC strawberries, raspberries, loganberries, almonds, cranberries,
CC blackberries, walnuts and chestnuts after transferring these genes suing
CC the transformation methods cited. The obtained important information on
CC gene regulation can be exploited to regulate gene expression in
CC transgene. The novel cDNAs and genomic DNAs are useful for synthesising
CC unique proteins for raising antibodies. The antibodies can be used as
CC probes to look for similar proteins in other plants, animal and/or
CC microbial systems or the like. These are also useful as probes to look
CC for expression of these sequences of nucleotides in other plants, animal
CC and/or microbial systems. The present sequence is a PCR primer used for
CC amplifying non-dormant (ND) and dormant (D) apical buds of tea. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 18 BP; 2 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTT 4514
||| ||||||||||||
Db 1 AAGCTTTTTTTTTTTT 17

RESULT 1042
ADM06395/c
ID ADM06395 standard; DNA; 18 BP.
XX
AC ADM06395;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PCR primer SEQ ID NO:5080.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Example 8; SEQ ID NO 5080; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines

```
CC   for regulating their expression and activity, or as a target of gene
CC   therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC   are useful as pharmaceutical agents. The present sequence represents an
CC   oligonucleotide used in the invention.
XX
SQ   Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3812 AGGCATCCTTGTCTTTT 3828
              ||||||| |||||||||
Db         17 AGGCATCGTTGTCTTTT 1


RESULT 1043
ADM16963
ID   ADM16963 standard; DNA; 18 BP.
XX
AC   ADM16963;
XX
DT   20-MAY-2004  (first entry)
XX
DE   T11A PCR primer, to identify C. jubata differentially expressed genes.
XX
KW   Plant; freeze tolerance; PCR; primer; ss.
XX
OS   Caragana jubata.
XX
PN   US2003140379-A1.
XX
PD   24-JUL-2003.
XX
PF   27-MAR-2002; 2002US-00106799.
XX
PR   29-MAR-2001; 2001US-0279426P.
XX
PA   (KUMA/) KUMAR S.
PA   (GUPT/) GUPTA R K.
PA   (AHUJ/) AHUJA P S.
XX
PI   Kumar S,  Gupta RK,  Ahuja PS;
XX
DR   WPI; 2003-851764/79.
XX
PT   New DNA sequences from the Caragana jubata plant, useful for developing
PT   probes to identify plants, animals and/or microbial systems with
PT   tolerance to grow under freezing conditions, or for modulating freeze
PT   tolerance in these systems.
XX
PS   Example 3; Page 8; 53pp; English.
XX
CC   The invention relates to novel DNA sequences that are differentially
CC   expressed in apical buds of the plant Caragana jubata (Pall.) growing
CC   under freezing conditions. DNA molecules of the invention are useful for
CC   developing probes to identify plants, animals and/or microbial systems
CC   with tolerance to grow under freezing conditions. They are particularly
CC   useful for developing e.g. plants that can tolerate and grow under
CC   freezing conditions at high altitude. The invention is also useful for
CC   modulating freeze tolerance in biological systems. The present sequence
CC   is a PCR primer used to identify C. jubata differentially expressed
CC   genes.
XX
SQ   Sequence 18 BP; 3 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 1044
ADM16964
ID   ADM16964 standard; DNA; 18 BP.
XX
AC   ADM16964;
XX
DT   20-MAY-2004  (first entry)
XX
DE   T11C PCR primer, to identify C. jubata differentially expressed genes.
XX
KW   Plant; freeze tolerance; PCR; primer; ss.
XX
OS   Caragana jubata.
XX
PN   US2003140379-A1.
XX
PD   24-JUL-2003.
XX
PF   27-MAR-2002; 2002US-00106799.
XX
PR   29-MAR-2001; 2001US-0279426P.
XX
PA   (KUMA/) KUMAR S.
PA   (GUPT/) GUPTA R K.
PA   (AHUJ/) AHUJA P S.
XX
PI   Kumar S,  Gupta RK,  Ahuja PS;
XX
DR   WPI; 2003-851764/79.
XX
PT   New DNA sequences from the Caragana jubata plant, useful for developing
PT   probes to identify plants, animals and/or microbial systems with
PT   tolerance to grow under freezing conditions, or for modulating freeze
PT   tolerance in these systems.
XX
PS   Example 3; Page 8; 53pp; English.
XX
CC   The invention relates to novel DNA sequences that are differentially
CC   expressed in apical buds of the plant Caragana jubata (Pall.) growing
CC   under freezing conditions. DNA molecules of the invention are useful for
CC   developing probes to identify plants, animals and/or microbial systems
CC   with tolerance to grow under freezing conditions. They are particularly
CC   useful for developing e.g. plants that can tolerate and grow under
CC   freezing conditions at high altitude. The invention is also useful for
CC   modulating freeze tolerance in biological systems. The present sequence
CC   is a PCR primer used to identify C. jubata differentially expressed
CC   genes.
XX
SQ   Sequence 18 BP; 2 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 1045
ADM16965
ID   ADM16965 standard; DNA; 18 BP.
XX
AC   ADM16965;
XX
DT   20-MAY-2004  (first entry)
XX
DE   T11G PCR primer, to identify C. jubata differentially expressed genes.
XX
KW   Plant; freeze tolerance; PCR; primer; ss.
XX
```

OS Caragana jubata.
XX
PN US2003140379-A1.
XX
PD 24-JUL-2003.
XX
PF 27-MAR-2002; 2002US-00106799.
XX
PR 29-MAR-2001; 2001US-0279426P.
XX
PA (KUMA/) KUMAR S.
PA (GUPT/) GUPTA R K.
PA (AHUJ/) AHUJA P S.
XX
PI Kumar S, Gupta RK, Ahuja PS;
XX
DR WPI; 2003-851764/79.
XX
PT New DNA sequences from the Caragana jubata plant, useful for developing
PT probes to identify plants, animals and/or microbial systems with
PT tolerance to grow under freezing conditions, or for modulating freeze
PT tolerance in these systems.
XX
PS Example 3; Page 8; 53pp; English.
XX
CC The invention relates to novel DNA sequences that are differentially
CC expressed in apical buds of the plant Caragana jubata (Pall.) growing
CC under freezing conditions. DNA molecules of the invention are useful for
CC developing probes to identify plants, animals and/or microbial systems
CC with tolerance to grow under freezing conditions. They are particularly
CC useful for developing e.g. plants that can tolerate and grow under
CC freezing conditions at high altitude. The invention is also useful for
CC modulating freeze tolerance in biological systems. The present sequence
CC is a PCR primer used to identify C. jubata differentially expressed
CC genes.
XX
SQ Sequence 18 BP; 2 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTT 4514
||| ||||||||||||
Db 1 AAGCTTTTTTTTTTTT 17

RESULT 1046
ADM91739
ID ADM91739 standard; cDNA; 18 BP.
XX
AC ADM91739;
XX
DT 03-JUN-2004 (first entry)
XX
DE Primer #3 of the invention.
XX
KW tea plant; water-deficient stress condition; Plant protectant;
KW water stress tolerance; ss; primer.
XX
OS Synthetic.
XX
PN WO2003082913-A1.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2002; 2002WO-IN000090.
XX
PR 28-MAR-2002; 2002WO-IN000090.
XX
PA (COUL) COUNCIL SCI & IND RES.
XX
PI Sharma P, Kumar S, Ahuja PS;
XX
DR WPI; 2003-804026/75.
XX
PT New genes from drought stress tolerant tea plant, useful for producing
PT drought-tolerant transgenic plants and for identifying drought-tolerant
PT plants.
XX
PS Example 5; SEQ ID NO 6; 57pp; English.
XX
CC The present invention relates to identifying the new genes differentially
CC expressed in tea plants under water-deficient stress conditions,
CC comprising: isolating total mRNA from the plant growing both under normal
CC and drought conditions; reverse transcribing the mRNAs to obtain
CC corresponding cDNA; sequencing the cDNA; and identifying differentially
CC expressed genes using the cDNA sequences; and introducing water-deficient
CC stress tolerance in plant systems using the new genes, comprising
CC transferring the genes into the plant systems. The genes are useful in
CC method M2 for introducing water stress tolerance into plants (especially
CC tea plants). The method is useful for identifying the genes
CC differentially expressed in tea plants. The genes are also useful in
CC developing probes to identify drought tolerant plants. The present
CC sequence represents a primer of the invention.
XX
SQ Sequence 18 BP; 3 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4498 AAGTTTTTTTTTTTTT 4514
||| ||||||||||||
Db 1 AAGCTTTTTTTTTTTT 17

RESULT 1047
ADM91741
ID ADM91741 standard; cDNA; 18 BP.
XX
AC ADM91741;
XX
DT 03-JUN-2004 (first entry)
XX
DE Primer #5 of the invention.
XX
KW tea plant; water-deficient stress condition; Plant protectant;
KW water stress tolerance; ss; primer.
XX
OS Synthetic.
XX
PN WO2003082913-A1.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2002; 2002WO-IN000090.
XX
PR 28-MAR-2002; 2002WO-IN000090.
XX
PA (COUL) COUNCIL SCI & IND RES.
XX
PI Sharma P, Kumar S, Ahuja PS;
XX
DR WPI; 2003-804026/75.
XX
PT New genes from drought stress tolerant tea plant, useful for producing
PT drought-tolerant transgenic plants and for identifying drought-tolerant
PT plants.
XX
PS Example 5; SEQ ID NO 8; 57pp; English.
XX
CC The present invention relates to identifying the new genes differentially
CC expressed in tea plants under water-deficient stress conditions,
CC comprising: isolating total mRNA from the plant growing both under normal
CC and drought conditions; reverse transcribing the mRNAs to obtain

```
CC   corresponding cDNA; sequencing the cDNA; and identifying differentially
CC   expressed genes using the cDNA sequences; and introducing water-deficient
CC   stress tolerance in plant systems using the new genes, comprising
CC   transferring the genes into the plant systems. The genes are useful in
CC   method M2 for introducing water stress tolerance into plants (especially
CC   tea plants). The method is useful for identifying the genes
CC   differentially expressed in tea plants. The genes are also useful in
CC   developing probes to identify drought tolerant plants. The present
CC   sequence represents a primer of the invention.
XX
SQ   Sequence 18 BP; 2 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 1048
ADM91740
ID   ADM91740 standard; cDNA; 18 BP.
XX
AC   ADM91740;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Primer #4 of the invention.
XX
KW   tea plant; water-deficient stress condition; Plant protectant;
KW   water stress tolerance; ss; primer.
XX
OS   Synthetic.
XX
PN   WO2003082913-A1.
XX
PD   09-OCT-2003.
XX
PF   28-MAR-2002; 2002WO-IN000090.
XX
PR   28-MAR-2002; 2002WO-IN000090.
XX
PA   (COUL ) COUNCIL SCI & IND RES.
XX
PI   Sharma P,  Kumar S,  Ahuja PS;
XX
DR   WPI; 2003-804026/75.
XX
PT   New genes from drought stress tolerant tea plant, useful for producing
PT   drought-tolerant transgenic plants and for identifying drought-tolerant
PT   plants.
XX
PS   Example 5; SEQ ID NO 7; 57pp; English.
XX
CC   The present invention relates to identifying the new genes differentially
CC   expressed in tea plants under water-deficient stress conditions,
CC   comprising: isolating total mRNA from the plant growing both under normal
CC   and drought conditions; reverse transcribing the mRNAs to obtain
CC   corresponding cDNA; sequencing the cDNA; and identifying differentially
CC   expressed genes using the cDNA sequences; and introducing water-deficient
CC   stress tolerance in plant systems using the new genes, comprising
CC   transferring the genes into the plant systems. The genes are useful in
CC   method M2 for introducing water stress tolerance into plants (especially
CC   tea plants). The method is useful for identifying the genes
CC   differentially expressed in tea plants. The genes are also useful in
CC   developing probes to identify drought tolerant plants. The present
CC   sequence represents a primer of the invention.
XX
SQ   Sequence 18 BP; 2 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTTT 4514
              ||| ||||||||||||
Db          1 AAGCTTTTTTTTTTTT 17


RESULT 1049
ADH43299/c
ID   ADH43299 standard; DNA; 18 BP.
XX
AC   ADH43299;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human PDE8A specific outer PCR primer.
XX
KW   human; cyclic nucleotide phosphodiesterase; PDE8A; prostate cancer;
KW   neoplastic disorder; immune disorder; neuronal disorder; lung tumour;
KW   type I diabetes; ss; PCR; primer.
XX
OS   Homo sapiens.
XX
PN   US2003139578-A1.
XX
PD   24-JUL-2003.
XX
PF   15-OCT-2002; 2002US-00272970.
XX
PR   25-MAR-1996;   96US-00624663.
PR   19-NOV-1997;   97US-00974565.
PR   23-FEB-1999;   99US-00255748.
PR   02-DEC-1999;   99US-00454060.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young JK,  Cocks BG,  Coleman RT,  Seilhamer JJ,  Fisher DA;
XX
DR   WPI; 2004-118981/12.
XX
PT   Novel isolated antibody that specifically binds human cyclic nucleotide
PT   phosphodiesterases 8 useful for treating prostate cancer and type I
PT   diabetes.
XX
PS   Example 1; SEQ ID NO 18; 75pp; English.
XX
CC   The invention relates to an isolated antibody that specifically binds a
CC   human cyclic nucleotide phosphodiesterases 8 (PDE8s). The antibody is
CC   useful for detecting differential expression of a protein in a prostate,
CC   pancreas or lung sample. An antibody composition is useful for assessing
CC   efficacy of a small drug molecule and for assessing toxicity of a
CC   compound. The antibody and antibody compulsions are useful for treating
CC   prostate cancer. Antibody compositions are useful for delivering an agent
CC   to the prostate. The antibody is useful for treating neoplastic, immune
CC   and neuronal disorders e.g. lung tumours and type I diabetes. The present
CC   sequence represents cDNA encoding the human PDE8A specific outer PCR
CC   primer.
XX
SQ   Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              | |||||||||||||||
Db         17 TTCTGCTGATGTGCTTC 1


RESULT 1050
ADK69848/c
ID   ADK69848 standard; DNA; 18 BP.
```

```
XX
AC   ADK69848;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cyclic PDE8A-specific outer PCR primer.
XX
KW   Cyclic phosphodiesterase; PDE; gene therapy; neurodegenerative disorder;
KW   Parkinson's disease; Alzheimer's disease; dementia; depression;
KW   schizophrenia; Huntington's disease; cancer; leukaemia;
KW   immunological disorder; scleroderma; diabetes; atopic dermatitis;
KW   Grave's disease; ulcerative colitis; infection;
KW   systemic lupus erythematosus; allergy; transgenic; human; PCR; primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US2004018605-A1.
XX
PD   29-JAN-2004.
XX
PF   25-JUL-2003; 2003US-00627929.
XX
PR   25-MAR-1996;   96US-00624663.
PR   19-NOV-1997;   97US-00974565.
PR   23-FEB-1999;   99US-00255748.
PR   02-DEC-1999;   99US-00454060.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Au-Young J,  Cocks BG,  Coleman R,  Seilhamer JJ,  Fisher DA;
XX
DR   WPI; 2004-122039/12.
XX
PT   New PDE8 polypeptides and encoding polynucleotides, useful for
PT   diagnosing, preventing, and treating disorders associated with an
PT   abnormal expression or activity of PDE8, such as neuromuscular,
PT   immunological, and cancer.
XX
PS   Example 5; SEQ ID NO 10; 71pp; English.
XX
CC   The invention relates to cyclic phosphodiesterase (PDE) polynucleotide
CC   and polypeptide. The invention is useful in gene therapy. The polypeptide
CC   or its fragments, and the polynucleotide encoding the polypeptide are
CC   useful in diagnosing, preventing, and treating disorders associated with
CC   an abnormal expression or activity of PDE8, such as neurodegenerative
CC   disorders (e.g. Parkinson's disease, Alzheimer's disease, dementia,
CC   depression, schizophrenia, Huntington's disease), cancers (e.g.
CC   leukaemia, cervical or breast cancers), and immunological disorders (e.g.
CC   scleroderma, diabetes, atopic dermatitis, Grave's disease, ulcerative
CC   colitis, viral, bacterial, parasitic, protozoal infections, systemic
CC   lupus erythematosus, allergies). PDE8 or its fragments may also be used
CC   in screening for compounds that specifically bind to and modulate the
CC   activity of PDE8. The polynucleotides can be used to create humanised
CC   animals or transgenic animals to model human disease. The present
CC   sequence is a PCR primer used in the extension of PDE8 cDNA.
XX
SQ   Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        900 TGCTGCTGATGTGCTTC 916
              | ||||||||||||||||
Db         17 TTCTGCTGATGTGCTTC 1


RESULT 1051
AAQ75551
ID   AAQ75551 standard; DNA; 19 BP.
XX
AC   AAQ75551;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              |||||||||||||||  |
Db          3 TTTTTTTTTTTTTTAG 19


RESULT 1052
AAQ75555
ID   AAQ75555 standard; DNA; 19 BP.
XX
AC   AAQ75555;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
```

```
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTGG 4517
              ||||||||||||||| |
Db          3 TTTTTTTTTTTTTTCG 19


RESULT 1053
AAX32228/c
ID   AAX32228 standard; DNA; 19 BP.
XX
AC   AAX32228;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Probe specific for BAP1 gene.
XX
KW   Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW   CFTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW   Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW   colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene; PTEN;
KW   BAP1 gene; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9906598-A2.
XX
PD   11-FEB-1999.
XX
PF   04-AUG-1998;   98WO-US016574.
XX
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 1999-153820/13.
XX
PT   Determining common functional alleles in a population - useful in the
PT   diagnosis of disease associated with allelic heterogeneity.
XX
PS   Example 5; Page 42; 78pp; English.
XX
CC   The invention relates to methods of determining a functional allele
CC   profile of a gene in a population. Functional allele profiles comprise
CC   the commonly occurring alleles in a population, and the relative
CC   frequencies at which such alleles of a given gene occur. The methods are
CC   used to identify and determine the frequency of the functional alleles of
CC   genes which display extensive allelic heterogeneity, particularly those
CC   implicated in disease or conditions, such as the BRCA1 gene associated
CC   with breast cancer, CFTR associated with cystic fibrosis, dystrophin
CC   associated with Duchenne muscular dystrophy and Becker muscular
CC   dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
CC   also be employed for diseases where allelic and genetic heterogeneity
CC   exist, such as breast cancer, neurofibromatosis, and hereditary non-
CC   polyposis colorectal cancer. Identification of functional alleles is
CC   necessary for identification of mutations which may be implicated in the
CC   disease. Sequences AAX32173-232 represent probes used to detect BRCA2,
CC   PTEN, and BAP1 single nucleotide polymorphisms (SNPs)
XX
SQ   Sequence 19 BP; 4 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4353 AAAGGGGCCTGAGTGGA 4369
              ||||||||||||| ||||
Db         19 AAAGGGGCCTGATTGGA 3


RESULT 1054
AAA83339
ID   AAA83339 standard; DNA; 19 BP.
XX
AC   AAA83339;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk8 ribozyme binding site #59.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 60; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 9 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1831 ACAAAGCTTCTAAAGCA 1847
              ||| |||||||||||||
Db          1 ACAGAGCTTCTAAAGCA 17
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RESULT 1055
AAA82668
ID   AAA82668 standard; DNA; 19 BP.
XX
AC   AAA82668;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk2 ribozyme binding site #105.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 49; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
              |||||| ||||||||||
Db          1 GGCCCTATTCCCTGGAG 17


RESULT 1056
AAA82667
ID   AAA82667 standard; DNA; 19 BP.
XX
AC   AAA82667;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk2 ribozyme binding site #104.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 49; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 3 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
              |||||| ||||||||||
Db          2 GGCCCTATTCCCTGGAG 18


RESULT 1057
AAH42195/c
ID   AAH42195 standard; DNA; 19 BP.
XX
AC   AAH42195;
XX
DT   17-SEP-2001  (first entry)
XX
DE   PCR primer for cDNA encoding a G-protein coupled receptor.
XX
KW   Human; G-protein coupled receptor; GPCR; thyroid disorder;
KW   thyrotoxicosis; myxedema; renal failure; inflammatory condition;
KW   Crohn's disease; arthritis; autoimmune disorder; stroke; migraine;
KW   central nervous system disorder; pain; psychotic disorder;
KW   neurological disorder; anxiety; mental disorder; manic depression;
KW   anxiety disorder; post-traumatic-stress disorder; depression;
KW   bipolar disorder; dementia; severe mental retardation;
KW   Huntington's disease; degenerative disorder; Parkinson's; Alzheimer's;
KW   infection; metabolic disorder; cardiovascular disease; diabetes; obesity;
KW   anorexia; hypotension; hypertension; thrombosis; myocardial infarction;
KW   atherosclerosis; proliferative disease; cancer;
KW   hyperproliferative disorder; psoriasis; prostate hyperplasia;
KW   hormonal disorder; polycystic ovarian syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200148015-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035456.
XX
PR   28-DEC-1999;   99US-0173339P.
PR   23-FEB-2000; 2000US-0184305P.
PR   13-MAR-2000; 2000US-0188880P.
PR   27-APR-2000; 2000US-0200534P.
PR   20-JUL-2000; 2000US-0219492P.
PR   11-AUG-2000; 2000US-0224321P.
```

PR 09-OCT-2000; 2000US-0239062P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lind P, Parodi LA, Lindberg E, Vogeli G, Wood LS, Hiebsch RR;
PI Ruff V;
XX
DR WPI; 2001-441707/47.
XX
PT G-protein coupled receptor (GPCR-x) nucleic acids and polypeptides
PT encoded by them, useful for treating neurological and psychiatric
PT disorders such as severe mental retardation, manic depression and
PT dementia.
XX
PS Example 5; Page 104; 175pp; English.
XX
CC PCR primers AAH42194-95 were used to amplify G-protein coupled receptor
CC (GPCR) cDNA. GPCRs may be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate GPCR expression such as thyroid
CC disorders (e.g. thyrotoxicosis, myxedema), renal failure; inflammatory
CC conditions (e.g., Crohn's disease); diseases related to cell
CC differentiation and homeostasis; rheumatoid arthritis; autoimmune
CC disorders; central nervous system (CNS) disorders (e.g., pain including
CC migraine, stroke; psychotic and neurological disorders such as anxiety,
CC mental disorder, manic depression, generalized anxiety disorder, post-
CC traumatic-stress disorder, depression, bipolar disorder, dementia, severe
CC mental retardation; Huntington's disease; degenerative disorders such as
CC Parkinson's, Alzheimer's; infections such as viral infections caused by
CC HIV-1 or HIV-2; metabolic and cardiovascular disease and disorders (e.g.,
CC type 2 diabetes, obesity, anorexia, hypotension, hypertension,
CC thrombosis, myocardial infarction, atherosclerosis); proliferative
CC diseases and cancers and hyperproliferative disorders such as psoriasis,
CC prostate hyperplasia); hormonal disorders (male/female hormonal
CC replacement, polycystic ovarian syndrome)
XX
SQ Sequence 19 BP; 1 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3422 GGGCAAGAACCCAAGTG 3438
||||||||||| ||||||
Db 19 GGGCAAGAACACAAGTG 3

RESULT 1058
AAH57829
ID AAH57829 standard; DNA; 19 BP.
XX
AC AAH57829;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk2 ribozyme binding site SEQ ID NO:253.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 90; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 3 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3455 GGCCCTGTTCCCTGGAG 3471
|||||| ||||||||||
Db 2 GGCCCTATTCCCTGGAG 18

RESULT 1059
AAH57830
ID AAH57830 standard; DNA; 19 BP.
XX
AC AAH57830;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk2 ribozyme binding site SEQ ID NO:254.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.

```
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 90; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3455 GGCCCTGTTCCCTGGAG 3471
              |||||| ||||||||||
Db          1 GGCCCTATTCCCTGGAG 17


RESULT 1060
AAH58501
ID   AAH58501 standard; DNA; 19 BP.
XX
AC   AAH58501;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cell-cycle dependent kinase cdk8 ribozyme binding site SEQ ID NO:925.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 139; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 9 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1831 ACAAAGCTTCTAAAGCA 1847
              ||| ||||||||||||
Db          1 ACAGAGCTTCTAAAGCA 17


RESULT 1061
ABK90423
ID   ABK90423 standard; DNA; 19 BP.
XX
AC   ABK90423;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human UGT1a1 promoter polymorphism (TA)8 repeat region.
XX
KW   Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
KW   uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
KW   UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
KW   TAS-103; xenobiotic.
XX
OS   Homo sapiens.
XX
PN   US6395481-B1.
XX
PD   28-MAY-2002.
XX
```

PF 16-FEB-1999; 99US-00251274.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Di Rienzo A, Iyer L, Ratain MJ;
XX
DR WPI; 2002-588597/63.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient,
PT comprises determining the presence of five thymidine-adenine repeats in
PT the promoter.
XX
PS Example 6; Col 11; 13pp; English.
XX
CC The invention relates to detecting (M1) polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
CC the presence of five thymidine-adenine (TA) repeats in the promoter,
CC where the presence of the five TA repeats correlates with increased
CC expression of the gene. The method is used for detecting polymorphisms in
CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is
CC useful for screening individuals for variation in glucuronidation
CC activity, for optimising drug dosages for a patient, where the drugs
CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
CC UGT1A1) and the activity of the drug is effected by its level of
CC glucurodination. The method preferably involves obtaining DNA from an
CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
CC promoter) contained in the DNA and determining the number of TA repeats
CC in the promoter. Thus the DNA being amplified comprises all or part of
CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
CC the number of TA repeats is determined by gel electrophoresis or by
CC sequencing the amplified DNA. The polymorphism comprises an allele
CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
CC (TA)8/(TA)8. (M1) is also useful for predicting an individuals
CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
CC UGT1A1) gene product, the method comprising determining the number of TA
CC repeats in a UGT gene promoter, where the number of TA repeats correlates
CC with expression of the UGT gene, and the individuals sensitivity to
CC xenobiotics is effected by glucuronidation activity. The methods
CC preferably involve determining the presence of five, six or seven TA
CC repeats in the promoter. Defects in glucurodination is associated with
CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
CC present sequence is the UGT1A1 promoter (TA)8 repeat region
XX
SQ Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2394 ATATATATACATATATA 2410
||||||||| |||||||
Db 2 ATATATATATATATATA 18

RESULT 1062
ABK90423/c
ID ABK90423 standard; DNA; 19 BP.
XX
AC ABK90423;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human UGT1a1 promoter polymorphism (TA)8 repeat region.
XX
KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
KW TAS-103; xenobiotic.
XX
OS Homo sapiens.
XX
PN US6395481-B1.
XX
PD 28-MAY-2002.
XX
PF 16-FEB-1999; 99US-00251274.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Di Rienzo A, Iyer L, Ratain MJ;
XX
DR WPI; 2002-588597/63.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient,
PT comprises determining the presence of five thymidine-adenine repeats in
PT the promoter.
XX
PS Example 6; Col 11; 13pp; English.
XX
CC The invention relates to detecting (M1) polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
CC the presence of five thymidine-adenine (TA) repeats in the promoter,
CC where the presence of the five TA repeats correlates with increased
CC expression of the gene. The method is used for detecting polymorphisms in
CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is
CC useful for screening individuals for variation in glucuronidation
CC activity, for optimising drug dosages for a patient, where the drugs
CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
CC UGT1A1) and the activity of the drug is effected by its level of
CC glucurodination. The method preferably involves obtaining DNA from an
CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
CC promoter) contained in the DNA and determining the number of TA repeats
CC in the promoter. Thus the DNA being amplified comprises all or part of
CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
CC the number of TA repeats is determined by gel electrophoresis or by
CC sequencing the amplified DNA. The polymorphism comprises an allele
CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
CC (TA)8/(TA)8. (M1) is also useful for predicting an individuals
CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
CC UGT1A1) gene product, the method comprising determining the number of TA
CC repeats in a UGT gene promoter, where the number of TA repeats correlates
CC with expression of the UGT gene, and the individuals sensitivity to
CC xenobiotics is effected by glucuronidation activity. The methods
CC preferably involve determining the presence of five, six or seven TA
CC repeats in the promoter. Defects in glucurodination is associated with
CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
CC present sequence is the UGT1A1 promoter (TA)8 repeat region
XX
SQ Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2394 ATATATATACATATATA 2410
||||||||| |||||||
Db 17 ATATATATATATATATA 1

RESULT 1063
AAL50681
ID AAL50681 standard; DNA; 19 BP.
XX
AC AAL50681;
XX
DT 16-JAN-2003 (first entry)

```
XX
DE   Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX
KW   Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW   uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW   drug dosage optimisation; xenobiotic sensitivity.
XX
OS   Homo sapiens.
XX
PN   US2002115097-A1.
XX
PD   22-AUG-2002.
XX
PF   01-FEB-2002; 2002US-00061693.
XX
PR   16-FEB-1999;   99US-00251274.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Rienzo AD,  Iyer L,  Ratain MJ;
XX
DR   WPI; 2002-740095/80.
XX
PT   Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT   gene promoter, useful for optimizing drug dosages for a patient, involves
PT   determining number of thymidine-adenine repeats in the promoter.
XX
PS   Example 6; Page 3; 13pp; English.
XX
CC   The invention comprises a method for detecting polymorphisms in a uridine
CC   diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC   UGT1A1). The method involves determining the number of thymidine-adenine
CC   (TA) repeats in the promoter - as the number of TA repeats correlates
CC   with expression of the UGT gene. The method of the invention is useful
CC   for detecting polymorphisms in a UGT gene promoter. The method of the
CC   invention is also useful in optimising drug dosages and predicting an
CC   individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC   are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC   TA repeat polymorphism
XX
SQ   Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db          2 ATATATATATATATATA 18


RESULT 1064
AAL50681/c
ID   AAL50681 standard; DNA; 19 BP.
XX
AC   AAL50681;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX
KW   Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW   uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW   drug dosage optimisation; xenobiotic sensitivity.
XX
OS   Homo sapiens.
XX
PN   US2002115097-A1.
XX
PD   22-AUG-2002.
XX
PF   01-FEB-2002; 2002US-00061693.
XX
PR   16-FEB-1999;   99US-00251274.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Rienzo AD,  Iyer L,  Ratain MJ;
XX
DR   WPI; 2002-740095/80.
XX
PT   Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT   gene promoter, useful for optimizing drug dosages for a patient, involves
PT   determining number of thymidine-adenine repeats in the promoter.
XX
PS   Example 6; Page 3; 13pp; English.
XX
CC   The invention comprises a method for detecting polymorphisms in a uridine
CC   diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC   UGT1A1). The method involves determining the number of thymidine-adenine
CC   (TA) repeats in the promoter - as the number of TA repeats correlates
CC   with expression of the UGT gene. The method of the invention is useful
CC   for detecting polymorphisms in a UGT gene promoter. The method of the
CC   invention is also useful in optimising drug dosages and predicting an
CC   individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC   are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC   TA repeat polymorphism
XX
SQ   Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATA 2410
              ||||||||| |||||||
Db         17 ATATATATATATATATA 1


RESULT 1065
ABL51521/c
ID   ABL51521 standard; DNA; 19 BP.
XX
AC   ABL51521;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Tailing reaction related exemplary primer dA18U SEQ ID NO:2.
XX
KW   Tailing reaction; tailed primer; primer; probe; identification;
KW   detection; linear amplification scheme; chain extending enzyme;
KW   telomerase; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        19
FT                   /*tag=  a
XX
PN   US2002031776-A1.
XX
PD   14-MAR-2002.
XX
PF   26-JUL-2001; 2001US-00917138.
XX
PR   28-MAY-1999;   99US-0136545P.
PR   25-MAY-2000; 2000US-00580358.
XX
PA   (TULL/) TULLIS R H.
PA   (STRE/) STREIFEL J A.
XX
PI   Tullis RH,  Streifel JA;
XX
DR   WPI; 2002-361176/39.
XX
PT   Identifying and detecting nucleic acids, particularly DNA hybridization
```

PT probes, involves employing chain extending enzymes (e.g. telomerase) to
PT elongate probes to render them readily detectable.
XX
PS Example 1; Page 5; 10pp; English.
XX
CC The present invention describes a method for detecting a nucleic acid
CC probe, which comprises using chain extending enzymes to elongate probes.
CC The method comprises: (a) treating the sample with a chain terminating
CC reagent to prevent polynucleotide chain growth from the nucleic acid in
CC the sample; (b) contacting the sample with the probe containing a
CC terminus capable of elongation by a chain extending enzyme, where the
CC probe hybridises to the nucleic acid in the sample; (c) contacting the
CC sample with a chain extending enzyme and its substrates, which elongates
CC the probe; and (d) detecting the elongated hybridised probe. Also
CC described is a method comprising: (a) treating nucleic acid molecules or
CC modified nucleic acids in a sample with a reagent or reagents that render
CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC (b) hybridising the treated molecules with a nucleic acid probe that
CC includes an extendable terminus, under conditions where hybrids form; and
CC (c) treating any hybrids formed with a non-template dependent chain
CC elongating enzyme and its substrates, where any hybridised probe is
CC extended. The method is useful for identifying and detecting nucleic
CC acids, particularly DNA hybridisation probes. The present sequence
CC represents a tailing reaction exemplary primer, which is used in an
CC example from the present invention
XX
SQ Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTTT 4515
| ||||||||||||||||
Db 19 ATTTTTTTTTTTTTTTT 3

RESULT 1066
ADA45468/c
ID ADA45468 standard; DNA; 19 BP.
XX
AC ADA45468;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human BAP1 DNA probe #12.
XX
KW Functional allele profile; genetic inheritance; haplotype; population;
KW disease; pharmacogenetic application; selective pressure; human; MSH2;
KW MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; probe; ss.
XX
OS Homo sapiens.
XX
PN US2003096236-A1.
XX
PD 22-MAY-2003.
XX
PF 08-AUG-2001; 2001US-00923327.
XX
PR 12-FEB-1996; 96US-00598591.
PR 12-FEB-1997; 97US-00798691.
PR 04-AUG-1997; 97US-00905772.
PR 22-MAY-1998; 98US-00084471.
PR 04-AUG-1998; 98US-00129134.
PR 14-MAR-2000; 2000US-00524794.
XX
PA (ONCO-) ONCORMED INC.
XX
PI Murphy PD;
XX
DR WPI; 2003-576875/54.
XX
PT Determining a functional allele profile of a gene in a population by
PT identifying the nucleotide sequence of a gene of genomic DNA from each of
PT the individuals with a family history of functional alleles of the gene
PT of interest.
XX
PS Example 5; Page 16; 28pp; English.
XX
CC The present invention relates to a method for determining a functional
CC allele profile of a gene in a population. The method comprises
CC identifying the nucleotide sequence of a gene of interest out of genomic
CC DNA from each of a population of individuals identified as having a
CC family history which indicates inheritance of functional alleles of the
CC gene of interest, and rank ordering the frequency of occurrence of each
CC haplotype, where the identity of the alleles containing each haplotype
CC and the determination of their relative frequencies constitutes the
CC functional allele profile of the gene of interest in the population. The
CC method is useful for determining functional allele profiles which are
CC useful in the treatment and diagnosis of diseases, for genetic and
CC pharmacogenetic applications, and for evaluating the degree to which the
CC gene(s) are under selective pressure. The present sequence represents a
CC probe used in the method of the invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4353 AAAGGGGCCTGAGTGGA 4369
||||||||||||| ||||
Db 19 AAAGGGGCCTGATTGGA 3

RESULT 1067
ADF36974
ID ADF36974 standard; RNA; 19 BP.
XX
AC ADF36974;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human VEGFR2 short interfering nucleic acid (siNA) SEQ ID NO:1263.
XX
KW double-stranded short interfering nucleic acid;
KW short interfering nucleic acid; siNA; downregulation;
KW vascular endothelial growth factor receptor; VEGFR; antiangiogenic;
KW cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
KW nephrotropic; gynaecological; angiogenesis-associated condition; cancer;
KW diabetic retinopathy; macular degeneration; neovascular glaucoma;
KW arthritis; psoriasis; endometriosis; angiofibroma;
KW polycystic kidney disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070910-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005022.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002WO-US017674.
PR 06-JUN-2002; 2002US-0386782P.
PR 03-JUL-2002; 2002US-0393796P.
PR 29-JUL-2002; 2002US-0399348P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 04-NOV-2002; 2002US-00287949.
PR 27-NOV-2002; 2002US-00306747.
PR 15-JAN-2003; 2003US-0440129P.
XX

PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Pavco P;
XX
DR WPI; 2003-679876/64.
XX
PT New double-stranded interfering nucleic acid, useful e.g. for treatment
PT and diagnosis of cancer, downregulates the vascular endothelial growth
PT factor receptor gene.
XX
PS Example 3; SEQ ID NO 1263; 207pp; English.
XX
CC The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of the vascular
CC endothelial growth factor receptor (VEGFR) gene. Also described: (1) a
CC siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors
CC that express siNA; and (5) single-stranded siNA with similar properties.
CC The siNAs have antiangiogenic, cytostatic, antidiabetic,
CC ophthalmological, antiarthritic, antipsoriatic, nephrotropic and
CC gynaecological activities. The siNA are useful for modulating
CC (downregulating) the expression of VEGFR genes. The siNA are potentially
CC useful for treating a wide range of angiogenesis-associated conditions,
CC particularly cancers, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma,
CC and polycystic kidney disease. The siNA may also be useful for diagnosis,
CC drug screening, target identification and validation, genetic
CC engineering, studying gene function, and also for gene mapping (e.g. of
CC single-nucleotide polymorphisms). The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 52.9%; Pred. No. 8.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3035 CTGCTTCTCTTTTGAAA 3051
              |:||::|:| :::||||
Db          2 CUGCUUCUCCUUUGAAA 18
```

RESULT 1068
ADF36650/c
ID ADF36650 standard; RNA; 19 BP.
XX
AC ADF36650;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human VEGFR2 short interfering nucleic acid (siNA) SEQ ID NO:939.
XX
KW double-stranded short interfering nucleic acid;
KW short interfering nucleic acid; siNA; downregulation;
KW vascular endothelial growth factor receptor; VEGFR; antiangiogenic;
KW cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
KW nephrotropic; gynaecological; angiogenesis-associated condition; cancer;
KW diabetic retinopathy; macular degeneration; neovascular glaucoma;
KW arthritis; psoriasis; endometriosis; angiofibroma;
KW polycystic kidney disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070910-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005022.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002WO-US017674.
PR 06-JUN-2002; 2002US-0386782P.
PR 03-JUL-2002; 2002US-0393796P.
PR 29-JUL-2002; 2002US-0399348P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 04-NOV-2002; 2002US-00287949.
PR 27-NOV-2002; 2002US-00306747.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Pavco P;
XX
DR WPI; 2003-679876/64.
XX
PT New double-stranded interfering nucleic acid, useful e.g. for treatment
PT and diagnosis of cancer, downregulates the vascular endothelial growth
PT factor receptor gene.
XX
PS Example 3; SEQ ID NO 939; 207pp; English.
XX
CC The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of the vascular
CC endothelial growth factor receptor (VEGFR) gene. Also described: (1) a
CC siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors
CC that express siNA; and (5) single-stranded siNA with similar properties.
CC The siNAs have antiangiogenic, cytostatic, antidiabetic,
CC ophthalmological, antiarthritic, antipsoriatic, nephrotropic and
CC gynaecological activities. The siNA are useful for modulating
CC (downregulating) the expression of VEGFR genes. The siNA are potentially
CC useful for treating a wide range of angiogenesis-associated conditions,
CC particularly cancers, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma,
CC and polycystic kidney disease. The siNA may also be useful for diagnosis,
CC drug screening, target identification and validation, genetic
CC engineering, studying gene function, and also for gene mapping (e.g. of
CC single-nucleotide polymorphisms). The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 9 A; 2 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3035 CTGCTTCTCTTTTGAAA 3051
              ||||||||| |||||||
Db         18 CTGCTTCTCCTTTGAAA 2
```

RESULT 1069
ADR81918
ID ADR81918 standard; DNA; 19 BP.
XX
AC ADR81918;
XX
DT 16-DEC-2004 (first entry)
XX
DE Hepatitis C virus (HCV) oligonucleotide seqid 6417.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.
XX
OS Hepatitis C virus.

XX
PN WO2004080406-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US007070.
XX
PR 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Bumcrot D;
XX
DR WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
PS Example 5; SEQ ID NO 6417; 378pp; English.
XX
CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or disregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholestorolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can
CC be used to control HCV gene expression.
XX
SQ Sequence 19 BP; 1 A; 4 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5069 TTTTTTCCCTTTTTATG 5085
||||||||||.||||||
Db 1 TTTTTTCCCTCTTTATG 17

RESULT 1070
AAD44149
ID AAD44149 standard; DNA; 16 BP.
XX
AC AAD44149;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #9 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
OS Unidentified.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broaddus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Fig 1C; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dT
CC PCR primer used to illustrate the method of the invention
XX
SQ Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 7.4e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4499 AGTTTTTTTTTTTTTT 4514
|:||||||||||||||
Db 1 AVTTTTTTTTTTTTTT 16

RESULT 1071
AAX18388
ID AAX18388 standard; DNA; 17 BP.
XX
AC AAX18388;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 29.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.

XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 1 TTTTTTTTTTTTTTV 16

RESULT 1072
AAS14174
ID AAS14174 standard; DNA; 17 BP.
XX
AC AAS14174;
XX
DT 18-DEC-2001 (first entry)
XX
DE Modified Poly-T Primer #1 used in construction of probe sets.
XX
KW WRAP-Probe; gene expression array; global amplification; RNA array; ss;
KW tissue microarray; drug discovery assay; reporter binding site; forensic;
KW diagnostic; genomic analysis; universal linker; poly-T primer.
XX
OS Synthetic.
XX
PN WO200166802-A1.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007508.
XX
PR 09-MAR-2000; 2000US-0187982P.
XX
PA (GENE-) GENETAG TECHNOLOGY INC.
XX
PI Shafer DA;
XX
DR WPI; 2001-596845/67.
XX
PT Novel probe sets with common universal linkers at one or both ends (WRAP
PT probes) for gene expression arrays to provide global amplification of
PT probe set and to provide common equivalent signaling regardless of
PT length.
XX
PS Disclosure; Page 88; 97pp; English.
XX
CC The invention relates to a probe set for gene expression arrays to
CC provide common equivalent signalling per probe and global amplification
CC of the set. The probe set has a pool of modified cDNA probes, each probe
CC having a central target specific segment copied from a portion of a
CC single mRNA transcript and a universal linker (a WRAP-Probe) located on
CC one or both terminal ends. The universal linker has reporter binding
CC sites to join common reporters to the probes and primer binding sites to
CC copy and amplify the probe. The probes and reporters are useful in
CC diagnostic or drug discovery assays for a wide range of biomedical
CC samples, including detection of nucleic acids and gene expression
CC profiles in human diagnostics, forensics and genomic analysis. The
CC methods are useful for amplifying and identifying any unknown DNA
CC fragment and also for improving sensitivity with tissue microarrays or
CC RNA arrays. The methods improve the quantification of gene expression and
CC allow highly improved detection of rare transcripts or very small
CC samples. This sequence represents a poly-T primer used in the
CC construction of probe sets
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 1 TTTTTTTTTTTTTTV 16

RESULT 1073
AAD44151
ID AAD44151 standard; DNA; 17 BP.
XX
AC AAD44151;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-AT PCR primer #2 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
OS Unidentified.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broaddus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Fig 1D; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits

```
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo AT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 7.8e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4515
              :|||||||||||||||
Db          2 VTTTTTTTTTTTTTT 17


RESULT 1074
AAX18389
ID   AAX18389 standard; DNA; 18 BP.
XX
AC   AAX18389;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 30.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 8.2e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          2 TTTTTTTTTTTTTTV 17


RESULT 1075
ADP04929
ID   ADP04929 standard; DNA; 18 BP.
XX
AC   ADP04929;
XX
DT   29-JUL-2004  (first entry)
XX
DE   PCR primer 1 used to amplify sea squirt DNA.
XX
KW   primer; ss; sea squirt; regeneration medicine; gene therapy;
KW   cell proliferation; differentiation; reproduction;
KW   environmental measurement; water survey; PCR.
XX
OS   Ciona intestinalis.
XX
PN   JP2004057129-A.
XX
PD   26-FEB-2004.
XX
PF   31-JUL-2002; 2002JP-00222593.
XX
PR   31-JUL-2002; 2002JP-00222593.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2004-287079/27.
XX
PT   Novel gene cluster which is specifically expressed in tissue or organ
PT   during developmental phase of sea squirt, useful for elucidation of
PT   mechanism of development of tissue or organ of sea squirt.
XX
PS   Disclosure; Page 38; 1846pp; Japanese.
XX
CC   This invention relates to novel genes and the encoded proteins thereof
CC   that are derived from the sea squirt Ciona intestinalis. Specifically, it
CC   refers to those genes that are expressed in the tissues or organs of the
CC   sea squirt during its developmental phase. The present invention
CC   describes the identification of these genes as useful for elucidation of
CC   the mechanism of development and hence for developing regeneration
CC   medicines and gene therapy techniques. Accordingly, they can be used in
CC   the research of various genetic diseases, as well as the analysis of cell
CC   proliferation, differentiation and reproduction. Furthermore, such
CC   compositions can be useful for environmental measurements and water
CC   surveys, particularly for sea water surveys, and also for the preparation
CC   of transformed sea squirt for improving edibility of sea squirt such as
CC   Halocynthia roretzi. This oligonucleotide sequence is a PCR primer used
CC   to amplify sea squirt DNA given in an exemplification of the invention.
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 8.2e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          3 TTTTTTTTTTTTTTV 18


RESULT 1076
AAT94431/c
ID   AAT94431 standard; mRNA; 19 BP.
XX
AC   AAT94431;
XX
DT   02-MAR-1998  (first entry)
XX
DE   Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
XX
KW   Primer; detection; characterisation; mRNA; restriction display PCR;
KW   synthesis; cDNA; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
```

XX
PN WO9729211-A1.
XX
PD 14-AUG-1997.
XX
PF 07-FEB-1997; 97WO-US002009.
XX
PR 09-FEB-1996; 96US-0011379P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Weinstein JN, Boulamwini J;
XX
DR WPI; 1997-415362/38.
XX
PT Detection and characterisation of mRNA by restriction display PCR -
PT comprising synthesis of cDNA, digestion with a restriction endonuclease,
PT ligation to an adaptor DNA and PCR amplification.
XX
PS Disclosure; Page 24; 40pp; English.
XX
CC A method has been improved for detecting and characterising mRNA
CC molecules which includes synthesising a double stranded (ds) cDNA from
CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
CC produce cDNA fragments in which at least one end of the cDNA fragments
CC has a sequence capable of hybridising to an adaptor DNA sequence. The
CC improvement comprises: (a) hybridising adaptor DNA sequences to at least
CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to
CC the cDNA fragments; (c) amplifying the cDNA fragments having ligated
CC adaptor DNA sequences by a PCR using primers that hybridise to the ends
CC of the cDNA fragments, where the primers have at least one nucleotide at
CC the 3' end that specifically hybridises to a subset of cDNA molecules;
CC and (d) detecting the presence of the resulting amplified cDNA fragments.
CC The present sequence represent a template poly-A tail used in the present
CC specification. The method designate restriction display PCR can be used
CC for characterising cells based on their mRNA content, for representing
CC expressed genes, and for discovery of therapeutics that alter cellular
CC gene expression. The method is also useful for characterising cells of a
CC variety of types and under a variety of physiological conditions. The
CC method is also useful for identifying cells or tissue from particular
CC individuals or species based on the fingerprint obtained from the mRNA
CC content of isolated cells or tissue and comparing it to cells or tissue
CC from a known source
XX
SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 17 TTTTTTTTTTTTTTV 2

RESULT 1077
AAX18390
ID AAX18390 standard; DNA; 19 BP.
XX
AC AAX18390;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 31.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 3 TTTTTTTTTTTTTTV 18

RESULT 1078
AAZ99489
ID AAZ99489 standard; DNA; 19 BP.
XX
AC AAZ99489;
XX
DT 03-JUL-2000 (first entry)
XX
DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX
KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW seed germination; seedling growth; gibberellin biosynthetic pathway;
KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
XX
OS Cucurbita maxima.
XX
PN WO200009722-A2.
XX
PD 24-FEB-2000.
XX
PF 10-AUG-1999; 99WO-US018066.
XX
PR 10-AUG-1998; 98US-0096111P.
PR 07-JUN-1999; 99US-0137977P.
XX
PA (MONS) MONSANTO CO.
XX
PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
PI Piller KJ, Rao S, Ream JE;
XX
DR WPI; 2000-224351/19.
XX
PT Obtaining transgenic plant useful for controlling seed germination and
PT seedling growth comprises transgene comprising a sequence expressing
PT altered levels of an essential hormone.

XX
PS Example 17; Page 262; 267pp; English.
XX
CC The present primer was used to reverse transcribe cDNA encoding a C-20
CC oxidase. The amplifie fragment is used in the method of the invention.
CC The specification describes methods for the inhibition and control of
CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
CC controlled by use of a chimeric expression construct expressing a RNA or
CC protein which suppresses the gibberellin biosynthetic pathway sequence,
CC diverts substrate from the pathway, or degrades pathway substrates or
CC products. The methods uses copalyl diphosphate synthase, 3beta-
CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
CC used to control seed germination and seedling growth especially to
CC regulate gene products of gibberellin biosynthetic pathway and
CC restoration of normal seed germination, in transgenic plants. The plants
CC produced are gibberellin deficient, and have shortened hypocotyl and/or
CC epicotyl phenotypes compared to normal plants
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1079
AAD15201
ID AAD15201 standard; DNA; 19 BP.
XX
AC AAD15201;
XX
DT 01-NOV-2001 (first entry)
XX
DE 3' sequencing primer #1 to identify and characterise polynucleotides.
XX
KW Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW nervous system disorder; Parkinson's disease; immune system disorder;
KW ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW coagulation disorder; blood platelet disorder; autoimmune disorder;
KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
KW cardiovascular; antiviral; primer; ss.
XX
OS Unidentified.
XX
PN WO200154651-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002439.
XX
PR 25-JAN-2000; 2000US-0177963P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
XX
DR WPI; 2001-514526/56.
XX
PT New polynucleotides regulated by fatty lesion development and their
PT encoded polypeptides, useful for preventing, treating or ameliorating
PT atherosclerosis, as well as for immune or hyperproliferative disorders.
XX
PS Example 1; Page 79; 188pp; English.
XX
CC The present invention relates to an isolated nucleic acid regulated by
CC fatty lesion development, which comprises any of 55 polynucleotide
CC sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
CC antibody is useful for preventing, treating, modulating or ameliorating a
CC medical condition, particularly atherosclerosis. The invention is used as
CC a marker or detector of nervous system disorder or disease (e.g.
CC Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
CC invention may also be useful for treating deficiencies or disorders of
CC the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
CC syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
CC (e.g.Gaucher's disease), infectious disease (e.g. herpes simplex),
CC coagulation disorders, blood platelet disorders and autoimmune disorders
CC (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
CC The polynucleotide sequence is also used in gene therapy. The present
CC sequence is a 3' sequencing primer used in the identification and
CC characterisation of polynucleotides up-regulated by fatty lesion
CC development
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1080
AAH21968
ID AAH21968 standard; DNA; 19 BP.
XX
AC AAH21968;
XX
DT 16-AUG-2001 (first entry)
XX
DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
XX
KW Mouse; human; total gene expression analysis; TOGA; DST; EST;
KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
KW central nervous system; antidepressant; gene therapy; diagnosis;
KW neuropsychiatric disorder; schizophrenia; bipolar disorder;
KW addiction-related behaviour; chromosome identification; immune response;
KW PCR primer; probe; ss.
XX
OS Mus musculus.
XX
PN WO200130972-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029690.
XX
PR 26-OCT-1999; 99US-0161379P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW;
XX
DR WPI; 2001-300499/31.
XX
PT New neuroleptic-regulated polynucleotides expressed in the central
PT nervous system for diagnosing and treating neuropsychiatric disorders
PT such as schizophrenia, bipolar disorder and addiction-related behavior.
XX
PS Example 1; Page 87; 210pp; English.
XX
CC The present invention describes isolated neuroleptic-regulated nucleic
CC acid molecules. (I) have neuroleptic, antimanic and antidepressant
CC activities, and can be used in gene therapy. (I), polypeptides (II)
CC encoded by (I), or a host cell (III) comprising (I), are useful for
CC preventing, treating, modulating or ameliorating a medical condition such
CC as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
CC diagnosing a pathological condition or susceptibility to a pathological

CC condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
CC disorder or addiction-related behaviour. (I) are useful for detecting the
CC presence of a nucleic acid encoding a protein in a mammalian tissue
CC sample. (I) can be used as probes and primers, for chromosome
CC identification, to control gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy to treat the above mentioned
CC disorders, identifying individuals from minute biological samples, as an
CC alternative to restriction fragment length polymorphism (RFLP) and as
CC polymorphic markers for forensic purposes. (I) is also useful as
CC molecular weight markers on Southern gels, diagnostic probes for the
CC presence of specific mRNA in a particular cell type, as a probe to
CC subtract-out known sequences in the process of discovering novel
CC polynucleotides, for selecting and making oligomers for attachment to a
CC gene chip or other support, to raise anti-DNA antibodies using DNA
CC immunisation technique, and as an antigen to elicit an immune response.
CC AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1081
AAS06525
ID AAS06525 standard; DNA; 19 BP.
XX
AC AAS06525;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mouse microglia and macrophage regulatory gene primer #60.
XX
KW Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
KW PCR-based total gene expression analysis; TOGA; infectious disorder;
KW neuroinflammatory pathology; neurodegenerative disease; gene therapy;
KW hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
KW ss.
XX
OS Mus musculus.
XX
PN WO200134770-A2.
XX
PD 17-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-US030585.
XX
PR 12-NOV-1999; 99WO-US026824.
PR 03-MAR-2000; 2000US-0186770P.
PR 19-JUN-2000; 2000US-0212465P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Carson MJ, Sutcliffe JG, Almazan MT, Tobal GM;
XX
DR WPI; 2001-308782/32.
XX
PT New regulated genes of microglia and macrophages, useful for diagnosing,
PT preventing or treating neuroinflammatory pathology and neurodegenerative
PT disease.
XX
PS Example 1; Page 88; 244pp; English.
XX
CC The present sequence represents a primer used to isolate novel mouse
CC microglia and macrophage regulatory gene DST (digital sequence tag)
CC sequences. AAS06401-AAS06590 represent these novel sequences and the
CC primer sequences used to isolate them. The PCR-based total gene
CC expression analysis (TOGA) system is used to examine the expression
CC pattern of molecules corresponding to genes that are regulated in
CC unstimulated microglia, activated microglia, unstimulated macrophage and
CC activated macrophage. The polynucleotides of the invention, the
CC polypeptides encoded by them and antibodies that bind to these
CC polypeptides are useful are useful for the diagnosis, prevention,
CC treatment or amelioration of a medical condition, preferably a
CC neuroinflammatory pathology or a neurodegenerative disease such as
CC Alzheimer's disease, senile dementia, Parkinson's disease, obsessive
CC compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,
CC depression and bipolar manic-depressive disorder. The sequences and
CC methods of the invention can also be used for detecting or treating
CC infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g.
CC cancer), immune disorders (e.g. severe combined immunodeficiency, SCID)
CC autoimmune diseases (e.g. insulin dependent diabetes mellitus),
CC inflammatory disorders (e.g. arthritis). The polynucleotides can be used
CC for gene therapy
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1082
ABK71509
ID ABK71509 standard; DNA; 19 BP.
XX
AC ABK71509;
XX
DT 30-JUL-2002 (first entry)
XX
DE CNS related 3' sequencing primer.
XX
KW Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
KW Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
KW addiction; multiple sclerosis; depression; manic-depressive disorder;
KW primer; ss.
XX
OS Synthetic.
XX
PN WO200226936-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-US030695.
XX
PR 29-SEP-2000; 2000US-0236790P.
PR 18-JAN-2001; 2001US-0263084P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;
XX
DR WPI; 2002-383271/41.
XX
PT New polynucleotide useful in gene therapy for preventing, treating
PT modulating or ameliorating a medical condition such as psychoses or a
PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
PT mammal.
XX
PS Example 1; Page 40; 254pp; English.
XX
CC This invention relates to the cDNA sequences of novel isolated
CC polynucleotides associated with psychoses or other neuropsychiatric
CC disorders. The sequences of the invention may act as blockers of D_2

CC receptors in the meso-limbic dopamine system. The nucleotide sequences of
CC the invention and the polypeptides encoded by them are useful in the
CC manufacture of a medicament useful for preventing, treating, modulating
CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An
CC antibody that binds the proteins of the invention is useful for
CC preventing, treating, modulating or ameliorating neurological disorders
CC such as psychoses or other neuropsychiatric disorders in a subject. The
CC sequences are also useful for diagnosing neurological disorders or a
CC susceptibility to a neurological disorder such as psychoses and other
CC neuro psychiatric disorders in a subject by determining the presence or
CC absence of mutation in the nucleotide sequence of apolipoprotein D or by
CC determining the alteration (increase or decrease) in the expression of
CC apolipoprotein D. The sequences of the invention are useful in treating
CC deficiencies or disorders of the central nervous system or peripheral
CC nervous system by activating or inhibiting the proliferation,
CC differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells
CC or glial cells. The sequences are useful as a marker or detector of a
CC particular nervous system disease or disorder such as Alzheimer's
CC disease, Pick's disease, Binswanger's disease, other senile dementia,
CC Parkinson's disease, obsessive compulsive disorders, epilepsy,
CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and
CC manic-depressive disorder. The present sequence represents an
CC oligonucleotide primer used in the identification of the cDNA sequences
CC of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1083
ABQ73231
ID ABQ73231 standard; DNA; 19 BP.
XX
AC ABQ73231;
XX
DT 27-SEP-2002 (first entry)
XX
DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
XX
KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
KW TOGA primer; ss.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200242420-A2.
XX
PD 30-MAY-2002.
XX
PF 21-NOV-2001; 2001WO-US044072.
XX
PR 21-NOV-2000; 2000US-0252216P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Leonardi A, Sartani A, Glass JR, Hasel KW;
XX
DR WPI; 2002-575233/61.
XX
PT New polynucleotides related to regulated genes characteristic of
PT atherosclerosis, useful for diagnosing, preventing, treating, modulating
PT or ameliorating atherosclerosis in a mammalian subject.
XX
PS Disclosure; Page 28; 130pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) and its
CC complements, and degenerate variants, comprising a sequence selected from
CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
CC (DST) corresponding to mRNAs whose expression is regulated by
CC proliferative lesion development caused by mechanically induced intimal
CC hyperplasia, or by lercanidipine treatment, or by proliferative lesions
CC and reversed by lercanidipine treatment. (I) has antiatherosclerotic
CC activity and can be used in gene therapy. (I) can be used for diagnosing
CC a medical condition (e.g. atherosclerosis) in a subject which involves
CC determining the presence or absence of a mutation in (I) and diagnosing
CC the medical condition based on the presence or absence of the mutation.
CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility
CC to atherosclerosis in a subject which involves detecting an alteration
CC (an increase or decrease) in amount of expression of (I). (I) is also
CC useful for diagnosing or monitoring the effects of treating a subject
CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
CC be used for preventing, treating, modulating, or ameliorating a medical
CC condition such as atherosclerosis in a mammalian subject. The present
CC sequence represents a TOGA primer which is used in the exemplification of
CC the present invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTTV 19

RESULT 1084
AAD34663
ID AAD34663 standard; DNA; 19 BP.
XX
AC AAD34663;
XX
DT 16-JUL-2002 (first entry)
XX
DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
XX
KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
KW TOGA; TOtal Gene expression Analysis; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200222783-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US029123.
XX
PR 15-SEP-2000; 2000US-0233176P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;
XX
DR WPI; 2002-339865/37.
XX
PT Preventing and treating hepatitis viral infection in a mammal, comprises
PT administering nucleic acid molecules that up- or down-regulate in
PT hepatitis B virus infection or polypeptides encoded by the nucleic acid
PT molecules.
XX
PS Disclosure; Page 28; 125pp; English.
XX
CC The present invention relates to a method for preventing, treating,
CC modulating or ameliorating a medical condition. The method involves
CC administering one or more nucleic acid molecules up- or down-regulated in
CC hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
CC acid molecules or antibodies that bind to the polypeptide. The method is

```
CC   useful for preventing, treating, modulating or ameliorating a medical
CC   condition. It is also useful for determining the presence or absence of a
CC   mutation in the nucleic acid molecules or detecting an alteration in
CC   expression of the polypeptide which is useful for the diagnosis of
CC   hepatitis viral infection. The method is useful for assessing the stage
CC   of hepatitis viral infection (e.g., acute hepatitis versus chronic
CC   hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
CC   for hepatitis viral infection and a gene expression profile is useful for
CC   identifying polypeptides and polynucleotides which are associated with
CC   hepatitis viral infection. Sequences of the invention are used in gene
CC   therapy and as vaccines. Nucleic acid sequences are useful as a
CC   diagnostic markers for HBV infection and for treating infectious
CC   diseases. The present DNA sequence is a PCR primer which is used for
CC   direct sequencing of TOGA (TOtal Gene expression Analysis) generated PCR
CC   products
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 1085
AAD40279
ID   AAD40279 standard; DNA; 19 BP.
XX
AC   AAD40279;
XX
DT   22-OCT-2002  (first entry)
XX
DE   HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX
KW   Gibberellin; transgenic plant; seed germination; seedling growth; GA;
KW   transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
XX
OS   Cucurbita pepo.
XX
PN   US2002053095-A1.
XX
PD   02-MAY-2002.
XX
PF   10-AUG-1999;   99US-00371307.
XX
PR   10-AUG-1999;   99US-00371307.
XX
PA   (BROW/) BROWN S M.
XX
PI   Brown SM,  Elich TD,  Heck GR,  Kishore GM,  Logusch EW,  Logusch SJ;
PI   Piller KJ,  Rao S,  Ream JE;
XX
DR   WPI; 2002-489107/52.
XX
PT   Control of gibberellin levels in plants useful to avoid unfavorable
PT   conditions in crops to increase yields, using transgenic plants having
PT   reduced seed germination and early seedling growth then treatment to
PT   restore these properties.
XX
PS   Example 19; Page 104; 155pp; English.
XX
CC   The invention relates to control of gibberellin (GA) levels in plants.
CC   The method involves producing transgenic plants having a phenotype of
CC   reduced seed germination and reduced early seedling growth, then
CC   restoring seed germination and early seedling growth by treating plants
CC   with an appropriate compound when conditions are favourable. The method
CC   is useful to control seed germination and/or early seedling growth in
CC   agricultural production so that unfavorable environmental conditions
CC   normally reducing agronomic output can be avoided and yields increased.
CC   Plants also demonstrate increased uniformity of germination, emergence
CC   and seedling vigor, so increasing yields at harvest. The method is
CC   especially useful in crop plants such as e.g. canola, soybean, cotton,
CC   etc:, and is also useful in storage and transport of seeds to reduce
CC   premature germination which may affect agronomic or food quality of the
CC   seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta
CC   -3beta hydroxylase cDNA. This primer is used in the exemplification of
CC   the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 1086
ABZ68389
ID   ABZ68389 standard; DNA; 19 BP.
XX
AC   ABZ68389;
XX
DT   22-APR-2003  (first entry)
XX
DE   Reverse transcription primer used to produce yeast cDNA.
XX
KW   Histone acetyltransferase; histone deacetylase; gene expression profile;
KW   chromatin-associated protein; gene expression; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003000715-A1.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US019750.
XX
PR   22-JUN-2001; 2001US-0300135P.
XX
PA   (CERE-) CERES INC.
XX
PI   Dang V,  Okamuro J;
XX
DR   WPI; 2003-175280/17.
XX
PT   New chimeric polypeptide comprising a histone acetyltransferase
PT   polypeptide segment and a segment comprising a histone deacetylase
PT   chromatin-associated protein complex subunit, useful for modulating gene
PT   expression in cells.
XX
PS   Example 10; Page 54; 85pp; English.
XX
CC   The specification describes chimeric histone acetyltransferase
CC   polypeptides. The chimeric polypeptides comprise a polypeptide segment
CC   that exhibits histone acetyltransferase activity, and a polypeptide
CC   segment having 40% or greater sequence identity to a subunit of a histone
CC   deacetylase chromatin-associated protein complex. The chimeric
CC   polypeptides are useful for determining gene expression profiles in
CC   specific cells, for modulating gene expression in specific cells, and for
CC   making genetically modified eukaryotes. The present sequence represents a
CC   reverse transcription primer used in the method of the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
```

```
Db          4 TTTTTTTTTTTTTTV 19


RESULT 1087
ACC79402
ID   ACC79402 standard; DNA; 19 BP.
XX
AC   ACC79402;
XX
DT   04-AUG-2003  (first entry)
XX
DE   M13 sequencing primer 3' primer SEQ ID NO:84.
XX
KW   Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
KW   cytostatic; vaccine; gene therapy; PCR primer; ss.
XX
OS   Enterobacteria phage M13.
OS   Synthetic.
XX
PN   WO2003033668-A2.
XX
PD   24-APR-2003.
XX
PF   17-OCT-2002; 2002WO-US033311.
XX
PR   17-OCT-2001; 2001US-0330206P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Barlow C,  Winrow CJ,  Callahan MLA,  Pankratz DG,  Vibat CRT;
PI   Warren AJ;
XX
DR   WPI; 2003-393520/37.
XX
PT   Preventing or treating a pathological condition e.g., ataxia
PT   telangiectasia (AT), AT tumors or other cancers comprises administering
PT   polynucleotides.
XX
PS   Example 1; Page 76; 184pp; English.
XX
CC   The present invention describes a method for preventing or treating a
CC   pathological condition (comprising ataxia telangiectasia (AT), AT tumours
CC   or other cancers), which comprises administering to a mammalian subject
CC   at least one of: (a) a first polynucleotide comprising a sequence having
CC   38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
CC   second polynucleotide at least 95% identical to the first polynucleotide;
CC   (b) a third polynucleotide comprising at least 10-bp sequence that is
CC   hybridisable to the first polynucleotide under stringent conditions; or
CC   (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
CC   identical to the gene. (I) have cytostatic activities, and can be used in
CC   vaccines and in gene therapy. The method is useful for preventing or
CC   treating e.g., ataxia telangiectasia (AT), AT tumours or other cancers.
CC   ACC79393 to ACC79423 represent primers used in the exemplification of the
CC   present invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 1088
AAD49149
ID   AAD49149 standard; DNA; 19 BP.
XX
AC   AAD49149;
XX
DT   07-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used in the invention.
XX
KW   Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
KW   autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
KW   haemolytic anaemia; graft-versus-host disease; inflammation; infection;
KW   epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
KW   food additive; food preservative; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200281726-A2.
XX
PD   17-OCT-2002.
XX
PF   15-NOV-2001; 2001WO-US043741.
XX
PR   15-NOV-2000; 2000US-0248892P.
PR   28-NOV-2000; 2000US-0253623P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Leonardi A,  Sartani A,  Glass J,  Sutcliffe JG,  Hasel KW;
XX
DR   WPI; 2003-058561/05.
XX
PT   New polypeptide associated with atherosclerosis, useful for treating
PT   atherosclerosis, nervous system disorders, immune disorders,
PT   hyperproliferative disorders and infectious diseases.
XX
PS   Disclosure; Page 139; 146pp; English.
XX
CC   The invention relates to polynucleotides and polypeptides associated with
CC   atherosclerosis. Polynucleotides of the invention are useful for delivery
CC   of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
CC   macromolecules. Sequences of the invention are useful for treating
CC   nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
CC   disorders such as rheumatoid arthritis, Addison's disease, haemolytic
CC   anaemia, graft-versus-host disease, inflammation), hyperproliferative
CC   disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
CC   bacterial, fungal or parasite infection). They are used for regeneration
CC   of tissues, to repair, replace or protect damage tissues, for increasing
CC   chemotaxis activity of cells, for increasing or decreasing the
CC   differentiation or proliferation of embryonic stem cells from a lineage,
CC   for modulating mammalian characteristics, (such as body weight or
CC   height), for modulating mammalian metabolism affecting catabolism,
CC   anabolism, processing utilisation and storage of energy, to change a
CC   mammal's mental or physical state, or as a food additive or preservative.
CC   The invention is useful in gene therapy. The present sequence is a
CC   sequencing primer used in the invention
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTG 4516
              ||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 1089
AAD50267
ID   AAD50267 standard; DNA; 19 BP.
XX
AC   AAD50267;
XX
DT   24-MAR-2003  (first entry)
XX
DE   3' sequencing primer #1 used to illustrate the method of the invention.
```

XX
KW Gene expression; drug interaction mechanism; drug screening; primer;
KW genomic mapping; ss.
XX
OS Unidentified.
XX
PN WO200261045-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-US002666.
XX
PR 01-FEB-2001; 2001US-00775217.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA (QUAN/) QUAN J.
XX
PI Quan J, Hilbush BS, Hasel KWPD, Sutcliffe GJ, Chang HW;
PI Callahan MA;
XX
DR WPI; 2003-092784/08.
XX
PT Simplified TOGA method for simultaneous sequence-specific identification
PT of multiple mRNA molecules in mRNA population, useful for determining
PT tissue-specific patterns of gene expression or mechanisms of drug
PT interaction.
XX
PS Disclosure; Page 39; 93pp; English.
XX
CC The present invention relates to a novel simplified TOGA (RTM) method for
CC simultaneous sequence-specific identification of multiple mRNA molecules
CC in a RNA population. The method involves characterising each of the
CC sequence-specific polymerase chain reaction (PCR) products by partial
CC sequence and length. The method is useful for determining tissue-specific
CC patterns of gene expression or mechanisms of drug interaction. It is also
CC useful for drug screening, studying physiological processes, genomic
CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
CC The present sequence is a primer used to illustrate the method of the
CC invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1090
ADC21495
ID ADC21495 standard; DNA; 19 BP.
XX
AC ADC21495;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRDI-BF1 RT-PCR primer.
XX
KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
KW multiple myeloma cell; human; PRDI-BF1;
KW positive regulatory domain I-binding factor-1; MHC;
KW major histocompatibility complex Class I; cytostatic; vaccine; ss;
KW primer; PCR.
XX
OS Homo sapiens.
XX
PN WO2003029282-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-EP010701.
XX
PR 29-SEP-2001; 2001DE-01048236.
XX
PA (IMMU-) IMMUGENICS AG.
XX
PI Theobald M, Lotz C;
XX
DR WPI; 2003-354724/33.
XX
PT New tumor-associated oligopeptide, useful particularly for treating
PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also
PT derivatives and related nucleic acid.
XX
PS Disclosure; Page 22; 64pp; German.
XX
CC This invention describes a novel tumor-associated oligopeptide that is
CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
CC regulatory domain I-binding factor-1) which is able to induce an MHC
CC (major histocompatibility complex) Class I allele variant A2-restricted
CC immune response of CD8+ CTL against tumor cells. The products of the
CC invention have cytostatic activity and can be used in a vaccine. The
CC peptide of the invention, also related retro-inverse and pseudopeptides,
CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
CC and T cell receptors specific for PRDI-BFI peptides are useful for
CC treating diseases associated with PRDI-BF1, particularly tumors. The
CC products of the invention are also useful as diagnostic, therapeutic and
CC prophylactic agents for detecting, modifying, generating, expanding
CC and/or regulating activation and functional status of T cells, and for
CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell
CC receptors and their functional equivalents. This sequence represents an
CC RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
CC invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTG 4516
||||||||||||||:
Db 4 TTTTTTTTTTTTTTV 19

RESULT 1091
ADF74670/c
ID ADF74670 standard; DNA; 19 BP.
XX
AC ADF74670;
XX
DT 26-FEB-2004 (first entry)
XX
DE DNA oligo (30) used in preparing a library of same length signatures.
XX
KW ss; tag-DNA signature; adapter-signature-adapter; parallel sequencing;
KW genomic mapping; genetic identification; medical diagnostic.
XX
OS Unidentified.
XX
PN WO2003091416-A2.
XX
PD 06-NOV-2003.
XX
PF 25-APR-2003; 2003WO-US013076.
XX
PR 26-APR-2002; 2002US-0375782P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Fischer A, Hiemisch H, Williams S, Brenner S, Walker R;

```
PI   Vermaas E,  Fu R;
XX
DR   WPI; 2003-865585/80.
XX
PT   Preparing a library of same-length signature sequences from a source
PT   nucleic acid population by ligating to the cleaved ends, a second adapter
PT   containing a recognition and cleavage site for a second restriction
PT   endonuclease.
XX
PS   Disclosure; Fig 2a; 54pp; English.
XX
CC   This invention relates to a novel method for preparing a library of same-
CC   length signature sequences from a source nucleic acid population.
CC   Specifically, it comprises producing solid phase cloned libraries of
CC   oligonucleotide tag-DNA signature sequence constructs, which are useful
CC   for sequencing many polynucleotides simultaneously. The present invention
CC   describes a kit for the construction of adapter-signature-adapter
CC   constructs using 'first' and 'second' adapters each containing a specific
CC   restriction endonuclease recognition site, and which flanks the same
CC   length signature sequence. As such, using the method described herein it
CC   is possible to do parallel sequencing of large populations of
CC   polynucleotides for genomic mapping, genetic identification and medical
CC   diagnostics. This oligonucleotide sequence is a DNA oligo involved in the
CC   step wise process of preparing a library of same length signature
CC   sequences from restriction fragments in an exemplification of the
CC   invention.
XX
SQ   Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db         16 TTTTTTTTTTTTTTV 1


RESULT 1092
ADL24850
ID   ADL24850 standard; DNA; 19 BP.
XX
AC   ADL24850;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Intestinal epithelium/peyer's patch M cell-related primer #15.
XX
KW   intestinal epithelium cell development; peyer's patch M cell development;
KW   inflammatory bowel disease; glutenenteropathy; infectious disease;
KW   autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW   Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
KW   immune system disorder; hypersensitivity; anaphylaxis;
KW   blood group incompatibility; ss; PCR; primer.
XX
OS   Unidentified.
XX
PN   WO200280852-A2.
XX
PD   17-OCT-2002.
XX
PF   04-APR-2002; 2002WO-US010873.
XX
PR   04-APR-2001; 2001US-0281416P.
XX
PA   (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI   Brayden DJ,  Byrne D,  O'mahony DJ,  Evans CF,  Mah SP,  Lo DD;
XX
DR   WPI; 2003-075470/07.
XX
PT   Novel isolated or purified polypeptide encoded by genes associated with
PT   intestinal epithelium or M cell development, differentiation or function,
PT   useful for treating autoimmune diseases and infectious diseases.
XX
PS   Disclosure; SEQ ID NO 360; 152pp; English.
XX
CC   The invention comprises DNA sequences which are associated with
CC   intestinal epithelium and peyer's patch M cells. The DNA sequences of the
CC   invention are useful for assessing, modifying, modulating or regulating
CC   intestinal epithelium or M cell development. The DNA sequences of the
CC   invention are also useful in the treatment of: inflammatory bowel
CC   disease, glutenenteropathy, infectious diseases, autoimmune diseases
CC   (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
CC   disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
CC   diseases or disorders of the immune system, hypersensitivity,
CC   anaphylaxis, and blood group incompatibility. The present DNA sequence
CC   represents a primer that was used in the exemplification of the
CC   invention.
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 8.6e+02;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTG 4516
              |||||||||||||||:
Db          4 TTTTTTTTTTTTTTV 19


RESULT 1093
ADM16445
ID   ADM16445 standard; RNA; 19 BP.
XX
AC   ADM16445;
XX
DT   17-JUN-2004  (first entry)
XX
DE   RNA intron poly-pyrimidine tract, seq id 2.
XX
KW   Cytostatic; antimicrobial; virucide; gene therapy; RNA intron; cancer;
KW   viral; microbial; infection; poly-pyrimidine tract; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    2. .4
FT                   /*tag=  a
FT                   /note= "optionally between 1-3 bases at this position"
FT   misc_feature    5
FT                   /*tag=  b
FT                   /note= "optionally absent base"
FT   misc_feature    6. .17
FT                   /*tag=  c
FT                   /note= "optionally between 7-12 bases at this position"
FT   misc_feature    19
FT                   /*tag=  d
FT                   /note= "optionally absent base"
XX
PN   WO2004024940-A2.
XX
PD   25-MAR-2004.
XX
PF   16-SEP-2003; 2003WO-US029274.
XX
PR   16-SEP-2002; 2002US-0411062P.
PR   12-OCT-2002; 2002US-0418405P.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Lin S,  Ying S;
XX
DR   WPI; 2004-270056/25.
XX
PT   New isolated RNAs comprising an intron RNA that is released in a cell,
```

```
PT   thus modulating the function of a target gene, useful for treating and
PT   preventing diseases such as cancer and viral/microbial infections.
XX
PS   Claim 2; SEQ ID NO 2; 54pp; English.
XX
CC   The invention relates to isolated RNAs comprising an intron RNA that is
CC   released in a cell, thus modulating the function of a target gene. Also
CC   disclosed is a DNA template for the isolated RNA, an expression vector
CC   comprising the DNA, and a composition comprising one or more agents that
CC   induce RNA-mediated modulation of the functions of two or more target
CC   genes in a cell, such as a mammalian cell. The isolated RNAs and
CC   compositions are useful for modulating the function of a target gene in a
CC   cell, e.g. to inhibit a cancer-related gene, potential viral gene, and
CC   microbe-related gene, and thus useful for treating and preventing
CC   diseases such as cancer and viral/microbial infections. The current
CC   sequence represents a potential poly-pyrimidine tract of the artificial
CC   RNA intron.
XX
SQ   Sequence 19 BP; 0 A; 3 C; 0 G; 0 T; 13 U; 3 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 19;
  Best Local Similarity   11.1%;  Pred. No. 8.6e+02;
  Matches    2;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2124 TTTTCTTTTCTTTTTTC 2141
              ::::|:::: :::::::|
Db          1 UYYYCUUUUUUUUUUUC 18


RESULT 1094
ABL57554
ID   ABL57554 standard; DNA; 20 BP.
XX
AC   ABL57554;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly u.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 6; Page 23; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the effects of
CC   the number of G(s) in each target nucleic acid, and the number of G(S) in
CC   its corresponding invention nucleic acid probe
XX
SQ   Sequence 20 BP; 4 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 9e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4493 TTTATAAGTTTTTTTTTTTT 4512
              | ||||  ||||||||||||
Db          1 TATATATATTTTTTTTTTTT 20


RESULT 1095
ABQ79871/c
ID   ABQ79871 standard; DNA; 20 BP.
XX
AC   ABQ79871;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Nucleotide sequence of a PCR primer #1.
XX
KW   Polymerase chain reaction; thermal cycle; immobilisation;
KW   genetic engineering; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2002191369-A.
XX
PD   09-JUL-2002.
XX
PF   27-DEC-2000; 2000JP-00399573.
XX
PR   27-DEC-2000; 2000JP-00399573.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
PA   (TAKA/) TAKAHASHI K.
XX
DR   WPI; 2002-630904/68.
XX
PT   Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT   a substrate on which a DNA is immobilized used in medical, biochemical,
PT   molecular biological and gene engineering fields.
XX
PS   Example; Page 9; 13pp; Japanese.
XX
CC   The invention relates to performing a thermal cycle of PCR by using a
CC   substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC   method is useful in the medical, biochemical, molecular biological and
CC   genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC   used in the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 9e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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```
Qy       3606 AAAAAACAAAAACAGAATTT 3625
              |||||| ||||| | |||||
Db         20 AAAAAAAAAAAAAAAAATTT 1
```

RESULT 1096
ABA97633
ID ABA97633 standard; DNA; 20 BP.
XX
AC ABA97633;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly o nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 4 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       4493 TTTATAAGTTTTTTTTTTTT 4512
              | ||||  ||||||||||||
Db          1 TATATATATTTTTTTTTTTT 20
```

RESULT 1097
ABA97639
ID ABA97639 standard; DNA; 20 BP.
XX
AC ABA97639;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly u nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 4 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       4493 TTTATAAGTTTTTTTTTTTT 4512
              | ||||  ||||||||||||
Db          1 TATATATATTTTTTTTTTTT 20
```

RESULT 1098
ABS98544
ID ABS98544 standard; DNA; 21 BP.
XX
AC ABS98544;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human acetyl choline muscarinic receptor 3 polymorphic sequence #10.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX

```
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 28; Page 160; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   polymorphic DNA sequence of the invention
XX
SQ   Sequence 21 BP; 10 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2394 ATATATATACATATATACAT 2413
              ||||||||  ||||||| ||
Db          1 ATATATATGTATATATATAT 20


RESULT 1099
AAQ79185/c
ID   AAQ79185 standard; DNA; 15 BP.
XX
AC   AAQ79185;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
XX
DE   Nuclease resistant oligonucleotide.
XX
KW   Nuclease resistant oligonucleotide; inhibition of gene expression;
KW   9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    13
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "9-methyl-acyclo-adenosine"
XX
PN   WO9422864-A1.
XX
PD   13-OCT-1994.
XX
PF   21-MAR-1994;   94WO-US002995.
XX
PR   30-MAR-1993;   93US-00040326.
XX
PA   (STER ) STERLING WINTHROP INC.
XX
PI   Cook PD,  Delecki DJ,  Guinosso C;
XX
DR   WPI; 1994-333078/41.
XX
PT   New acyclic nucleoside analogues - used to prepare nuclease resistant
PT   oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS   Example 11; Page 20; 37pp; English.
XX
CC   AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic
CC   nucleoside analogues which inhibit nuclease degradation. The nuclease
CC   resistant oligonucleotides can themselves be used to inhibit gene
CC   expression as antisense agents, in nucleic acid sequencing and diagnostic
CC   assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1100
AAQ79184/c
ID   AAQ79184 standard; DNA; 15 BP.
XX
AC   AAQ79184;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
XX
DE   Nuclease resistant oligonucleotide.
XX
KW   Nuclease resistant oligonucleotide; inhibition of gene expression;
KW   9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    14
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "9-methyl-acyclo-adenosine"
XX
```

PN WO9422864-A1.
XX
PD 13-OCT-1994.
XX
PF 21-MAR-1994; 94WO-US002995.
XX
PR 30-MAR-1993; 93US-00040326.
XX
PA (STER) STERLING WINTHROP INC.
XX
PI Cook PD, Delecki DJ, Guinosso C;
XX
DR WPI; 1994-333078/41.
XX
PT New acyclic nucleoside analogues - used to prepare nuclease resistant
PT oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS Example 10; Page 20; 37pp; English.
XX
CC AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic
CC nucleoside analogues which inhibit nuclease degradation. The nuclease
CC resistant oligonucleotides can themselves be used to inhibit gene
CC expression as antisense agents, in nucleic acid sequencing and diagnostic
CC assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 15 TTTTTTTTTTTTTTT 1

RESULT 1101
AAT52136
ID AAT52136 standard; RNA; 15 BP.
XX
AC AAT52136;
XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
DE Human ICAM hammerhead ribozyme target sequence (nt. position 2910).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9523225-A2.
XX
PD 31-AUG-1995.
XX
PF 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
PT Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 7.5e+02;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:::::::::::::::
Db 1 UUUUUUUUUUUUUUU 15

RESULT 1102
AAT52138
ID AAT52138 standard; RNA; 15 BP.
XX
AC AAT52138;
XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
DE Human ICAM hammerhead ribozyme target sequence (nt. position 2911).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;

KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9523225-A2.
XX
PD 31-AUG-1995.
XX
PF 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
PT Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 7.5e+02;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:::::::::::::::
Db 1 UUUUUUUUUUUUUUU 15

RESULT 1103
AAX65144/c
ID AAX65144 standard; RNA; 15 BP.
XX
AC AAX65144;
XX
DT 20-JUL-1999 (first entry)
XX
DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1776.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Mus sp.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US015516.
XX
PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363253.
PR 23-DEC-1994; 94US-00363254.
PR 17-FEB-1995; 95US-00390850.
PR 20-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00432874.
PR 04-MAY-1995; 95US-00434509.
PR 07-JUL-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-AUG-1995; 95US-00512861.
PR 05-OCT-1995; 95US-00541365.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
PI Karpeisky A, Thompson JD, Modak A, Burgin A;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX
PS Claim 10; Page 177; 307pp; English.
XX
CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.

```
CC   The concentration of ribozyme required to affect a therapeutic treatment
CC   is lower than that required of antisense molecules, and is highly
CC   specific. The present sequence is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 15 BP; 4 A; 4 C; 1 G; 0 T; 6 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1404 GATGCTAAAGATGAT 1418
              |||||||||||||||
Db         15 GATGCTAAAGATGAT 1


RESULT 1104
AAV01604/c
ID   AAV01604 standard; DNA; 15 BP.
XX
AC   AAV01604;
XX
DT   25-MAR-2003  (revised)
DT   31-MAR-1998  (first entry)
XX
DE   Oligonucleotide containing phosphoramidate linkages.
XX
KW   phosphoramidate linkage; solid phase synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "these residues have N3'->P5' phosphoramidate
FT                   linkages"
XX
PN   WO9731009-A1.
XX
PD   28-AUG-1997.
XX
PF   14-JUN-1996;   96WO-US010418.
XX
PR   21-FEB-1996;   96US-00603566.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Hirschbein BL,  Fearon KL,  Gryaznov SM,  Mccurdy SN,  Nelson JS;
PI   Schultz RG;
XX
DR   WPI; 1997-435080/40.
XX
PT   Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT   immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT   phosphoramidite then oxidation, useful as research, diagnostic and
PT   therapeutic agents.
XX
PS   Disclosure; Page 28; 60pp; English.
XX
CC   A new method is provided for the synthesis of oligonucleotides having N3'
CC   ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC   protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC   amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC   phosphoramidite monomer to form an internucleoside N3'-> P5'
CC   phosphoramidite link; (d) oxidising this link to phosphoramidate; and
CC   optionally repeating steps (b)-(d) until the required oligonucleotide is
CC   completed. This method provides better yields with lower reagent
CC   consumption than known processes, and can be operated on a large scale.
CC   The obtained oligos, containing phosphoramidate linkages, have favourable
CC   binding properties, nuclease resistance and solubility, and are useful as
CC   research, diagnostic and therapeutic agents. The present sequence is an
CC   example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
CC   have been introduced by the new method. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1105
AAV01603
ID   AAV01603 standard; DNA; 15 BP.
XX
AC   AAV01603;
XX
DT   25-MAR-2003  (revised)
DT   31-MAR-1998  (first entry)
XX
DE   Oligonucleotide containing phosphoramidate linkages.
XX
KW   phosphoramidate linkage; solid phase synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "these residues have N3'->P5' phosphoramidate
FT                   linkages"
XX
PN   WO9731009-A1.
XX
PD   28-AUG-1997.
XX
PF   14-JUN-1996;   96WO-US010418.
XX
PR   21-FEB-1996;   96US-00603566.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Hirschbein BL,  Fearon KL,  Gryaznov SM,  Mccurdy SN,  Nelson JS;
PI   Schultz RG;
XX
DR   WPI; 1997-435080/40.
XX
PT   Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT   immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT   phosphoramidite then oxidation, useful as research, diagnostic and
PT   therapeutic agents.
XX
PS   Disclosure; Page 28; 60pp; English.
XX
CC   A new method is provided for the synthesis of oligonucleotides having N3'
CC   ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC   protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC   amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC   phosphoramidite monomer to form an internucleoside N3'-> P5'
CC   phosphoramidite link; (d) oxidising this link to phosphoramidate; and
CC   optionally repeating steps (b)-(d) until the required oligonucleotide is
CC   completed. This method provides better yields with lower reagent
CC   consumption than known processes, and can be operated on a large scale.
CC   The obtained oligos, containing phosphoramidate linkages, have favourable
CC   binding properties, nuclease resistance and solubility, and are useful as
CC   research, diagnostic and therapeutic agents. The present sequence is an
CC   example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
CC   have been introduced by the new method. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
```

```
  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1106
AAV07431
ID   AAV07431 standard; DNA; 15 BP.
XX
AC   AAV07431;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Synthetic peptide-labeled oligonucleotide primer.
XX
KW   oligonucleotide; peptide; conjugate; release tag compound;
KW   mass spectrometry; detection; identification; diagnosis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9826095-A1.
XX
PD   18-JUN-1998.
XX
PF   10-DEC-1997;   97WO-US022639.
XX
PR   10-DEC-1996;   96US-0033037P.
PR   16-MAY-1997;   97US-0046719P.
XX
PA   (GENE-) GENETRACE SYSTEMS INC.
XX
PI   Montforte JA,  Becker CH,  Pollart DJ,  Shaler TA;
XX
DR   WPI; 1998-348547/30.
XX
PT   New release tag compounds for detecting target molecule(s) - comprising a
PT   reactive group, a release group and a releasable non-volatile mass label
PT   detectable by mass spectrometry.
XX
PS   Example 3; Page 92; 170pp; English.
XX
CC   The sequence is that of an oligonucleotide primer which was produced as
CC   part of an oligonucleotide peptide conjugate as an example of a release
CC   tag compound (RTC). These comprise a reactive group, a release group and
CC   a non-volatile mass label comprising a synthetic polymer or biopolymer
CC   detectable by mass spectrometry. The RTCs can be used as probes for the
CC   detection of TMs. They can be used for e.g. identification of gene
CC   sequences, identification of non-coding nucleotide sequences,
CC   identification of mutations within a gene or protein sequence, detection
CC   of metals, detection of toxins, detection of receptors on an organism or
CC   a cell, characterisation of antibody-antigen interactions, enzyme-
CC   substrate interactions and characterisation of ligand interactions.
CC   Multiplex applications include multiple pathogen diagnostics, multigene
CC   genetic polymorphism screening, single nucleotide polymorphism (SNP)
CC   genotyping, clone and gene mapping, and gene expression analysis. The
CC   RTCs permit the ready detection of releasable mass labels by mass
CC   spectroscopy. The releasable mass labels permit the multiplexing of tens,
CC   hundreds and perhaps even thousands of different mass labels that can be
CC   used to uniquely identify each desired target
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1107
AAT86675
ID   AAT86675 standard; DNA; 15 BP.
XX
AC   AAT86675;
XX
DT   04-JUN-1998  (first entry)
XX
DE   Oligonucleotide linked to polyacrylamide.
XX
KW   Capillary afinity gel electrophoresis; separation; polymer-gel;
KW   polyacrylamide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Thymine at 5' end attached to a polyacrylamide
FT                   gel via a linking group"
XX
PN   WO9745721-A1.
XX
PD   04-DEC-1997.
XX
PF   23-MAY-1997;   97WO-EP002647.
XX
PR   24-MAY-1996;   96CH-00001320.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Muscate A,  Paulus A,  Natt F;
XX
DR   WPI; 1998-041763/04.
XX
PT   Separation of electrically charged target molecules - by capillary
PT   affinity gel electrophoresis using polymer-gel to which receptors for
PT   target molecules are bound.
XX
PS   Example A1; Page 22; 41pp; English.
XX
CC   This sequence represents an oligonucleotide receptor molecule covalently
CC   bound to a polyacrylamide gel via a linking group. The invention relates
CC   to selective separation of electrically charged target molecules in an
CC   analytical mixture. It comprises capillary affinity gel electrophoresis
CC   using a capillary tube which is at least partly filled with a polymer
CC   gel. Receptors for target molecules are covalently bound to the polymer.
CC   An electric field of at least 50 volts/cm is applied. The capillary tube
CC   is charged with the analytical mixture. In a first separation stage, the
CC   target molecules in the mixture are bound to the receptors and the
CC   remaining components are eluted, optionally whilst splitting open. In a
CC   second stage, the elution conditions are changed, optionally in stages,
CC   so that the affinity of the target molecules for the receptor is
CC   eliminated and the target molecules are eluted and detected, optionally
CC   whilst splitting open. The process is useful for selective separation
CC   and/or determination of charged organic compounds, such as
CC   oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
CC   isolation of specific proteins and DNA molecules, purification of
CC   antibodies, analysis of antisense compounds or screening for enzyme
CC   inhibitors. The process achieves higher resolution and selectivity than
CC   prior art processes, especially in the case of complex biological
CC   analytical mixtures. It has high sensitivity, even with small amounts of
CC   samples. The derivatised polymers may be synthesised specifically using
CC   standard methods
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1108
AAT86605
ID   AAT86605 standard; DNA; 15 BP.
XX
AC   AAT86605;
XX
DT   04-JUN-1998  (first entry)
XX
DE   Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW   Capillary afinity gel electrophoresis; separation; polymer-gel;
KW   polyacrylamide; ss.
XX
OS   Synthetic.
XX
PN   WO9745721-A1.
XX
PD   04-DEC-1997.
XX
PF   23-MAY-1997;   97WO-EP002647.
XX
PR   24-MAY-1996;   96CH-00001320.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Muscate A,  Paulus A,  Natt F;
XX
DR   WPI; 1998-041763/04.
XX
PT   Separation of electrically charged target molecules - by capillary
PT   affinity gel electrophoresis using polymer-gel to which receptors for
PT   target molecules are bound.
XX
PS   Example D3; Page 25; 41pp; English.
XX
CC   A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC   process using capillary affinity gel electrophoresis. The invention
CC   relates to selective separation of electrically charged target molecules
CC   in an analytical mixture. It comprises capillary affinity gel
CC   electrophoresis using a capillary tube which is at least partly filled
CC   with a polymer gel. Receptors for target molecules are covalently bound
CC   to the polymer. An electric field of at least 50 volts/cm is applied. The
CC   capillary tube is charged with the analytical mixture. In a first
CC   separation stage, the target molecules in the mixture are bound to the
CC   receptors and the remaining components are eluted, optionally whilst
CC   splitting open. In a second stage, the elution conditions are changed,
CC   optionally in stages, so that the affinity of the target molecules for
CC   the receptor is eliminated and the target molecules are eluted and
CC   detected, optionally whilst splitting open. The process is useful for
CC   selective separation and/or determination of charged organic compounds,
CC   such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC   for isolation of specific proteins and DNA molecules, purification of
CC   antibodies, analysis of antisense compounds or screening for enzyme
CC   inhibitors. The process achieves higher resolution and selectivity than
CC   prior art processes, especially in the case of complex biological
CC   analytical mixtures. It has high sensitivity, even with small amounts of
CC   samples. The derivatised polymers may be synthesised specifically using
CC   standard methods
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1109
AAX00787
ID   AAX00787 standard; DNA; 15 BP.
XX
AC   AAX00787;
XX
DT   13-APR-1999  (first entry)
XX
DE   N3-P5 phosphoramidate oligonucleotide #3.
XX
KW   Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .15
FT                   /*tag=  a
FT                   /note= "contains internucleotide N3-P5 phosphoramidate
FT                   internucleotide linkages"
XX
PN   US5859233-A.
XX
PD   12-JAN-1999.
XX
PF   20-DEC-1996;   96US-00771789.
XX
PR   21-FEB-1996;   96US-00603566.
PR   14-JUN-1996;   96US-00663918.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Nelson JS,  Mccurdy SN,  Hirschbein BL,  Schultz RG;
PI   Fearon KL;
XX
DR   WPI; 1999-120007/10.
XX
PT   New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT   the synthesis of oligo-nucleotide(s).
XX
PS   Example 10; Col 33; 34pp; English.
XX
CC   This sequence represents an example of an oligonucleotide containing
CC   novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC   sequence is generated synthetically by using an amine-exchange reaction
CC   of phosphoramidites in which a deprotected 3'-amino group of an
CC   oligonucleotide chain is exchanged for the amino portion of a 5'-
CC   phosphoramidite with a protected 3' amino group. The resulting
CC   phosphoramidite internucleotide linkage is oxidised to form a stable
CC   protected phosphoramidate linkage
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1110
AAX00788/c
ID   AAX00788 standard; DNA; 15 BP.
XX
AC   AAX00788;
XX
DT   13-APR-1999  (first entry)
XX
DE   N3-P5 phosphoramidate oligonucleotide #4.
```

```
XX
KW   Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .15
FT                   /*tag=  a
FT                   /note= "contains internucleotide N3-P5 phosphoramidate
FT                   internucleotide linkages"
XX
PN   US5859233-A.
XX
PD   12-JAN-1999.
XX
PF   20-DEC-1996;   96US-00771789.
XX
PR   21-FEB-1996;   96US-00603566.
PR   14-JUN-1996;   96US-00663918.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Nelson JS,  Mccurdy SN,  Hirschbein BL,  Schultz RG;
PI   Fearon KL;
XX
DR   WPI; 1999-120007/10.
XX
PT   New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT   the synthesis of oligo-nucleotide(s).
XX
PS   Example 10; Col 33; 34pp; English.
XX
CC   This sequence represents an example of an oligonucleotide containing
CC   novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC   sequence is generated synthetically by using an amine-exchange reaction
CC   of phosphoramidites in which a deprotected 3'-amino group of an
CC   oligonucleotide chain is exchanged for the amino portion of a 5'-
CC   phosphoramidite with a protected 3' amino group. The resulting
CC   phosphoramidite internucleotide linkage is oxidised to form a stable
CC   protected phosphoramidate linkage
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1111
AAX18364
ID   AAX18364 standard; DNA; 15 BP.
XX
AC   AAX18364;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 5.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4503 TTTTTTTTTTTTTGG 4517
              |||||||||||||||
Db          1 TTTTTTTTTTTTTGG 15


RESULT 1112
AAZ61854
ID   AAZ61854 standard; RNA; 15 BP.
XX
AC   AAZ61854;
XX
DT   28-MAR-2000  (first entry)
XX
DE   HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 49; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
```

```
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC   HCV sequence was screened for optimal ribozyme target sites using a
CC   computer folding algorithm and regions of the mRNA which did not form
CC   secondary folding structures and contained potential ribozyme cleavage
CC   sites were identified. Ribozymes were synthesised to target these sites
CC   and their activities optimised by either varying the length of the
CC   binding arms or by modification to prevent degradation by nucleases. The
CC   ribozymes of the invention inhibit gene expression and/or viral
CC   replication, and are used to treat diseases associated with Hepatitis C
CC   virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC   carcinoma. The ribozymes may be used in combination with interferon to
CC   treat HCV infection, other infectious diseases, autoimmune diseases, and
CC   cancer
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 7.5e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1113
AAZ64910
ID   AAZ64910 standard; RNA; 15 BP.
XX
AC   AAZ64910;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 102; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC   the descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 7.5e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1114
AAA46502
ID   AAA46502 standard; cDNA; 15 BP.
XX
AC   AAA46502;
XX
DT   04-SEP-2000  (first entry)
XX
DE   PCR primer used to amplify DNA encoding an endo-beta-mannanase.
XX
KW   Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW   PCR primer; ss.
XX
OS   Coffea arabica.
XX
PN   WO200028046-A1.
XX
PD   18-MAY-2000.
XX
PF   28-OCT-1999;   99WO-EP008314.
XX
PR   11-NOV-1998;   98EP-00203742.
XX
PA   (NEST ) SOC PROD NESTLE SA.
XX
PI   Marraccini P,  Rogers J;
XX
DR   WPI; 2000-399535/34.
XX
PT   New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT   pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
XX
PS   Disclosure; Page 32; 41pp; French.
XX
CC   PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
CC   mannanase enzyme, which is involved in the hydrolysis of polysaccharides
CC   that consist of molecules of mannan, either simple or branched, linked
CC   together by beta(1-4) bonds. The mannanase polynucleotide sequence is
CC   used for in vivo modification of the coffee endo-beta-mannanase gene. It
CC   is also used to produce transgenic plant cells (especially coffee cells)
CC   which have modified properties of mannan polysaccharide, and thus altered
CC   flavour or structure. The enzyme is used for modification, degradation or
CC   synthesis of mannan polysaccharides in vitro, particularly to treat
CC   coffee beans to increase the percentage of dry matter extraction, and
CC   thus reduce the quantity of sediment
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 1115
AAA75048
ID   AAA75048 standard; DNA; 15 BP.
XX
AC   AAA75048;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Primer used to reverse transcribe human RNA.
XX
KW   Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW   heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW   wound healing; infection; burn; angiogenesis; restenosis;
KW   atherosclerosis; inflammation; neurodegenerative disease;
KW   Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200052178-A1.
XX
PD   08-SEP-2000.
XX
PF   14-FEB-2000; 2000WO-US003542.
XX
PR   01-MAR-1999;   99US-00258892.
XX
PA   (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA   (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA   (FRIE/) FRIEDMAN M M.
XX
PI   Pecker I,  Vlodavsky I,  Feinstein E;
XX
DR   WPI; 2000-579289/54.
XX
PT   New polynucleotides encoding a polypeptide having heparanase activity,
PT   useful in wound healing and in gene therapy, particularly in treating
PT   tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS   Disclosure; Page 44; 152pp; English.
XX
CC   The present primer was used to reverse transcribe human RNA, from which a
CC   cDNA sequence encoding a protein with heparanase catalytic activity was
CC   amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC   particularly in treating tumour, inflammation or autoimmunity.
CC   Particularly, the polynucleotide is useful in modulating the
CC   bioavailability of heparin-binding growth factors, cellular responses to
CC   heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC   interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC   susceptibility to certain viral and some bacterial and protozoa
CC   infections, or disintegration of neurodegenerative plaques. The
CC   polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC   radiation burns), and in the treatment of angiogenesis, restenosis,
CC   atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC   Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC   bacterial or protozoa infections
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1116
AAA07792
ID   AAA07792 standard; DNA; 15 BP.
XX
AC   AAA07792;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-e.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 7.5e+02;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :|||||||||||||:
Db          1 UTTTTTTTTTTTTTU 15


RESULT 1117
AAA07794
ID   AAA07794 standard; DNA; 15 BP.
XX
AC   AAA07794;
XX
```

```
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-g.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
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CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 1118
AAA07828
ID   AAA07828 standard; DNA; 15 BP.
XX
AC   AAA07828;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 15.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 7.5e+02;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15


RESULT 1119
AAA07790
ID   AAA07790 standard; DNA; 15 BP.
XX
AC   AAA07790;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-c.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
```

KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15
```

RESULT 1120
AAA07789
ID AAA07789 standard; DNA; 15 BP.
XX
AC AAA07789;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-b.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
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CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
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CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 7.5e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15
```

RESULT 1121
AAA07795
ID AAA07795 standard; DNA; 15 BP.
XX
AC AAA07795;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-h.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.

XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
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CC monomers in oligomers, which are used in pharmaceutical compositions to
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CC interleukins associated with pathological conditions such as inflammatory
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CC infections and bacterial infections (see AAA07786 for details of other
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CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||:|||:|||||
Db 1 TTTTTUTTTUTTTTT 15

RESULT 1122
AAA07797
ID AAA07797 standard; DNA; 15 BP.
XX
AC AAA07797;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-j.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
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CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:|||||||||||||:
Db 1 UTTTTTTTTTTTTTU 15

RESULT 1123
AAA07799
ID AAA07799 standard; DNA; 15 BP.
XX
AC AAA07799;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-l.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.

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XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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PS   Disclosure; Page 20; 42pp; English.
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CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 1124
AAA07802
ID   AAA07802 standard; DNA; 15 BP.
XX
AC   AAA07802;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-0.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
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CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 7.5e+02;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :|||||||||||||:
Db          1 UTTTTTTTTTTTTTU 15


RESULT 1125
AAA07825
ID   AAA07825 standard; DNA; 15 BP.
XX
AC   AAA07825;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 14.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
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XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
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CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 1126
AAA07831
ID   AAA07831 standard; DNA; 15 BP.
XX
AC   AAA07831;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 16.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 30; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
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CC   infected cells. They are used in oligomers for gene regulation, antisense
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CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 1127
AAA07803
ID   AAA07803 standard; DNA; 15 BP.
XX
AC   AAA07803;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-p.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
```

```
XX
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PT   oligomers used to inhibit expression of nucleic acids and in gene
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 7.5e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1128
AAA07834
ID   AAA07834 standard; DNA; 15 BP.
XX
AC   AAA07834;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 17.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 7.5e+02;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15


RESULT 1129
AAA07796
ID   AAA07796 standard; DNA; 15 BP.
XX
AC   AAA07796;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-i.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
```

PS Disclosure; Page 20; 42pp; English.
XX
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CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC interleukins associated with pathological conditions such as inflammatory
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CC infections and bacterial infections (see AAA07786 for details of other
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CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 7.5e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              :||||:|||:||||:
Db          1 UTTTTUTTTUTTTTU 15
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RESULT 1130
AAA07800
ID AAA07800 standard; DNA; 15 BP.
XX
AC AAA07800;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-m.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
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CC The invention provides modified nucleomonomers of specified formula and
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CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
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CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 7.5e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15
```

RESULT 1131
AAA07793
ID AAA07793 standard; DNA; 15 BP.
XX
AC AAA07793;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-f.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
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CC inhibit expression of nucleic acid molecules including DNA and RNA in
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CC technology, diagnostic applications to detect target sequences in
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CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
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CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 7.5e+02;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:::::::::::::::
Db 1 UUUUUUUUUUUUUUU 15

RESULT 1132
AAA07798
ID AAA07798 standard; DNA; 15 BP.
XX
AC AAA07798;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-k.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
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CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 7.5e+02;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:::::::::::::::
Db 1 UUUUUUUUUUUUUUU 15

RESULT 1133
AAA07788
ID AAA07788 standard; DNA; 15 BP.
XX
AC AAA07788;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-a.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
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DR WPI; 2000-246530/21.
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```
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CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1134
AAA07791
ID   AAA07791 standard; DNA; 15 BP.
XX
AC   AAA07791;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-d.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
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XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 7.5e+02;
  Matches   11;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :||||:|||:||||:
Db          1 UTTTTUTTTUTTTTU 15


RESULT 1135
AAA07801
ID   AAA07801 standard; DNA; 15 BP.
XX
AC   AAA07801;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-n.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
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PA   (UYNE-) UNIV NEBRASKA.
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PI   Gold B;
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DR   WPI; 2000-246530/21.
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CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
```

```
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 7.5e+02;
  Matches   11;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             :||||:|||:||||:
Db          1 UTTTTUTTTUTTTTU 15


RESULT 1136
AAA62350
ID   AAA62350 standard; DNA; 15 BP.
XX
AC   AAA62350;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   7
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 16; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1137
AAA62347
ID   AAA62347 standard; DNA; 15 BP.
XX
AC   AAA62347;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   11
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   13
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   15
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
```

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PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 15; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1138
AAA62348
ID   AAA62348 standard; DNA; 15 BP.
XX
AC   AAA62348;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   7
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 15; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1139
AAH20308
ID   AAH20308 standard; DNA; 15 BP.
XX
AC   AAH20308;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Oligo dT15 EDTA labelled probe.
XX
KW   Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
FT   modified_base   5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
FT   modified_base   8
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
XX
PN   US2001002314-A1.
XX
PD   31-MAY-2001.
XX
PF   04-AUG-1998;   98US-00128732.
XX
PR   30-OCT-1987;   87US-00115922.
PR   16-NOV-1990;   90US-00614205.
PR   12-NOV-1993;   93US-00152250.
XX
PA   (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
```

PI Dervan PB, Moser HE;
XX
DR WPI; 2001-342909/36.
XX
PT New hybridization probe for specific triplex formation with large double
PT helices, useful e.g. for site-specific diagnostic cleavage, contains
PT attached functional residue.
XX
PS Example 1; Fig 3B; 20pp; English.
XX
CC This invention relates to hybridisation probes which target a specific
CC sequence within a large double-helical nucleic acid. The probe is
CC complementary to the target sequence and contains at least one nucleotide
CC with an attached molecule that is able to cleave double-helical DNA e.g.
CC EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC where the attached molecule is a label or compound that alters gene
CC expression, are used for specific detection and/or cleavage of double-
CC helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC caused by viruses, genetic defects or oncogenes), for chromosomal
CC analysis, and for the isolation and mapping of genes. The present
CC sequence represents probe of the invention used in an example
CC illustrating how the probe binds to and cleaves double stranded DNA
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1140
AAF30882
ID AAF30882 standard; DNA; 15 BP.
XX
AC AAF30882;
XX
DT 09-JUL-2001 (first entry)
XX
DE Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW hybridisation; detection; fluorescence; probe; ss.
XX
OS Synthetic.
XX
PN WO200131063-A1.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029786.
XX
PR 26-OCT-1999; 99US-00428236.
XX
PA (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI Dempcy RO, Afonina IA, Vermeulen NMJ;
XX
DR WPI; 2001-328656/34.
XX
PT Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT mismatch discrimination.
XX
PS Disclosure; Page 58; 105pp; English.
XX
CC The present sequence is that of the oligonucleotide (ODN) component of an
CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC invention. MGBs bind in a non-intercalating manner to the minor groove of
CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC but in an intercalating manner, or lies in the minor groove, or is
CC oriented in some other way to the DNA molecule by MGB, such that it
CC becomes fluorescent (or its fluorescent properties change detectably).
CC The conjugates are used as hybridisation probes and amplification primers
CC for fluorescent detection of specifically hybridising sequences, for
CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC mismatch discrimination, target or signal amplification, array-based
CC assays and sequencing, including detection of double-stranded DNA by
CC triplex formation. Many different targets can be detected a single
CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC hybridisation-triggered fluorescence. Upon hybridisation to the
CC complementary target sequence there was an increase in fluorescence
CC yield, measured as the ratio of the fluorescence emitted by the hybrid
CC between the ODN-MGB-LF conjugate and its target sequence to the
CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC of 8.3
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1141
AAH20511
ID AAH20511 standard; DNA; 15 BP.
XX
AC AAH20511;
XX
DT 31-JUL-2001 (first entry)
XX
DE Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX
KW Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
KW phosphorothioate; solid phase synthesis; modified oligonucleotide;
KW clinical diagnostic; cancer treatment; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .14
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate deoxynucleotides"
XX
PN DE10051726-A1.
XX
PD 10-MAY-2001.
XX
PF 18-OCT-2000; 2000DE-01051726.
XX
PR 30-OCT-1999; 99DE-01052376.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Seliger H, Sobkowski M, Hinz M;
XX
DR WPI; 2001-336414/36.
XX
PT Intermediate for oligonucleotide synthesis comprises partially hydrolysed
PT cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
XX
PS Example 2; Page 5; 8pp; German.
XX
CC This invention describes a novel chemical product comprising a partially
CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
CC with nucleotide derivative(s). The product is an intermediate for the
CC large (gram) scale solid phase synthesis of modified oligonucleotides

CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the
CC treatment of AIDS and cancers. The presence of the partially hydrolysed
CC copolymer facilitates the synthesis of larger amounts of oligonucleotides
CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
CC described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
CC Oligonucleotides are obtained in very good quality and high yields, Also,
CC the nucleosides do not display the reduced activity seen in some prior
CC art procedures, less carrier material, reagents and solvent are required.
CC Further, the carrier material is biodegradable and thus does not present
CC disposal problems. It also swells uniformly in a range of solvents, which
CC obviates expansion or contraction during use or solvent exchange.
CC AAH20510-AAH20513 represent oligonucleotides containing modified
CC deoxynucleotides which are used to illustrate the method of the invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1142
AAF49041
ID AAF49041 standard; DNA; 15 BP.
XX
AC AAF49041;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #1.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 60; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4502 TTTTTTTTTTTTTTG 4516
|||||||||||||||
Db 1 TTTTTTTTTTTTTTG 15

RESULT 1143
AAH49243
ID AAH49243 standard; DNA; 15 BP.
XX
AC AAH49243;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #7.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9
FT /*tag= a
FT /mod_base= OTHER
FT /note= "t-but"
FT modified_base 15
FT /*tag= b
FT /mod_base= OTHER
FT /note= "t-hex"
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 26; Page 40; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage

CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (I) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC restenosis, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (I)
CC show different responses to base-pair mismatches in the DNA and PNA
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1144
ABL40743
ID ABL40743 standard; DNA; 15 BP.
XX
AC ABL40743;
XX
DT 03-JUL-2002 (first entry)
XX
DE Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.
XX
KW Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;
KW anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
XX
OS Gallus gallus.
XX
PN US2002034810-A1.
XX
PD 21-MAR-2002.
XX
PF 16-AUG-2001; 2001US-00930218.
XX
PR 20-SEP-2000; 2000US-00666390.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX
PI Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
XX
DR WPI; 2002-338926/37.
XX
PT Nucleic acid encoding avian and reptile heparanase polypeptide is useful
PT to treat various heparin-related disorders and the signal peptide is
PT useful in production of membrane-targeted or secreted recombinant
PT proteins.
XX
PS Disclosure; Page 13; 39pp; English.
XX
CC The invention relates to an isolated avian and reptile nucleic acid,
CC encoding a polypeptide with heparanase catalytic activity. The signal
CC peptide of the nucleic acid can be used to express membrane-associated or
CC secreted proteins in heterologous expression systems. The encoded
CC polypeptides can be used to prevent tumour angiogenesis, metastasis and
CC invasion, and to intervene with pathologies associated with impaired
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoa and bacterial infections or
CC disintegration of neurodegenerative plaques. The present sequence
CC represents a chicken heparanase (hpa) cDNA cloning oligo dT(15) primer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1145
ABA97403
ID ABA97403 standard; DNA; 15 BP.
XX
AC ABA97403;
XX
DT 18-JUN-2002 (first entry)
XX
DE Nucleotide sequence of oligomer # 10 used to compare mismatches.
XX
KW Protein nucleic acid molecule; PNA; ds.
XX
OS Synthetic.
XX
PN WO200168673-A1.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US008111.
XX
PR 14-MAR-2000; 2000US-0189190P.
PR 30-NOV-2000; 2000US-0250334P.
XX
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
PI Chakhmakhcheau O, Buryakova A, Choob M, Hondorp K;
XX
DR WPI; 2002-041177/05.
XX
PT Oligonucleotides analogs useful in detection, separation and purification
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS Example 20; Page 123; 197pp; English.
XX
CC This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adapters and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenen, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide

```
CC   backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC   nucleic acid molecules with greater affinity than DNA or RNA
CC   concentration. The compounds are relatively simple to synthesize and are
CC   used in a wide variety of applications. This sequence represents a DNA
CC   oligomer which is used to represent the effect of single base mismatches
CC   on oligonucleotides
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1146
AAL49453/c
ID   AAL49453 standard; DNA; 15 BP.
XX
AC   AAL49453;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
XX
KW   Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW   protein production; cancer; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15
FT                   /*tag=  a
FT                   /product= "tag peptide"
FT                   /partial
FT                   /note= "no start or stop"
XX
PN   WO200266675-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-EP001651.
XX
PR   16-FEB-2001; 2001DE-01007317.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Kahmann S,  Mueller O;
XX
DR   WPI; 2002-674959/72.
DR   P-PSDB; AAO19054.
XX
PT   Detecting mutations in nucleic acid, useful for diagnosis and
PT   characterization of tumors, by amplification, in vitro transcription and
PT   translation, then protein detection.
XX
PS   Claim 11; Fig 5; 62pp; German.
XX
CC   The present invention relates to a method of detecting mutations in a
CC   nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC   amplicon, in vitro transcription and translation of this amplicon, and
CC   detection of the translated protein. The primers used for amplification
CC   are designed to produce an amplicon that is translatable and allows
CC   differentiation between translation products of wild-type and mutated
CC   nucleic acids. The method is used to detect mutations in tumour
CC   suppressor genes, for (early) diagnosis, monitoring and characterisation
CC   of tumours (especially of bladder and intestines) and in the germ line
CC   (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC   is used to detect or verify the reading frame of a nucleic acid cloned in
CC   it, and to determine the suitability of detectable peptides for analysis
CC   and/or purification of a recombinant protein, expressed from a sequence
CC   cloned in the vector. The present sequence encodes a tag peptide and was
CC   used in the invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1147
AAL49455/c
ID   AAL49455 standard; DNA; 15 BP.
XX
AC   AAL49455;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
XX
KW   Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW   protein production; cancer; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15
FT                   /*tag=  a
FT                   /product= "tag peptide"
FT                   /partial
FT                   /note= "no start or stop"
XX
PN   WO200266675-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-EP001651.
XX
PR   16-FEB-2001; 2001DE-01007317.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Kahmann S,  Mueller O;
XX
DR   WPI; 2002-674959/72.
DR   P-PSDB; AAO19056.
XX
PT   Detecting mutations in nucleic acid, useful for diagnosis and
PT   characterization of tumors, by amplification, in vitro transcription and
PT   translation, then protein detection.
XX
PS   Claim 11; Fig 5; 62pp; German.
XX
CC   The present invention relates to a method of detecting mutations in a
CC   nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC   amplicon, in vitro transcription and translation of this amplicon, and
CC   detection of the translated protein. The primers used for amplification
CC   are designed to produce an amplicon that is translatable and allows
CC   differentiation between translation products of wild-type and mutated
CC   nucleic acids. The method is used to detect mutations in tumour
CC   suppressor genes, for (early) diagnosis, monitoring and characterisation
CC   of tumours (especially of bladder and intestines) and in the germ line
CC   (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC   is used to detect or verify the reading frame of a nucleic acid cloned in
CC   it, and to determine the suitability of detectable peptides for analysis
CC   and/or purification of a recombinant protein, expressed from a sequence
CC   cloned in the vector. The present sequence encodes a tag peptide and was
CC   used in the invention
```

```
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1148
AAD29506
ID   AAD29506 standard; DNA; 15 BP.
XX
AC   AAD29506;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Primer used for the expression of adipocytes in human preadipose cells.
XX
KW   Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
KW   diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200206450-A1.
XX
PD   24-JAN-2002.
XX
PF   13-JUL-2001; 2001WO-EP008165.
XX
PR   18-JUL-2000; 2000EP-00115489.
XX
PA   (NEST ) SOC PROD NESTLE SA.
XX
PI   Darimont C,  Mace K,  Pfeifer A;
XX
DR   WPI; 2002-188539/24.
XX
PT   New human pre-adipose cell line capable of differentiating to adipose
PT   cells, useful in developing drug, food ingredients, and supplements
PT   against obesity, diabetes and cardiovascular diseases.
XX
PS   Example 5; Page 10; 30pp; English.
XX
CC   The present invention relates to new human pre-adipose cell lines capable
CC   to differentiate to white adipose cells, exhibiting essentially the same
CC   cellular properties of normal white adipose cells. The human pre-adipose
CC   cell lines are useful for the identification of substances controlling
CC   the regulation of lipid uptake and release by human white adipocytes, and
CC   substances controlling the differentiation of preadipocytes into mature
CC   adipocytes. They are useful for screening compounds capable to regulate
CC   the secretion of any metabolites or hormones from human white adipocytes.
CC   Sequences of the invention are useful for developing drugs, food
CC   ingredients and supplements against obesity, diabetes and cardio-
CC   vascular diseases. The present DNA sequence is a reverse transcription
CC   (RT)-PCR primer which is used for the expression of adipocytes in
CC   differentiated immortalised human preadipose cells. This primer is used
CC   in the exemplification of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1149
AAD22531/c
ID   AAD22531 standard; RNA; 15 BP.
XX
AC   AAD22531;
XX
DT   29-AUG-2003  (revised)
DT   07-AUG-2003  (revised)
DT   12-FEB-2002  (first entry)
XX
DE   Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
XX
KW   RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
KW   virucide; oncogene; cancer; transcription; translation; leukaemia virus;
KW   hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
KW   poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
XX
OS   unidentified retrovirus.
OS   Unidentified.
XX
PN   US6291438-B1.
XX
PD   18-SEP-2001.
XX
PF   06-OCT-1998;   98US-00167375.
XX
PR   24-FEB-1993;   93US-00022055.
PR   23-FEB-1994;   94US-00200650.
PR   22-FEB-1996;   96US-00604871.
XX
PA   (WANG/) WANG J H.
XX
PI   Wang JH;
XX
DR   WPI; 2002-009339/01.
XX
PT   Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
PT   reverse transcriptase comprises at the 2'-O position of the
PT   oligoribonucleotide, a hydrophobic carrier reagent containing a poly
PT   substituted phenyl compound.
XX
PS   Example 3; Col 24; 56pp; English.
XX
CC   The invention relates to derivatised antisense oligoribonucleotides with
CC   enhanced membrane permeability and stability. The derivatised antisense
CC   oligoribonucleotide complementary to a sequence of nucleotides found in a
CC   virus or a cell is useful for inhibiting e.g., viral reverse
CC   transcriptase. Derivatised antisense oligoribonucleotide is conjugated at
CC   the 2'-O position with a hydrophobic carrier reagent containing a poly
CC   substituted phenyl compound. The derivatised oligoribonucleotides are
CC   used to decrease the expression of oncogenes and thereby decrease the
CC   expression of cancer cells which rely upon oncogene expression for their
CC   phenotypic and pathological properties. The oligoribonucleotides are also
CC   used for increasing the effectiveness of antisense oligonucleotide
CC   targetted to a gene associated with a disease or a condition in an
CC   animal. To alter gene transcription and/or translation for any gene or
CC   gene segment responsible for expression, to inhibit viral reverse
CC   transcriptase, to inhibit the expression of leukaemia virus, hepatitis
CC   virus, oncogenes and human immunodeficiency virus. The present sequence
CC   is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
CC   which is used in the treatment of moloney murine leukaemia virus (MuLV)
CC   in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-
CC   AUG-2003 to standardise OS field)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
```

```
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1150
ABQ82140/c
ID   ABQ82140 standard; DNA; 15 BP.
XX
AC   ABQ82140;
XX
DT   11-DEC-2002  (first entry)
XX
DE   Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.
XX
KW   Chimeric nucleic acid construct; recombinational cloning; silencing;
KW   recombination site; double stranded RNA; plant; ds.
XX
OS   Synthetic.
XX
PN   WO200259294-A1.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-AU000073.
XX
PR   26-JAN-2001; 2001US-0264067P.
PR   29-NOV-2001; 2001US-0333743P.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Wesley S,  Waterhouse P,  Helliwell C;
XX
DR   WPI; 2002-682669/73.
XX
PT   New vectors comprising operably linked DNA fragments having an origin of
PT   replication, a selectable marker and a chimeric DNA construct, useful for
PT   silencing target nucleic acids and for producing large amounts of double-
PT   stranded RNA.
XX
PS   Claim 14; Page 74; 104pp; English.
XX
CC   The present invention describes a vector (I) comprising operably linked
CC   DNA fragments having: (a) origin of replication allowing replication in a
CC   recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC   selectable marker region capable of being expressed in the recipient cell
CC   ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC   region capable of being recognized by RNA polymerases of a eukaryotic
CC   cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC   fourth recombination sites; (iii) 3' transcription terminating and
CC   polyadenylation region functional in the eukaryotic cell. The first and
CC   fourth recombination sites, or the second and third recombination sites
CC   are capable of reacting with a same recombination site, and preferably
CC   are identical. The first and second recombination sites, or the third and
CC   fourth recombination sites, do not recombine with each other or with a
CC   same recombination site. The vector is useful for producing large amounts
CC   of double-stranded RNA which can be used for silencing target nucleic
CC   acid sequences. The vectors can also be used to convert a DNA fragment
CC   into an inverted repeat structure. Plants transformed with a vector from
CC   the present invention can be used in a conventional breeding scheme to
CC   produce more plants with the same characteristics or to introduce a
CC   chimeric gene for reduction of the phenotypic expression of nucleic
CC   acids. The present sequence represents an acceptor vector nucleotide
CC   sequence from the present invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1151
ABX00240
ID   ABX00240 standard; RNA; 15 BP.
XX
AC   ABX00240;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 21; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 7.5e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1152
```

```
ABX03406
ID   ABX03406 standard; RNA; 15 BP.
XX
AC   ABX03406;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 64; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 7.5e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1153
ABL57064
ID   ABL57064 standard; DNA; 15 BP.
XX
AC   ABL57064;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)methyl)isophthalate, synthetic branching
FT                   amidite"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 4; Page 44; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O35, which was produced in an
CC   example from the invention and which includes a synthetic branching
CC   amidite compound. The invention describes an improved process for
CC   immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1154
ABL57054
```

```
ID   ABL57054 standard; DNA; 15 BP.
XX
AC   ABL57054;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide phosphoramidite oligonucleotide O9.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)-N'-tritylhexanohydrazide"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 2; Page 40; 120pp; English.
XX
CC   The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC   15-mer, designated oligo O9, which was produced in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1155
ABL57063
ID   ABL57063 standard; DNA; 15 BP.
XX
AC   ABL57063;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O39.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzyloxy)-5
FT                   -((2'-cyanoethyl)(diisopropylamino) phosphanyloxymethyl)-
FT                   benzene"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O39, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1156
ABL57066
ID   ABL57066 standard; DNA; 15 BP.
XX
AC   ABL57066;
XX
DT   22-JUL-2002  (first entry)
```

```
XX
DE   Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Amino-C6 modification"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 12; Page 57; 120pp; English.
XX
CC   The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
CC   oligonucleotide that was used in a comparison of hydrazine and amine
CC   attachment moieties on active ester surfaces in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1157
ABL57059
ID   ABL57059 standard; DNA; 15 BP.
XX
AC   ABL57059;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O33.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "4-((2-cyanoethyl)(diisopropylamino)
FT                   phosphanyloxymethyl)-benzoic acid methyl ester"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O33, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1158
ABL57061
ID   ABL57061 standard; DNA; 15 BP.
XX
AC   ABL57061;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT                   phenylcarbonylamido)-2-((2''-cyanoethyloxy)
FT                   (diisopropyl)amino)-phosphanyloxy)-propane"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O37, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1159
ABL57056
ID   ABL57056 standard; DNA; 15 BP.
XX
AC   ABL57056;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide phosphoramidite oligonucleotide O31.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)-N'-tritylhexanohydrazide"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 2; Page 40; 120pp; English.
XX
CC   The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC   15-mer, designated oligo O31, which was produced in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1160
ABL57060
ID   ABL57060 standard; DNA; 15 BP.
XX
AC   ABL57060;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O34.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
```

```
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)methyl)isophthalate"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O34, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1161
ABK98141
ID   ABK98141 standard; DNA; 15 BP.
XX
AC   ABK98141;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Triple helix forming associated oligonucleotide #26.
XX
KW   Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW   gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW   pathogenic bacteria; virus; replication; virulence; cancer;
KW   oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS   Synthetic.
XX
PN   US6403302-B1.
XX
PD   11-JUN-2002.
XX
PF   16-DEC-1993;   93US-00168920.
XX
PR   17-SEP-1992;   92US-00946976.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Dervan PB,  Beal PA;
XX
DR   WPI; 2002-536030/57.
XX
PT   A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT   oligonucleotide which binds in parallel and antiparallel orientation,
PT   respectively, for targetting sequences on alternate strands of DHNA to
PT   control gene expression.
XX
PS   Example 1; Fig 3B; 108pp; English.
XX
CC   The present invention relates to methods and oligonucleotides for forming
CC   a triple-helix comprising a double helical nucleic acid comprising first
CC   and second substantially complementary strands, and an oligonucleotide
CC   bound to a purine-rich target sequence within the double helical nucleic
CC   acid, where the oligonucleotide binds in a parallel and antiparallel
CC   orientation, respectively, to target sequences on alternate strands of
CC   the double helical nucleic acid. The method has therapeutic applications,
CC   where gene expression is controlled by selective triple-helix formation
CC   within expression regulatory sequences of a target gene. The
CC   oligonucleotides can be used to form triple-helices, and are useful to
CC   detect the presence or absence of specific sequences within genomic DNA
CC   for diagnostic and therapeutic purposes. The oligonucleotides can be
CC   selected to specifically bind to pathogenic double-stranded DNA including
CC   specific sequences required by pathogenic bacteria or viruses for
CC   replication or virulence, reducing their pathogenicity. Alternatively,
CC   the oligonucleotide can be chosen to target a unique sequence of the
CC   pathogen which is not found in the genome of pathogen's host. The
CC   oligonucleotides can be used in cancer treatment by way of triple-helix
CC   suppression of specific oncogenes including those of endogenous or viral
CC   origin. Such therapeutic oligonucleotides are capable of forming triple-
CC   helices with such sequences in cancerous cells containing the activated
CC   oncogene, so preferentially killing or repressing the cancer causing
CC   cell. The present sequence represents an oligonucleotide used in the
CC   methods of the present invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1162
ABK98184
ID   ABK98184 standard; DNA; 15 BP.
XX
AC   ABK98184;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Triple helix forming associated oligonucleotide #48.
XX
KW   Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW   gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW   pathogenic bacteria; virus; replication; virulence; cancer;
```

KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1163
ABV74142/c
ID ABV74142 standard; DNA; 15 BP.
XX
AC ABV74142;
XX
DT 23-JAN-2003 (first entry)
XX
DE 5' End of cDNA library clone.
XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; arometic; pesticide; ss.
XX
OS Synthetic.
XX
PN WO200277200-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009559.
XX
PR 27-MAR-2001; 2001US-0279168P.
PR 31-JAN-2002; 2002US-0353392P.
XX
PA (INSC-) INSCENT INC.
XX
PI Woods D, Dimitratos S;
XX
DR WPI; 2003-029930/02.
XX
PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odorant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.
XX
PS Disclosure; Fig 5; 83pp; English.
XX
CC The present sequence is that of the 5' end of a cDNA clone isolated from
CC a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC using a method designed to rapidly array and normalize a complex cDNA
CC library obtained from a target species. Clones are arrayed into multi-
CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC and a unique 3' sequence, which allows an anchored oligonucleotide in
CC each well to selectively hybridise only to those cDNA clones with a
CC complementary 5' end. The unique 3' key sequences are designed to give a
CC comprehensive level of degeneracy since they are diverse and numerous
CC enough to ensure that every possible cDNA sequence can be bound by an
CC individual, specific oligonucleotide in a single well. The cDNA library
CC is heated to denature the clones into single stranded DNA, and an aliquot
CC is added to every well. The anchored oligonucleotide serves as the 3'
CC primer in PCR, and the common 5' region present in every cDNA clone
CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC in each well. The library is now arrayed and normalised. The method was
CC used to identify and isolate clones encoding G-protein coupled receptors,
CC especially odourant receptors, and active effectors involved in the
CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
CC proteins, or other olfactory or neuronal proteins. The identified
CC receptors and proteins are useful for identifying compounds that reduce a
CC target animal's sensitivity to odours, for manufacturing compounds or
CC devices that mask odours, or trapping invertebrates with odourants.
CC Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC with desirable effects on specific species, for the development of pest
CC monitoring systems or non-toxic, species-specific pesticide alternatives,
CC for controlling insect feeding and breeding behaviour, detecting the
CC presence of small air-borne molecules, etc
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 15 TTTTTTTTTTTTTTT 1

RESULT 1164
ABV74141
ID ABV74141 standard; DNA; 15 BP.
XX
AC ABV74141;
XX
DT 23-JAN-2003 (first entry)

```
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of a poly-T oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1165
ABV75865
ID   ABV75865 standard; DNA; 15 BP.
XX
AC   ABV75865;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Oligonucleotide T15-Q-CDPI3.
XX
KW   Deprotection; phosphoramidite; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphoramidite linkage"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3' Q-CDPI3"
XX
PN   WO200272864-A2.
XX
PD   19-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US006739.
XX
PR   08-MAR-2001; 2001US-0274309P.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Nelson J;
XX
DR   WPI; 2003-046740/04.
XX
PT   New oligonucleotide deprotection reagent useful for deprotecting
PT   oligonucleotide comprises an active methylene compound and an amine
PT   reagent.
XX
PS   Example 2; Page 25; 46pp; English.
XX
CC   The present invention provides a method for deprotection of an
CC   oligonucleotide. This involves reacting a protected oligonucleotide,
CC   which is preferably covalently attached to a solid support through a
CC   linkage, with a deprotection reagent comprising an active methylene
CC   compound and an amine reagent. The process and reagent minimise side-
CC   reactions leading to certain impurities that contaminate synthetic
CC   oligonucleotides. The present sequence is a T15 phosphoramidite
CC   oligonucleotide having a quencher moiety (Q) and minor groove binder
CC   (CDPI3) at the 3' end, which was synthesised in an example of the
CC   invention. This protected oligonucleotide was treated either with 15%
CC   ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%
CC   ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that
CC   deprotection without DEM yielded a complex mixture of products containing
CC   only 26.5% of the desired product. When DEM was used, 76.8% of the
CC   desired product was obtained
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
```

```
RESULT 1166
ADA14836/c
ID   ADA14836 standard; DNA; 15 BP.
XX
AC   ADA14836;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin target sequence, #1, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .15
FT                   /*tag=  a
FT                   /bound_moiety= "Hairpin oligonucleotide #1"
FT                   /note= "Forms a doube-stranded region with the hairpin
FT                   oligonucleotide shown in example 2"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 2; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
CC   complementary probe. Also claimed is a microarray comprising the hairpin
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide target
CC   sequence, #1, used in an example of the invention.
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1167
ADB68520
ID   ADB68520 standard; DNA; 15 BP.
XX
AC   ADB68520;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Single-base mismatch oligonucleotide SEQ ID 10 DNA.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; single-base mismatch; ss;
KW   phosphono-peptide nucleic acid; pPNA.
XX
OS   Synthetic.
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 20; Page 234; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the
CC   invention. This sequence may also comprise a peptide nucleic acid (PNA),
CC   a phosphono-PNA (pPNA) or a HypNA.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
```

```
  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1168
ADC18592
ID   ADC18592 standard; DNA; 15 BP.
XX
AC   ADC18592;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Annealing control primer Oligo-dT15 SEQ ID NO:54.
XX
KW   annealing control primer; ACP; annealing specificity;
KW   nucleic acid amplification; hybridisation; DNA fingerprinting;
KW   genomic DNA; RNA fingerprint; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003050305-A1.
XX
PD   19-JUN-2003.
XX
PF   19-SEP-2002; 2002WO-KR001781.
XX
PR   08-DEC-2001; 2001WO-KR002133.
PR   01-MAY-2002; 2002WO-KR000816.
XX
PA   (SEEG-) SEEGENE INC.
XX
PI   Chun J;
XX
DR   WPI; 2003-627256/59.
XX
PT   Annealing control primer to improve annealing specificity in nucleic acid
PT   amplification, has region complementary to target, arbitrary nucleotide
PT   sequence, regulator with universal base/non-discriminatory base analog.
XX
PS   Example 2; SEQ ID NO 54; 190pp; English.
XX
CC   The present invention describes an annealing control primer (ACP) (I) for
CC   improving the annealing specificity in nucleic acid amplification. (I)
CC   has a 3'-end portion with a nucleotide sequence complementary to a site
CC   on a template nucleic acid for hybridisation, a 5'-end portion having a
CC   pre-selected arbitrary nucleotide sequence, and a regulator portion
CC   between the 3' and 5'-end portions, comprising a universal or non-
CC   discriminatory base analogue, where the regulator portion is capable of
CC   regulating an annealing portion of the primer in association with
CC   annealing temperature. (I) is useful for improving annealing specificity
CC   in nucleic acid amplification. (I) is useful for amplifying a nucleic
CC   acid sequence from a DNA or a mixture of nucleic acids, for selectively
CC   amplifying a target nucleic acid sequence from a DNA, and for selectively
CC   amplifying a target nucleic acid sequence from a mRNA, by reverse
CC   transcribing the mRNA and performing an amplification reaction using (I).
CC   (I) is also useful for detecting DNA complementary to differentially
CC   expressed mRNA in two or more nucleic acid samples, by reverse
CC   transcribing the mRNA and performing an amplification reaction using (I).
CC   (I) is also useful for rapidly amplifying a target cDNA fragment
CC   comprising a cDNA region corresponding to the 3'-end or 5'-end region of
CC   an mRNA, for amplifying a population of full-length double-stranded cDNAs
CC   complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs
CC   complementary to mRNA. (I) is also useful for amplifying more than one
CC   target nucleotide sequence simultaneously using more than one pair of
CC   primers in the same reaction, where the primers are derived from (I), for
CC   producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
CC   fingerprint of an mRNA sample, identifying conserved homology segments in
CC   a multigene family from an mRNA sample, and for identifying conserved
CC   homology segments in a multigene family from gDNA. (I) is also useful for
CC   identifying a nucleotide variation in a target nucleic acid, and for
CC   mutagenesis in a target nucleic acid. The present sequence represents a
CC   primer which is used in the exemplification of the present invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1169
ADF44290
ID   ADF44290 standard; DNA; 15 BP.
XX
AC   ADF44290;
XX
DT   12-FEB-2004  (first entry)
XX
DE   HPV labelling 3'-end primer.
XX
KW   detection; human papillomavirus; HPV subtype; primer; ss.
XX
OS   Human papillomavirus.
XX
PN   JP2002360271-A.
XX
PD   17-DEC-2002.
XX
PF   28-NOV-2001; 2001JP-00362595.
XX
PR   04-MAY-2001; 2001TW-00110785.
XX
PA   (KING-) KING CAR FOOD IND CO LTD.
XX
DR   WPI; 2003-600935/57.
XX
PT   A detecting apparatus and a detecting method for identifying the subtypes
PT   of many species of human papilloma viruses at the same time and a
PT   composition for the detection.
XX
PS   Example 1; SEQ ID NO 647; 166pp; Japanese.
XX
CC   This invention describes a novel detecting apparatus for identifying the
CC   subtypes of human papillomaviruses (HPV) contained in a sample which
CC   comprises a carrier which can load sample, a first oligonucleotide loaded
CC   on first part of the carrier and a second oligonucleotide loaded on
CC   second part of carrier, in which first and second oligonucleotides
CC   hybridise with the DNA of the first and the second HPV subtype and can
CC   identify HPV subtype contained in sample at the same time. This sequence
CC   represents a labelling primer used in the method of the invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1170
AAD63523
ID   AAD63523 standard; DNA; 15 BP.
XX
```

AC AAD63523;
XX
DT 12-FEB-2004 (first entry)
XX
DE Chicken heparanase DNA specific PCR primer.
XX
KW Chicken; heparanase; tumour cell metastasis; inflammation; autoimmunity;
KW wound healing; angiogenesis; restenosis; Genstmann-Straussler Syndrome;
KW neurodegenerative disease; atherosclerosis; Creutzfeldt-Jakob disease;
KW infection; Scrapie; Alzheimer's disease; protein therapy; cytostatic;
KW immunosuppressive; vulnerary; bactericide; anti-angiogenic; virucide;
KW antisclerotic; neuroprotective; protozoacide; PCR; primer; ss.
XX
OS Gallus gallus.
XX
PN US2003180788-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2003; 2003US-00431438.
XX
PR 20-SEP-2000; 2000US-00666390.
PR 16-AUG-2001; 2001US-00930218.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
XX
DR WPI; 2003-843931/78.
XX
PT Recombinant jungle red fowl (Gallus gallus) heparanase protein, useful
PT for treating cancers, microbial infections and aiding wound healing.
XX
PS Example; Page 13; 0pp; English.
XX
CC The present invention relates to novel jungle red fowl heparanase protein
CC and polynucleotides encoding such proteins. Heparanase sequences can be
CC used to develop treatments for various diseases, to develop diagnostic
CC assays for these diseases and to provide new tools for basic and directed
CC research especially in the fields of medicine and biology. They can be
CC used to develop new drugs to inhibit tumour cell metastasis, inflammation
CC and autoimmunity. Recombinant heparanase offers a potential treatment for
CC wound healing, angiogenesis, restenosis, atherosclerosis, inflammation,
CC neurodegenerative diseases (e.g. Genstmann-Straussler Syndrome, Scrape,
CC Creutzfeldt-Jakob disease and Alzheimer's disease) and certain viral and
CC some bacterial and protozoa infections. Recombinant heparanase can also
CC be used to neutralise plasma heparin, as a potential replacement of
CC protamine. Sequences of the invention are used in protein therapy. The
CC present sequence is chicken heparanase DNA specific PCR primer used in
CC the exemplification of the invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1171
ADF91234
ID ADF91234 standard; DNA; 15 BP.
XX
AC ADF91234;
XX
DT 26-FEB-2004 (first entry)
XX
DE cDNA synthesis associated primer.
XX
KW RNA repair; exon; outron; RNA trans-splicing; tumour cell; cell-death;
KW genetic defect; ss; primer.
XX
OS Unidentified.
XX
PN WO2003016537-A2.
XX
PD 27-FEB-2003.
XX
PF 13-AUG-2002; 2002WO-EP009082.
XX
PR 13-AUG-2001; 2001DE-01039492.
XX
PA (AESC-) AESCU LIFE GMBH.
PA (EULJ/) EUL J.
XX
PI Eul J;
XX
DR WPI; 2003-268335/26.
XX
PT Repairing mutated exons in pre-mRNA, useful e.g. for treatment of tumors,
PT by expressing, in a cell, repair DNA that replaces mutated exon by trans-
PT splicing.
XX
PS Disclosure; Fig R; 114pp; German.
XX
CC This invention describes a novel method of repairing a mutated exon (mE)
CC in the pre-mRNA of a mammalian cell. The method comprises introducing
CC into the cell a DNA (I) that encodes repair RNA (II) in the form of a pre
CC -mRNA (III) comprises a non-mutated exon (nmE) with at least one flanking
CC outron so that mE is exchanged for nmE, via RNA trans-splicing, using
CC splice components naturally present in the cell. The invention also
CC discloses DNA, encoding trans-splicing RNA that comprises an origin of
CC replication, an RNA polymerase-II promoter and a 3'-terminal signal for
CC polyadenylation of pre-mRNA, selective killing of tumour cells in a cell
CC population, identifying potential trans-splicing sites in cellular pre-
CC mRNA and subsequent identification of natural, cellular trans-spliced RNA
CC and identifying trans-splicing sites in cellular mRNA. The nucleic acid
CC of the invention produces a repair RNA containing a 5'-outron and/or 3'-
CC outron with at least 10 nucleotides (nt). Each outron has at least one
CC antisense sequence that pairs, in antisense, over a length of at least 18
CC bases to mE and/or to an intron region that flanks mE. Especially the
CC antisense part of the 5'-outron pairs to the intronic polypyrimidine
CC sequence of a 3'-splice site in mE, while that of the 3'-outron pairs to
CC the intronic sequence of a 5'-splice site. Especially the 5'-outron
CC comprises a branch-A site, a polypyrimidine stretch and an AG
CC dinucleotide at the border of the repair exon, while the 3'-outron
CC includes a GU dinucleotide at the border of this exon. The repair exon
CC comprises, apart from the wild-type sequence, a 3-mer, 3'-sequence as
CC exonic splice site, provided that the exon follows an outron, optionally
CC also an exonic splice enhancer site which does not introduce
CC additional/altered amino acids. Alternatively, the nucleic acid encodes a
CC truncated cell-death pre-mRNA that includes a frame shift sequence (up to
CC nt) at the 5'-end, also a recognition site for a cellular protease; it
CC then has a 5'-outron that hybridises to specific tumour cell pre-mRNA or
CC it is a probe pre-mRNA of 150-250 nt, if no protein-encoding sequences
CC are present in the exon, or several hundred nt if such sequences are
CC present. It also includes a single 5'- or 3'-splice site and,
CC accordingly, an exon or outron, where the outron includes a sequence of
CC 12-18 uracils and an 8-12-mer recognition/cleavage site for a restriction
CC enzyme. The trans-spliced RNA is amplified by cDNA-PCR (polymerase chain
CC reaction), and the products sequenced in the region that represents the
CC unknown cellular RNA. Further PCR analysis is performed using primers
CC that hybridise to two, predetermined, previously sequenced, exonic
CC fragments of the two trans-spliced RNAs. Natural cellular trans-spliced
CC RNAs are identified by PCR analysis if two specific trans-spliceable
CC cellular RNAs form, in vivo , a detectable trans-spliced hybrid. The
CC primers used for analysis hybridise to previously sequenced exonic
CC fragments from the trans-spliced RNA probes. The method is used for
CC selective killing of tumour cells and for identifying potential trans-
CC splicing sites in cellular pre-mRNAs and subsequently, natural, cellular
CC trans-spliced mRNAs. The method can correct genetic defects that cause
CC disease.

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1172
ADG88842
ID ADG88842 standard; DNA; 15 BP.
XX
AC ADG88842;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human hpa cDNA amplifying RT-PCR primer, oligo (dT)15.
XX
KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KW RT-PCR; reverse transcription; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003161823-A1.
XX
PD 28-AUG-2003.
XX
PF 14-JAN-2003; 2003US-00341582.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-IL000830.
PR 19-NOV-2001; 2001US-00988113.
XX
PA (ILAN/) ILAN N.
PA (VLOD/) VLODAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
XX
PI Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
DR WPI; 2003-897910/82.
XX
PT Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.
XX
PS Disclosure; SEQ ID NO 5; 143pp; English.
XX
CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa cDNA amplifying RT-PCR
CC primer.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1173
ABZ37501
ID ABZ37501 standard; DNA; 15 BP.
XX
AC ABZ37501;
XX
DT 18-FEB-2003 (first entry)
XX
DE Oligonucleotide SEQ ID NO:622.
XX
KW Library; cleavage; display; diverse family; ss.
XX
OS Synthetic.
XX
PN WO200283872-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012405.
XX
PR 17-APR-2001; 2001US-00837306.
PR 24-OCT-2001; 2001US-00000516.
PR 25-OCT-2001; 2001US-00045674.
XX
PA (LADN/) LADNER R C.
PA (COHE/) COHEN E H.
PA (NAST/) NASTRI H G.
PA (ROOK/) ROOKEY K L.
PA (HOET/) HOET R.
PA (HOOG/) HOOGENBOOM H R J M.
XX
PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
PI Hoogenboom HRJM;
XX
DR WPI; 2003-093015/08.
XX
PT Cleaving single-stranded nucleic acid sequences at a desired location by
PT contacting the nucleic acid with an single strand oligonucleotide
PT complementary to a nucleic acid region where cleavage is desired.
XX
PS Disclosure; Page 481; 485pp; English.
XX
CC The present invention describes a method for cleaving single-stranded
CC nucleic acid sequences at a desired location. Also described: (1) methods
CC for displaying or expressing a member of a diverse family of peptides,
CC polypeptides or proteins on the surface of a genetic package and
CC collectively displaying at least a part of the diversity of the family,
CC where the displayed or expressed peptide, polypeptide or protein is
CC encoded at least in part by a nucleic acid that has been cleaved at a
CC desired location; (2) a method for preparing single-stranded nucleic
CC acids; (3) a method for preparing a library comprising a collection of
CC genetic packages that display a member of a diverse family of peptides,
CC polypeptides or proteins and that collectively display at least a portion
CC of the family; (4) a vector comprising a DNA sequence encoding an
CC antibody variable region linked to a version of PIII anchor which does
CC not mediate infection of phage particles, and wild-type gene III; (5) a
CC method for producing a population or a library of immunoglobulin genes;
CC and (6) a library of immunoglobulins that comprise members having at
CC least one variable domain in which at least one of CDR1 and CDR2 contain
CC synthetic diversity and CDR3 diversity is captured from B cells. The
CC method is useful for cleaving single-stranded nucleic acid sequences at a
CC desired location, which can be subsequently used to produce libraries or
CC genetic packages that display and/or express a diverse family of
CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to
CC ABP55499 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1174
ADG28662
ID   ADG28662 standard; DNA; 15 BP.
XX
AC   ADG28662;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Annealing control primer Oligo dT15 used to amplify murine Esx1 RNA.
XX
KW   annealing control primer; ACP; deoxyinosine; murine; mouse; ss; PCR;
KW   primer; Esx1; Oligo dT15; RT-PCR.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO2003093509-A1.
XX
PD   13-NOV-2003.
XX
PF   01-MAY-2002; 2002WO-KR000816.
XX
PR   01-MAY-2002; 2002WO-KR000816.
XX
PA   (SEEG-) SEEGENE INC.
XX
PI   Chun JY;
XX
DR   WPI; 2004-022665/02.
XX
PT   New annealing control primer capable of improving primer annealing
PT   specificity in association with the alteration of primer annealing
PT   temperature, useful for selectively amplifying a target nucleic acid
PT   sequence.
XX
PS   Example 2; SEQ ID NO 54; 137pp; English.
XX
CC   The invention relates to a novel annealing control primer (ACP) capable
CC   of improving primer annealing specificity in association with the
CC   alteration of primer annealing temperature comprising 3' and 5'-end
CC   portions separated by at least 2 deoxyinosine residues, universal bases
CC   or non-discriminatory base analogues. The annealing control primer of the
CC   invention may be useful for selectively amplifying a target nucleic acid
CC   sequence from a nucleic acid molecule or mixture of nucleic acids, for
CC   detecting DNA complementary to differentially expressed mRNA in two or
CC   more nucleic acid samples or for amplifying a population of full-length
CC   double-stranded cDNAs complementary to mRNAs using annealing control
CC   primers. The current sequence is that of the annealing control primer of
CC   the invention which was used to amplify a murine sequence.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1175
ADH70349/c
ID   ADH70349 standard; DNA; 15 BP.
XX
AC   ADH70349;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #139.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 543; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 15 BP; 7 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATAT 2409
              ||||||||||||||||
Db         15 TATATATACATATAT 1
```

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RESULT 1176
ADH70351/c
ID   ADH70351 standard; DNA; 15 BP.
XX
AC   ADH70351;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human Vbeta gene repeat sequence #141.
XX
KW   human; T-cell associated disease; Vbeta; autoimmune disease;
KW   degenerative nervous system disease; graft versus host disease;
KW   hypersensitivity disease; infectious disease; neoplastic disease;
KW   Addison's disease; atrophic gastritis;
KW   degenerative nervous system disease; multiple sclerosis;
KW   Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW   allergy; type II hypersensitivity; Goodpasture's syndrome;
KW   type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW   HIV; fungal infection; Candida; parasitic infection; schistosome;
KW   filaria; bacterial infection; Mycobacterium; neoplastic disease;
KW   lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW   breast cancer; ds.
XX
OS   Homo sapiens.
XX
PN   US2002150891-A1.
XX
PD   17-OCT-2002.
XX
PF   05-MAR-1999;   99US-00263959.
XX
PR   19-SEP-1994;   94US-00309335.
PR   19-SEP-1995;   95US-00531241.
XX
PA   (HOOD/) HOOD L E.
PA   (ROWE/) ROWEN L.
XX
PI   Hood LE,  Rowen L;
XX
DR   WPI; 2004-059052/06.
XX
PT   Kit for diagnozing and treating T-cell associated diseases e.g.
PT   autoimmune, degenerative nervous system and infectious disease, comprises
PT   nucleic acid primers specifically priming and allowing amplification of a
PT   Vbeta gene.
XX
PS   Disclosure; SEQ ID NO 545; 164pp; English.
XX
CC   The invention relates to a kit for diagnosing and treating T-cell
CC   associated diseases which comprises a panel of nucleic acid primers
CC   specifically priming and allowing amplification of each Vbeta gene,
CC   VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC   rejection and diagnosing and treating T-cell associated diseases
CC   including autoimmune diseases, degenerative nervous system diseases,
CC   graft versus host disease, hypersensitivity diseases, infectious diseases
CC   and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC   atrophic gastritis. Degenerative nervous system diseases include multiple
CC   sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
CC   I hypersensitivities such as contact with allergens that lead to
CC   allergies, Type II hypersensitivities such as those present in
CC   Goodpasture's syndrome and Type IV hypersensitivities such as those
CC   manifested in leprosy. Infectious diseases include viral infections
CC   caused by viruses such as HIV, fungal infections such as those caused by
CC   the yeast genus Candida, parasitic infections such as those caused by
CC   schistosomes, filaria and bacterial infections such as those caused by
CC   Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC   such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC   breast. The present sequence represents a Vbeta gene repeat sequence.
XX
SQ   Sequence 15 BP; 7 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2395 TATATATACATATAT 2409
              |||||||||||||||
Db         15 TATATATACATATAT 1


RESULT 1177
ADH50577/c
ID   ADH50577 standard; DNA; 15 BP.
XX
AC   ADH50577;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Bacterial DNA primer, SEQ ID No 428.
XX
KW   non-viral organism; detection; purulent infection; bacteraemia;
KW   meningitis; endocarditis; neonatal meningitis;
KW   inflammatory intestinal disease; endocarditis; respiratory diphtheria;
KW   pneumonia; abscess; oral infection; festering nasopharyngitis; mouth;
KW   urinary track; deep infection; arthritis; enteritis; diarrhoea; brain;
KW   respiratory; male reproductive; bite wound; otitis media;
KW   acute appendicitis; aphtha; mycosis; probe; ss.
XX
OS   Unidentified.
XX
PN   WO2003095677-A1.
XX
PD   20-NOV-2003.
XX
PF   09-MAY-2003; 2003WO-KR000923.
XX
PR   09-MAY-2002; 2002KR-00025561.
PR   09-MAY-2002; 2002KR-00025562.
PR   09-MAY-2002; 2002KR-00025566.
PR   09-MAY-2002; 2002KR-00025567.
PR   09-MAY-2002; 2002KR-00025569.
PR   09-MAY-2002; 2002KR-00025579.
PR   09-MAY-2002; 2002KR-00025580.
PR   09-MAY-2002; 2002KR-00025582.
PR   09-MAY-2002; 2002KR-00025583.
PR   09-MAY-2002; 2002KR-00025634.
PR   09-MAY-2002; 2002KR-00025687.
PR   28-AUG-2002; 2002KR-00051054.
PR   25-JAN-2003; 2003KR-00005082.
PR   27-JAN-2003; 2003KR-00005341.
PR   27-JAN-2003; 2003KR-00005342.
PR   27-JAN-2003; 2003KR-00005344.
XX
PA   (MEDI-) MEDIGENES.
XX
PI   Lee S,  Chang K,  Yoo S,  Yoo S,  Keum K,  Yoo N,  Yoo W,  Lee G;
PI   Kim J;
XX
DR   WPI; 2004-012140/01.
XX
PT   New nucleic acid molecule, useful for preparing a composition for
PT   diagnosing diseases caused by non-viral organisms, e.g., Acinetobacter
PT   baumannii, Bacteroides fragilis, Cardiobacterium hominis or Clostridium
PT   ramosum.
XX
PS   Example 8; SEQ ID NO 428; 135pp; English.
XX
CC   The invention relates to a novel detection method of non-viral organisms.
CC   The invention further relates to a novel isolated nucleic acid molecule
CC   which has a fully defined sequence comprising 1830-5502 bp. The detection
CC   method comprises a kit, which contains: a composition comprising the
CC   nucleic acid probe; a pair of forward and reverse primers used for
CC   amplifying the polynucleic acids in the biological sample; a buffer
CC   enabling hybridization reaction between the probes contained in the
```

CC composition and the polynucleic acids present in the biological sample or
CC their amplified products or components necessary for producing the buffer
CC ; a solution for washing hybrids; and optionally means for detection of
CC the hybrids. The novel nucleic acid is useful for preparing a composition
CC for diagnosing diseases caused by non-viral organisms, e.g.,
CC Acinetobacter baumannii, Anaerobiospirillum succiniciproducens,
CC Bacteroides fragilis, Cardiobacterium hominis, Chryseobacterium
CC meningosepticum, Clostridium ramosum, Corynebacterium diphtheriae,
CC Klebsiella oxytoca, Ochrobactrum anthropi, Peptostreptococcus prevotii,
CC Porphyromonas gingivalis, Peptostreptococcus anaerobius,
CC Peptostreptococcus magnus, Fusobacterium necrophorum, Proteus vulgaris,
CC Enterobacter aerogenes, Streptococcus mutans, Kingella kingap,
CC Bacteroides ovatus, Bacteroides thetaiotaomicron, Clostridium diffcile,
CC Hemophilus aphrophilas, Neiserria gonorrhea, Eikenella corrodens,
CC Bacteroides vulgatus, Branhamella catarrhalis, Sutterella wadsworthensis,
CC Actinomyces israelii, Staphylococcus epidermidis, Burkholderia cepacia,
CC Salmonella enteritidis, Escherichia coli, Klebsiella pneumoniae, Proteus
CC mirabilis, Streptococcus pneumoniae, Vibrio vulnificus, Pseudomas
CC aeruginosa, Aeromonas hydrophila, Listeria monocytogenes, Enterococcus
CC faecium, Staphylococcus aureus, Neiserria meningitidis, Legionella
CC pneumophila, Candida albicans or Candida glabrata. These non-viral
CC organisms can cause, but are not limited to, disorders such as: purulent
CC infection, bacteraemia, meningitis, endocarditis, neonatal meningitis,
CC inflammatory intestinal diseases, endocarditis, respiratory diphtheria,
CC pneumonia, abscesses, oral infection, festering nasopharyngitis, mouth
CC infection, urinary track infection, deep infection, arthritis, enteritis,
CC diarrhoea, localised brain or respiratory infection, male reproductive
CC disorder, bite wounds, otitis media, acute appendicitis, aphtha, and
CC mycosis. This polynucleotide sequence represents a primer used in the
CC exemplification of the invention.
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 15 TTTTTTTTTTTTTTT 1

RESULT 1178
ADI34486
ID ADI34486 standard; DNA; 15 BP.
XX
AC ADI34486;
XX
DT 22-APR-2004 (first entry)
XX
DE Nucleotide sequence of an oligo dT15.
XX
KW Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
OS Synthetic.
XX
PN WO2003102243-A1.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-US017103.
XX
PR 31-MAY-2002; 2002US-0384454P.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Kamme FC, Zhu JY;
XX
DR WPI; 2004-035466/03.
XX
PT Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT RNA transcription from a polynucleotide template, comprises eliminating
PT single-stranded oligonucleotide from the transcription sample.
XX
PS Example 1; SEQ ID NO 5; 26pp; English.
XX
CC The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction.
CC Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
CC transcription reaction.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1179
ADL16374
ID ADL16374 standard; DNA; 15 BP.
XX
AC ADL16374;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase cDNA isolation primer Oligo (dT)15.
XX
KW Heparanase; ss; PCR; primer; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation.
XX
OS Synthetic.
XX
PN US2003236215-A1.
XX
PD 25-DEC-2003.
XX
PF 09-JUN-2003; 2003US-00456573.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2004-070610/07.
XX
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
PS Example; SEQ ID NO 5; 108pp; English.
XX
CC The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridisable in vivo , under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method

```
CC   of treating a subject suffering from a pathological condition
CC   (characterised by heparanase activity, comprising administering ASO to
CC   the subject), a pharmaceutical composition comprising the ASO and a
CC   carrier, an antisense nucleic acid construct (comprising a promoter
CC   sequence and a polynucleotide sequence directing the synthesis of an
CC   antisense RNA sequence of at least 10 bases being hybridisable in vivo ,
CC   under physiological conditions, with a polynucleotide strand encoding a
CC   polypeptide having heparanase catalytic activity), a method of in vivo
CC   downregulating heparanase activity (comprising administering in vivo the
CC   antisense nucleic acid construct), a pharmaceutical composition
CC   comprising the antisense nucleic acid construct and a carrier, and an
CC   antisense oligonucleotide comprising a polynucleotide or a polynucleotide
CC   analogue of at least 10 bases being hybridisable in vivo , under
CC   physiological conditions, with a portion of a polynucleotide strand being
CC   characterised by forming at least a portion of an untranslated region
CC   (UTR) for a polynucleotide strand encoding a polypeptide having
CC   heparanase catalytic activity. The methods and compositions of the
CC   present invention are useful for the prevention and/or treatment of
CC   diseases or conditions associated with aberrant heparanase activity, such
CC   as heparanase-dependent cancer, cancer, autoimmune reaction and
CC   inflammation. The present sequence is a PCR primer used in the isolation
CC   of human heparanase cDNA.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1180
ADM48711
ID   ADM48711 standard; DNA; 15 BP.
XX
AC   ADM48711;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human hp3 DNA amplifying RT-PCR primer.
XX
KW   Transgenic animal; heparanase; cancer; viral infection; restenosis;
KW   neurodegenerative disease; atherosclerosis; pulmonary disorder; hp3;
KW   RT-PCR; reverse transcription; primer; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2003217375-A1.
XX
PD   20-NOV-2003.
XX
PF   24-FEB-2003; 2003US-00371218.
XX
PR   31-AUG-1998;   98WO-US017954.
PR   01-MAR-1999;   99US-00258892.
PR   06-FEB-2001; 2001US-00776874.
PR   19-NOV-2001; 2001US-00988113.
XX
PA   (ZCHA/) ZCHARIA E.
PA   (VLOD/) VLODAVSKY I.
PA   (METZ/) METZGER S.
PA   (PECK/) PECKER I.
PA   (ILAN/) ILAN N.
PA   (CHAJ/) CHAJEK-SHAUL T.
PA   (GOLD/) GOLDSHMIDT O.
XX
PI   Zcharia E,  Vlodavsky I,  Metzger S,  Pecker I,  Ilan N;
PI   Chajek-Shaul T,  Goldshmidt O;
XX
DR   WPI; 2004-021918/02.
XX
PT   New transgenic non-human animal expressing heparinase, useful as models
PT   for human disease, such as cancers, viral infection, neurodegenerative
PT   diseases, restenosis, atherosclerosis and pulmonary disorders.
XX
PS   Example; SEQ ID NO 5; 106pp; English.
XX
CC   The present invention relates to a transgenic non-human animal whose
CC   genome comprises an exogenous polynucleotide sequence, including a
CC   promoter active in tissues of the non-human, a region encoding a human
CC   heparanase, where the promoter and the region encoding human heparanase
CC   are operably linked in the exogenous polynucleotide such that human
CC   heparanase is expressed in at least a portion of the cells of the non-
CC   human animal. The methods and compositions of the present invention are
CC   useful for the production of transgenic animals expressing heparanase, to
CC   be used as models for human diseases such as cancers, viral infection,
CC   restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC   disorders. The present sequence is human hp3 DNA amplifying (reverse
CC   transcription) RT-PCR primer used in the exemplification of the
CC   invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1181
ADL33722
ID   ADL33722 standard; DNA; 15 BP.
XX
AC   ADL33722;
XX
DT   03-JUN-2004  (first entry)
XX
DE   LNA oligomer #1.
XX
KW   Detection; isolation; locked nucleic acid; LNA; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "LNA thymidine analog"
FT   modified_base   4
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "LNA thymidine analog"
FT   modified_base   7
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "LNA thymidine analog"
FT   modified_base   10
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "LNA thymidine analog"
FT   modified_base   13
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "LNA thymidine analog"
XX
PN   WO2004020575-A2.
XX
PD   11-MAR-2004.
XX
PF   20-JUN-2003; 2003WO-IB006354.
```

XX
PR 24-JUN-2002; 2002US-0390928P.
XX
PA (EXIQ-) EXIQON AS.
XX
PI Kauppinen S, Jacobsen N;
XX
DR WPI; 2004-315512/29.
XX
PT Detecting and/or isolating nucleic acid molecule having homopolymeric
PT sequence or repetitive element or conserved nucleotide sequence involves
PT treating sample containing nucleic acid compounds with locked nucleic
PT acid oligonucleotide.
XX
PS Disclosure; Page 17; 104pp; English.
XX
CC The present invention relates to a method (M1) for detecting and/or
CC isolating a nucleic acid having a homopolymeric sequence or repetitive
CC element or conserved nucleotide sequence. (M1) comprises treating a
CC sample containing nucleic acid compounds with an locked nucleic acid
CC (LNA) oligonucleotide (LO) to thereby detect and/or isolate a nucleic
CC acid having the homopolymeric sequence or repetitive element or conserved
CC nucleotide sequence. (M1) is useful for detecting and isolating nucleic
CC acids released from a lysed complex biological mixture comprising nucleic
CC acids. The present sequence is a LNA oligomer, used to illustrate the
CC invention.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1182
ADO81112
ID ADO81112 standard; DNA; 15 BP.
XX
AC ADO81112;
XX
DT 29-JUL-2004 (first entry)
XX
DE Sheep prion protein microsatellite locus primer #83.
XX
KW gene typing; polymorphic microsatellite loci; PML;
KW disease predisposition; microsatellite marker; prion disease;
KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
KW microsatellite; PCR; primer; ss.
XX
OS Ovis aries.
XX
PN DE10236711-A1.
XX
PD 26-FEB-2004.
XX
PF 09-AUG-2002; 2002DE-01036711.
XX
PR 09-AUG-2002; 2002DE-01036711.
XX
PA (UYHO-) UNIV HOHENHEIM.
XX
PI Geldermann H, Preuss S, Han Y;
XX
DR WPI; 2004-215730/21.
XX
PT Typing genes that contain polymorphic microsatellite loci, useful for
PT identifying predisposition to disease, by amplification and determining
PT length of amplicons.
XX
PS Example 3; Page 31; 64pp; German.
XX
CC The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PML, using
CC as template a DNA sample containing at least one segment of (I); and
CC determining the length of the resulting amplicon(s). Also described are:
CC a method of determining (M2) microsatellite markers (MM) for
CC predisposition to a disease, associated with a gene that includes one or
CC more PML; and prediagnosis (M3) of diseases associated with gene that
CC include PML. The method is used to identify microsatellite markers, in a
CC disease-related gene, that are associated with a predisposition to
CC diseases and for prediagnosis of such diseases, especially prion diseases
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC metabolic diseases; also to type genes that encode milk proteins,
CC hormones or transcription factors. The method is simpler, quicker and
CC particularly less expensive than known methods based on sequencing. This
CC sequence represents a primer used to genotype a region of the sheep prion
CC protein (PrP) comprising a polymorphic microsatellite locus.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1183
ADO81158
ID ADO81158 standard; DNA; 15 BP.
XX
AC ADO81158;
XX
DT 29-JUL-2004 (first entry)
XX
DE Prion protein polymorphic microsatellite marker consensus sequence #36.
XX
KW gene typing; polymorphic microsatellite loci; PML;
KW disease predisposition; microsatellite marker; prion disease;
KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
KW microsatellite; ds.
XX
OS Synthetic.
XX
PN DE10236711-A1.
XX
PD 26-FEB-2004.
XX
PF 09-AUG-2002; 2002DE-01036711.
XX
PR 09-AUG-2002; 2002DE-01036711.
XX
PA (UYHO-) UNIV HOHENHEIM.
XX
PI Geldermann H, Preuss S, Han Y;
XX
DR WPI; 2004-215730/21.
XX
PT Typing genes that contain polymorphic microsatellite loci, useful for
PT identifying predisposition to disease, by amplification and determining
PT length of amplicons.
XX
PS Claim 9; Page 50; 64pp; German.
XX
CC The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PML, using

```
CC   as template a DNA sample containing at least one segment of (I); and
CC   determining the length of the resulting amplicon(s). Also described are:
CC   a method of determining (M2) microsatellite markers (MM) for
CC   predisposition to a disease, associated with a gene that includes one or
CC   more PML; and prediagnosis (M3) of diseases associated with gene that
CC   include PML. The method is used to identify microsatellite markers, in a
CC   disease-related gene, that are associated with a predisposition to
CC   diseases and for prediagnosis of such diseases, especially prion diseases
CC   but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC   metabolic diseases; also to type genes that encode milk proteins,
CC   hormones or transcription factors. The method is simpler, quicker and
CC   particularly less expensive than known methods based on sequencing. This
CC   sequence represents a prion protein polymorphic microsatellite marker
CC   consensus sequence.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1184
ADO81108
ID   ADO81108 standard; DNA; 15 BP.
XX
AC   ADO81108;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Sheep prion protein microsatellite locus primer #79.
XX
KW   gene typing; polymorphic microsatellite loci; PML;
KW   disease predisposition; microsatellite marker; prion disease;
KW   cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW   milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
KW   microsatellite; PCR; primer; ss.
XX
OS   Ovis aries.
XX
PN   DE10236711-A1.
XX
PD   26-FEB-2004.
XX
PF   09-AUG-2002; 2002DE-01036711.
XX
PR   09-AUG-2002; 2002DE-01036711.
XX
PA   (UYHO-) UNIV HOHENHEIM.
XX
PI   Geldermann H,  Preuss S,  Han Y;
XX
DR   WPI; 2004-215730/21.
XX
PT   Typing genes that contain polymorphic microsatellite loci, useful for
PT   identifying predisposition to disease, by amplification and determining
PT   length of amplicons.
XX
PS   Example 3; Page 31; 64pp; German.
XX
CC   The invention describes a method of typing (M1) a gene (I) that has one
CC   or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC   amplification of at least one DNA region of (I) that includes PML, using
CC   as template a DNA sample containing at least one segment of (I); and
CC   determining the length of the resulting amplicon(s). Also described are:
CC   a method of determining (M2) microsatellite markers (MM) for
CC   predisposition to a disease, associated with a gene that includes one or
CC   more PML; and prediagnosis (M3) of diseases associated with gene that
CC   include PML. The method is used to identify microsatellite markers, in a
CC   disease-related gene, that are associated with a predisposition to
CC   diseases and for prediagnosis of such diseases, especially prion diseases
CC   but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC   metabolic diseases; also to type genes that encode milk proteins,
CC   hormones or transcription factors. The method is simpler, quicker and
CC   particularly less expensive than known methods based on sequencing. This
CC   sequence represents a primer used to genotype a region of the sheep prion
CC   protein (PrP) comprising a polymorphic microsatellite locus.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1185
ADO78367
ID   ADO78367 standard; RNA; 15 BP.
XX
AC   ADO78367;
XX
DT   26-AUG-2004  (first entry)
XX
DE   RNA oligonucleotide of the invention.
XX
KW   ss; 2'-O-Silyloxymethyl ribonucleotide derivative;
KW   automated oligoribonucleotides solid phase synthesis;
KW   oligonucleotide preparation.
XX
OS   Synthetic.
XX
PN   WO2004049274-A2.
XX
PD   10-JUN-2004.
XX
PF   21-NOV-2003; 2003WO-EP013113.
XX
PR   22-NOV-2002; 2002GB-00027352.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
XX
PI   Natt FJ,  Hunziker J,  Hall J,  Martin P;
XX
DR   WPI; 2004-460864/43.
XX
PT   New 2'-O-silyloxymethyl ribonucleotide derivatives useful in automated
PT   oligoribonucleotides solid phase synthesis.
XX
PS   Example 3; Page 15; 20pp; English.
XX
CC   The invention relates to novel 2'-O-Silyloxymethyl ribonucleotide
CC   derivatives. The derivatives are useful in automated oligoribonucleotides
CC   solid phase synthesis. The derivatives provide cost effective and easier
CC   synthesis processing for the preparation of oligonucleotides. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||:|||||||||
Db          1 TTTTTUTTTTTTTTT 15
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RESULT 1186
ADO78368
ID   ADO78368 standard; RNA; 15 BP.
XX
AC   ADO78368;
XX
DT   26-AUG-2004  (first entry)
XX
DE   RNA oligonucleotide of the invention.
XX
KW   ss; 2'-O-Silyloxymethyl ribonucleotide derivative;
KW   automated oligoribonucleotides solid phase synthesis;
KW   oligonucleotide preparation.
XX
OS   Synthetic.
XX
PN   WO2004049274-A2.
XX
PD   10-JUN-2004.
XX
PF   21-NOV-2003; 2003WO-EP013113.
XX
PR   22-NOV-2002; 2002GB-00027352.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
XX
PI   Natt FJ,  Hunziker J,  Hall J,  Martin P;
XX
DR   WPI; 2004-460864/43.
XX
PT   New 2'-O-silyloxymethyl ribonucleotide derivatives useful in automated
PT   oligoribonucleotides solid phase synthesis.
XX
PS   Example 3; Page 15; 20pp; English.
XX
CC   The invention relates to novel 2'-O-Silyloxymethyl ribonucleotide
CC   derivatives. The derivatives are useful in automated oligoribonucleotides
CC   solid phase synthesis. The derivatives provide cost effective and easier
CC   synthesis processing for the preparation of oligonucleotides. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 7.5e+02;
  Matches   11;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||::::||||||
Db          1 TTTTTUUUUTTTTTT 15


RESULT 1187
ADQ81798
ID   ADQ81798 standard; DNA; 15 BP.
XX
AC   ADQ81798;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Oligonucleotide synthesis method polynucleotide #2.
XX
KW   ss; primer; DNA synthesis; nucleotide chemistry.
XX
OS   Synthetic.
XX
PN   WO2004058794-A1.
XX
PD   15-JUL-2004.
XX
PF   31-DEC-2002; 2002WO-EP014905.
XX
PR   31-DEC-2002; 2002WO-EP014905.
XX
PA   (PROL-) PROLIGO LLC.
XX
PI   Arar K;
XX
DR   WPI; 2004-553145/53.
XX
PT   Synthesis of oligonucleotides in nucleotide chemistry involves providing
PT   solid support of anchor group protected by orthogonal protective group,
PT   removing the protective group, synthesizing an oligonucleotide followed
PT   by capping and cleaving.
XX
PS   Example 9; SEQ ID NO 13; 77pp; English.
XX
CC   The present invention relates to a method for the synthesis of at least
CC   two different oligonucleotides, which involves providing a solid support
CC   comprising anchor groups that are protected by at least two orthogonal
CC   protective groups, removing one of the protective groups from the anchor
CC   groups, synthesizing an oligonucleotide on the deprotected anchor groups,
CC   capping the synthesized oligonucleotide, repeating these steps until all
CC   of anchor groups are deprotected, and cleaving the synthesized
CC   oligonucleotides. The method can be used for the synthesis of at least
CC   two different oligonucleotides, in the field of nucleotide chemistry, in
CC   applying the required pairs of oligonucleotide primers, several probes at
CC   a time, duplexed nuclei acid fragments (including PCR, sequencing,
CC   multiplexed genotyping, cloning and RNA interference), for applying to
CC   any known methods for the solid phase synthesis of oligonucleotides
CC   (including phosphoramidite chemistry, H-phosphonate chemistry,
CC   phosphotriester chemistry, or any other synthetic chemistry used to
CC   prepare oligonucleotides on solid supports). The present sequence is a
CC   polynucleotide used to demonstrate the method of the invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1188
AAX18365
ID   AAX18365 standard; DNA; 16 BP.
XX
AC   AAX18365;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 6.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
```

```
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTG 15


RESULT 1189
AAX18366
ID   AAX18366 standard; DNA; 16 BP.
XX
AC   AAX18366;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 7.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTG 15


RESULT 1190
AAX18367
ID   AAX18367 standard; DNA; 16 BP.
XX
AC   AAX18367;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 8.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4502 TTTTTTTTTTTTTTG 4516
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTG 15


RESULT 1191
AAX07568/c
ID   AAX07568 standard; cDNA; 16 BP.
XX
AC   AAX07568;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.
XX
```

```
KW   Secreted protein; fetal kidney; ds.
XX
OS   Homo sapiens.
XX
PN   WO9900405-A1.
XX
PD   07-JAN-1999.
XX
PF   29-JUN-1998;   98WO-US013530.
XX
PR   30-JUN-1997;   97US-00885610.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
PI   Evans C,  Agostino MJ;
XX
DR   WPI; 1999-095671/08.
XX
PT   New polynucleotides encoding secreted human proteins - are derived from
PT   foetal kidney or adult retina cDNA libraries, used as, e.g. potential
PT   vaccines.
XX
PS   Disclosure; Page 54; 76pp; English.
XX
CC   The sequence is that of the 3' end of a sequence encoding a secreted
CC   protein from a human fetal kidney clone AK296. Such a sequence is
CC   predicted to have biological activities which would make them suitable
CC   for treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, cytokine and cell
CC   proliferation/differentiation activity, immune stimulating (e.g. as
CC   vaccines) or suppressing activity, haematopoiesis regulating activity,
CC   tissue growth activity, activin/inhibin activity,
CC   chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC   receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC   invasion suppressor activity, and tumour inhibition activity. It is also
CC   stated to be useful for gene therapy
XX
SQ   Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 1192
AAC66068/c
ID   AAC66068 standard; DNA; 16 BP.
XX
AC   AAC66068;
XX
DT   22-FEB-2001  (first entry)
XX
DE   DNA chip primer #4.
XX
KW   DNA chip; primer; nucleoside derivative; photolabile protecting group;
KW   photolithographic nucleic acid chip; ss.
XX
OS   Synthetic.
XX
PN   WO200061594-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-DE001148.
XX
PR   08-APR-1999;   99DE-01015867.
PR   28-JAN-2000; 2000DE-01003631.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Beier M,  Hoheisel J;
XX
DR   WPI; 2000-679457/66.
XX
PT   New nucleoside derivatives with photolabile protecting groups, useful in
PT   oligonucleotide synthesis, particularly on solid phases, e.g. for
PT   hybridization testing.
XX
PS   Disclosure; Fig 9; 48pp; German.
XX
CC   This invention describes nucleoside derivatives (I) with photolabile
CC   protecting groups. (I) are used to synthesize oligonucleotides using the
CC   photolithographic nucleic acid chip method, particularly where these are
CC   intended for performing enzymatic reactions initiated from a free 3'-
CC   hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC   but also reverse transcription, cDNA synthesis etc.), also for
CC   hybridization testing, sequencing and in DNA computing. (I) are produced
CC   with high selectivity by reaction with a mild acylating agent that has
CC   high specificity for the 3'-position, without significant side-reactions
CC   (cf. more reactive acylating agents such as chloroformates)
XX
SQ   Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 1193
ABA04585
ID   ABA04585 standard; DNA; 16 BP.
XX
AC   ABA04585;
XX
DT   15-FEB-2002  (first entry)
XX
DE   Oligonucleotide #5.
XX
KW   Analytical support; genomic sequencing; mutation detection;
KW   pharmaceutical development; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
FT                   and PO is a phosphate group"
XX
PN   FR2805348-A1.
XX
PD   24-AUG-2001.
XX
PF   23-FEB-2000; 2000FR-00002236.
XX
PR   23-FEB-2000; 2000FR-00002236.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI   Cuzin M,  Peltie P,  Fontecave M,  Decout JL,  Dueymes C;
XX
DR   WPI; 2001-628265/73.
XX
PT   Support for hybridization analysis of nucleic acids for sequencing
PT   techniques, comprises an array of oligonucleotides having a label where
```

```
PT   the fluorescence changes follow hybridization.
XX
PS   Example 1; Page 12; 33pp; French.
XX
CC   The present invention relates to an analytical support, to which a number
CC   of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC   fluorescent compound, the fluorescence of which varies when the
CC   oligonucleotide hybridises to its complement. The analytical support is
CC   useful in hybridisation testing for identification of specific nucleic
CC   acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC   development. The present oligonucleotide was used to illustrate the
CC   invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1194
AAF30895
ID   AAF30895 standard; DNA; 16 BP.
XX
AC   AAF30895;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide-minor groove binder complex.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "thymine modified by a minor groove binder (2-
FT                   dimethylaminonaphthalene-6- sulfonamide"
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 101; 105pp; English.
XX
CC   The present sequence is that of an oligonucleotide (ODN)-minor groove
CC   binder (MGF) complex. MGBs bind in a non-intercalating manner to the
CC   minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF
CC   conjugates of the invention also comprise a latent fluorophore (LF),
CC   which binds similarly to the MGB but in an intercalating manner, or lies
CC   in the minor groove, or is oriented in some other way to the DNA molecule
CC   by MGB, such that it becomes fluorescent (or its fluorescent properties
CC   change detectably). The conjugates are used as hybridisation probes and
CC   amplification primers for fluorescent detection of specifically
CC   hybridising sequences, for analysis or diagnosis, especially (real-time)
CC   PCR, for single-nucleotide mismatch discrimination, target or signal
CC   amplification, array-based assays and sequencing, including detection of
CC   double-stranded DNA by triplex formation
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1195
AAF30880
ID   AAF30880 standard; DNA; 16 BP.
XX
AC   AAF30880;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 58; 105pp; English.
XX
CC   The present sequence is that of the oligonucleotide (ODN) component of an
CC   ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC   invention. MGBs bind in a non-intercalating manner to the minor groove of
CC   non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC   but in an intercalating manner, or lies in the minor groove, or is
CC   oriented in some other way to the DNA molecule by MGB, such that it
CC   becomes fluorescent (or its fluorescent properties change detectably).
CC   The conjugates are used as hybridisation probes and amplification primers
CC   for fluorescent detection of specifically hybridising sequences, for
CC   analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC   mismatch discrimination, target or signal amplification, array-based
CC   assays and sequencing, including detection of double-stranded DNA by
CC   triplex formation. Many different targets can be detected a single
CC   reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC   hybridisation-triggered fluorescence. Upon hybridisation to the
CC   complementary target sequence there was an increase in fluorescence
CC   yield, measured as the ratio of the fluorescence emitted by the hybrid
CC   between the ODN-MGB-LF conjugate and its target sequence to the
CC   fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC   of 8.3
XX
```

```
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1196
AAH42481
ID   AAH42481 standard; DNA; 16 BP.
XX
AC   AAH42481;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Oligonucleotide used to produce branched chain compounds.
XX
KW   Branched chain compound; nucleic acid synthesis; primer extension;
KW   reverse transcription; nucleic acid hybridization;
KW   nucleic acid amplification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "COOH attached"
FT   misc_feature    2. .3
FT                   /*tag=  c
FT                   /note= "branch present"
FT   modified_base   2
FT                   /*tag=  b
FT                   /note= "COOH attached"
XX
PN   EP1111068-A1.
XX
PD   27-JUN-2001.
XX
PF   21-DEC-1999;   99EP-00125484.
XX
PR   21-DEC-1999;   99EP-00125484.
XX
PA   (LION-) LION BIOSCIENCE AG.
PA   (VBCG-) VBC GENOMICS GMBH.
XX
PI   Schmidt W,  Hiller R,  Huber M,  Mueller M;
XX
DR   WPI; 2001-466959/51.
XX
PT   Branched compounds useful in e.g. nucleic acid synthesis reaction
PT   comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS   Example 1; Page 10; 31pp; English.
XX
CC   The specification describes branched compounds containing nucleic acid
CC   moieties optionally extended by a polymerase. The branched chain
CC   compounds of the invention are used in nucleic acid synthesis reaction,
CC   primer extension reaction, reverse transcription reaction of RNA into
CC   DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC   nucleic acid), and nucleic acid amplification experiment (for analysing
CC   the expression pattern of genes). The compounds are also used in solid-
CC   phase enzymatic reactions. The present sequence was used in the course of
CC   the invention to produce branched chain compounds
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1197
ABL57075/c
ID   ABL57075 standard; DNA; 16 BP.
XX
AC   ABL57075;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .16
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 5-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2
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RESULT 1198
ABA97402
ID   ABA97402 standard; DNA; 16 BP.
XX
AC   ABA97402;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX
KW   Protein nucleic acid molecule; PNA; ds.
XX
OS   Synthetic.
XX
PN   WO200168673-A1.
XX
PD   20-SEP-2001.
XX
PF   13-MAR-2001; 2001WO-US008111.
XX
PR   14-MAR-2000; 2000US-0189190P.
PR   30-NOV-2000; 2000US-0250334P.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeacon J;
PI   Chakhmakhcheau O,  Buryakova A,  Choob M,  Hondorp K;
XX
DR   WPI; 2002-041177/05.
XX
PT   Oligonucleotides analogs useful in detection, separation and purification
PT   of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS   Example 17; Page 118; 197pp; English.
XX
CC   This invention relates to oligonucleotide analogues comprising a protein
CC   nucleic acid molecule (PNA) monomer. They are used in the detection and
CC   separation of nucleic acid molecules and as probes, primers, linkers,
CC   adapters and antisense agents on solid supports. Modifications enhance
CC   their use as capture and detection probes e.g. by the incorporation of
CC   biotin, digoxigenen, radioisotopes, fluorescent labels such as
CC   fluorescein and reporter molecules such as alkaline phosphatase. They are
CC   also used for enhancing or inhibiting the activity of an enzyme or
CC   cellular activity. The compounds are stable to nucleases and proteases,
CC   have high affinity, binding specificity and solubility. The polyamide
CC   backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC   nucleic acid molecules with greater affinity than DNA or RNA
CC   concentration. The compounds are relatively simple to synthesize and are
CC   used in a wide variety of applications. This sequence represents a DNA
CC   oligomer which is used to represent the thermal stability of the
CC   oligomers of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1199
ABK87931
ID   ABK87931 standard; DNA; 16 BP.
XX
AC   ABK87931;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Anchored oligo-dT primer, H-T11G, used for differential display.
XX
KW   Human; PCR; primer; H-T11G; ss; CC214; cervical cancer 2; HCCR-2;
KW   protooncogene; cytostatic; tumourigenesis; cervical cancer; cancer;
KW   leukaemia; lymphoma; antisense; gene therapy; carcinogen; anticancer;
KW   antioxidant.
XX
OS   Synthetic.
XX
PN   WO200244370-A1.
XX
PD   06-JUN-2002.
XX
PF   09-JUL-2001; 2001WO-KR001172.
XX
PR   28-NOV-2000; 2000KR-00071202.
XX
PA   (KIMJ/) KIM J W.
XX
PI   Kim JW;
XX
DR   WPI; 2002-557542/59.
XX
PT   Novel human cervical cancer 2 protooncogene protein and polynucleotide
PT   encoding it useful for diagnosing various cancers e.g. leukemia, lymphoma
PT   or uterine cervix cancer, and for producing transformed animals.
XX
PS   Disclosure; Page 47; 49pp; English.
XX
CC   The invention discloses a human cervical cancer 2 (HCCR-2) protooncogene
CC   and encoded protein. The protooncogene was discovered using mRNA
CC   differential display, identifying it as being amplified in cancer cells
CC   and, more specifically, involved in the tumourigenesis of cervical
CC   cancer. HCCR-2 is useful for preventing, diagnosing or treating cancer,
CC   including leukaemia, lymphoma, colon, breast, kidney, stomach, lung,
CC   ovary or uterine cervix cancer. HCCR-2 is also useful for producing
CC   antibodies which are useful as diagnostic tools. HCCR-2 protooncogene is
CC   useful in the diagnosis of various cancers, in antisense gene therapy and
CC   for producing transformed animals which are useful in screening for
CC   carcinogens or anticancer agents, such as antioxidants. The protooncogene
CC   is also useful for establishing a continuous viable cancer cell line
CC   which is useful in searching for anticancer agents. The sequence
CC   presented is the anchored oligo-dT primer, H-T11G, which was used to
CC   amplify cDNA for differential display. This technique identified a cDNA
CC   fragment, designated CC214, which was then used as a probe to isolate the
CC   full length cDNA (cervical cancer 2 (HCCR-2) protooncogene) from a human
CC   lung embryonic fibroblast cDNA library
XX
SQ   Sequence 16 BP; 2 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4498 AAGTTTTTTTTTTTT 4512
              |||||||||||||||
Db          1 AAGTTTTTTTTTTTT 15


RESULT 1200
AAD56451
ID   AAD56451 standard; DNA; 16 BP.
XX
AC   AAD56451;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
```

```
FH   Key             Location/Qualifiers
FT   modified_base   1. .16
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature    8. .9
FT                   /*tag= b
FT                   /note= "Bases 8 and 9 are linked by two secouridine
FT                   linkers which is represented as S in page 49 and X in
FT                   page 57 and Fig 7 and 8 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1201
AAL54078
ID   AAL54078 standard; DNA; 16 BP.
XX
AC   AAL54078;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Oligo-homodeoxyribonucleotide sequence, oligo dT.
XX
KW   Detection; single-stranded sensor; detectable fluorescence emission;
KW   forensic testing; paternity testing; tissue typing; hereditary disorder;
KW   human population genetics; human evolutionary history; cystic fibrosis;
KW   human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
OS   Unidentified.
XX
PN   WO200284271-A2.
XX
PD   24-OCT-2002.
XX
PF   16-APR-2002; 2002WO-US012176.
XX
PR   16-APR-2001; 2001US-00836579.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CHAJ/) CHA J N.
XX
PI   Cha JN,  Morse DE,  Stucky GD;
XX
DR   WPI; 2003-103378/09.
XX
PT   Detecting polynucleotides, for pharmacogenetic testing, comprises
PT   contacting a target polynucleotide with a complementary single-stranded
PT   sensor polynucleotide and an agent that allows the sensor to fluoresce
PT   upon excitation.
XX
PS   Example 1; Page 25; 41pp; English.
XX
CC   The invention relates to a novel assay for detecting a polynucleotide in
CC   a sample, which comprises: contacting a sample suspected of containing a
CC   target polynucleotide with a predetermined single-stranded sensor
CC   polynucleotide complementary to the target polynucleotide, in a solution
CC   comprising an agent that is a nonaqueous solvent that allows the sensor
CC   polynucleotide to produce a detectable fluorescence emission; exciting
CC   the sensor polynucleotide; and determining fluorescence emission. The
CC   assay is useful for detecting a single or double-stranded target
CC   polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
CC   wide variety of different applications including pharmacogenetic testing,
CC   forensic testing to identify the species or individual which was the
CC   source of a forensic specimen, in anthropological setting, paternity
CC   testing, testing for compatibility between prospective tissue or blood
CC   donors and patients and in screening for hereditary disorders. The method
CC   is also useful to study alterations of gene expression in response to a
CC   stimulus, disease, drug or medication, and other applications include
CC   human population genetics, analyses of human evolutionary history and
CC   characterisation of human haplotype diversity. The method is useful for
CC   detecting polynucleotide sequences from contaminants or pathogens
CC   including bacteria, yeast, and viruses to detect single nucleotide
CC   polymorphisms, which may be associated with particular alleles or subsets
CC   of alleles. The method is useful for detection of mutations and to detect
CC   nucleotide sequences associated with increased risk of diseases or
CC   disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
CC   This polynucleotide sequence represents an oligonucleotide sequence used
CC   in a fluorescence technique of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1202
AAD57845/c
ID   AAD57845 standard; DNA; 16 BP.
XX
AC   AAD57845;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
```

```
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20-B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 1203
ADB68508
ID   ADB68508 standard; DNA; 16 BP.
XX
AC   ADB68508;
XX
DT   04-DEC-2003  (first entry)
XX
DE   PNA-HypNA hybridisation oligomer.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
KW   phosphono-peptide nucleic acid; pPNA.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = P (Phosphono PNA monomer with phenyl
FT                   group attached to terminal phosphate"
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 17; Page 148; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the PNA-HypNA hybridisation oligomer of the invention. This
CC   sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
CC   (SerNA) components.
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1204
ADB68519
ID   ADB68519 standard; DNA; 16 BP.
XX
AC   ADB68519;
XX
DT   04-DEC-2003  (first entry)
XX
DE   DNA hybridisation oligomer SEQ ID 9.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "Optional N-terminal acetyl"
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
```

```
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 17; Page 233; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC   sequence may also comprise a peptide nucleic acid (PNA).
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1205
ADF23331/c
ID   ADF23331 standard; DNA; 16 BP.
XX
AC   ADF23331;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Binding partner sceening method molecular beacon analogue #2.
XX
KW   binding partner screening; light beam; nonlinear optical light beam; ss;
KW   molecular beacon analogue.
XX
OS   Synthetic.
XX
PN   US2003148391-A1.
XX
PD   07-AUG-2003.
XX
PF   06-JUN-2002; 2002US-00164915.
XX
PR   24-JAN-2002; 2002US-0351879P.
PR   06-FEB-2002; 2002US-0354668P.
PR   06-FEB-2002; 2002US-0354679P.
PR   05-MAR-2002; 2002US-0362003P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-897567/82.
XX
PT   Screening of candidate binding partners for binding to test molecule
PT   comprises illuminating sample with light beams and measuring physical
PT   properties of nonlinear optical light beam emanating from sample.
XX
PS   Disclosure; SEQ ID NO 2; 58pp; English.
XX
CC   The invention describes screening a candidate binding partner by
CC   illuminating the sample with light beams at fundamental frequencies to
CC   binding partners, and measuring physical properties of a nonlinear
CC   optical light beam emanating from sample. On binding to the test molecule
CC   the properties change relative to that in absence of exposure of the test
CC   molecule. The invention is used in the screening of candidate binding
CC   partners for binding to test molecule. This sequence represents a
CC   molecular beacon analogue, an exemplary test molecule of the invention.
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 1206
ADI34487
ID   ADI34487 standard; DNA; 16 BP.
XX
AC   ADI34487;
XX
DT   22-APR-2004  (first entry)
XX
DE   Nucleotide sequence of an oligo dT16.
XX
KW   Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO2003102243-A1.
XX
PD   11-DEC-2003.
XX
PF   30-MAY-2003; 2003WO-US017103.
XX
PR   31-MAY-2002; 2002US-0384454P.
XX
PA   (JANC ) JANSSEN PHARM NV.
XX
PI   Kamme FC,  Zhu JY;
XX
DR   WPI; 2004-035466/03.
XX
PT   Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT   RNA transcription from a polynucleotide template, comprises eliminating
PT   single-stranded oligonucleotide from the transcription sample.
XX
PS   Example 1; SEQ ID NO 6; 26pp; English.
XX
CC   The invention relates to amplifying for RNA in a sample comprises
CC   eliminating single-stranded oligonucleotide from the transcription
CC   sample. The method involves synthesizing single-stranded cDNA by
CC   incubating the sample RNA with reverse transcriptase and an
CC   oligonucleotide primer that primes synthesis in a direction toward 5' end
CC   of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC   to form a transcription sample containing a cDNA template; eliminating
CC   single-stranded oligonucleotide from the transcription sample; and
CC   transcribing the cDNA template into RNA using an RNA polymerase. The
CC   method is useful for improving RNA polymerase based RNA transcription
CC   from a polynucleotide template. The method inhibits the undesired non-
CC   template derived production of RNA in the transcription reaction.
CC   Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
CC   transcription reaction.
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1207
AAX69800
ID   AAX69800 standard; RNA; 17 BP.
XX
AC   AAX69800;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 8.4e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             :::::::::::::::
Db          2 UUUUUUUUUUUUUUU 16


RESULT 1208
AAX69801
ID   AAX69801 standard; RNA; 17 BP.
XX
AC   AAX69801;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 8.4e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1209
AAX72892/c
ID   AAX72892 standard; RNA; 17 BP.
XX
AC   AAX72892;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #325.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
```

```
OS   Mus sp.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 132; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 5 A; 5 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4708 CTGGGCAAGTCACTT 4722
              |||||||||||||||
Db         15 CTGGGCAAGTCACTT 1


RESULT 1210
AAX69802
ID   AAX69802 standard; RNA; 17 BP.
XX
AC   AAX69802;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 8.4e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1211
AAX18371
ID   AAX18371 standard; DNA; 17 BP.
XX
AC   AAX18371;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 12.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
```

```
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1212
AAX18370
ID   AAX18370 standard; DNA; 17 BP.
XX
AC   AAX18370;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 11.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1213
AAZ89372
ID   AAZ89372 standard; DNA; 17 BP.
XX
AC   AAZ89372;
XX
DT   15-JUN-2000  (first entry)
XX
DE   RNA detecting primer #2.
XX
KW   Amplification; detection; gene expression; primer; ss.
XX
OS   Unidentified.
XX
PN   DE19840731-A1.
XX
PD   09-MAR-2000.
XX
PF   07-SEP-1998;   98DE-01040731.
XX
PR   07-SEP-1998;   98DE-01040731.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX
DR   WPI; 2000-257789/23.
XX
PT   Analysis of RNA samples, useful for detection of differential gene
PT   expression uses two differently labeled primers.
XX
PS   Disclosure; Page 10; 10pp; German.
XX
CC   This invention describes a novel method for analysis of an RNA sample
CC   which comprises amplifying cDNA with first and second differently labeled
CC   primers and analysis of the amplified labeled cDNA. The method is useful
CC   for analyzing differential gene expression, for identifying and/or
CC   characterizing pharmacological activities or for identifying target
CC   genes. The use of different primer combinations allow more cDNAs to be
CC   amplified. The method also provides a more detailed analysis than prior
CC   art methods. This sequence represents a primer used to illustrate the
CC   method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1214
AAZ36739
ID   AAZ36739 standard; DNA; 17 BP.
XX
AC   AAZ36739;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Anchored oligo(dT) primer AT15A used for modified differential display.
XX
KW   Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW   differentially expressed nucleic acid; disease state; cancer;
KW   autoimmune disease; infectious disease; aging; developmental disorder;
KW   proliferative disorder; neurological disorder; toxicity; primer;
KW   treatment resistance; differential expression; drug discovery;
KW   growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS   Synthetic.
XX
PN   WO9955913-A2.
XX
PD   04-NOV-1999.
```

XX
PF 27-APR-1999; 99WO-US009119.
XX
PR 27-APR-1998; 98US-0083331P.
PR 27-AUG-1998; 98US-0098070P.
PR 04-FEB-1999; 99US-0118624P.
XX
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI Mcclelland M, Welsh J, Trenkle T;
XX
DR WPI; 2000-086388/07.
XX
PT Measuring expression of low abundance reduced complexity target nucleic
PT acid molecules.
XX
PS Example 3; Page 91; 187pp; English.
XX
CC AAZ36739-41 represent oligo(dT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in a
CC target. The method comprises contacting a probe with an arbitrarily or
CC statistically sampled target and detecting the amount of specific binding
CC of the target to the probe. The methods can be used to identify
CC differentially expressed nucleic acid molecules associated with disease
CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery
XX
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 1215
AAA25450
ID AAA25450 standard; DNA; 17 BP.
XX
AC AAA25450;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1216
AAA25453
ID AAA25453 standard; DNA; 17 BP.
XX
AC AAA25453;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4502 TTTTTTTTTTTTTTG 4516
||||||||||||||||
Db 1 TTTTTTTTTTTTTTG 15

RESULT 1217
AAA98232
ID AAA98232 standard; DNA; 17 BP.
XX
AC AAA98232;
XX
DT 30-JAN-2001 (first entry)
XX
DE Human retrovirus HERV LTR PCR primer #31.
XX
KW Cell-specific expression; tissue-specific expression; gene therapy; LTR;
KW U3-R segment; long terminal repeat; retroviral expression vector;
KW PCR primer; ss.
XX
OS Human endogenous retrovirus.
XX
PN WO200053789-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-EP002064.
XX
PR 10-MAR-1999; 99DE-01010650.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI Leib-Moesch C, Schoen U, Baust C;
XX
DR WPI; 2000-587442/55.
XX
PT Retroviral expression vector, useful in gene therapy, contains a promoter
PT from a human endogenous retrovirus to provide cell-specific expression.
XX
PS Disclosure; Page 27; 67pp; German.
XX
CC This invention describes a novel retroviral expression vector (A)
CC containing DNA sequences (I) for packaging vector RNA and for cell-
CC specific expression of proteins or peptides encoding by heterologous DNA
CC (II). The sequences controlling cell-specific expression contain a cell-
CC specifically regulatable promoter region (P) from a human endogenous
CC retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
CC RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
CC eukaryotic cells containing (A) in integrated form; (d) virions
CC containing a retroviral expression vector RNA derived from (A); (e) a
CC method for producing the virions of (d); (f) a method for incorporating
CC protein-encoding nucleic acid sequences into a eukaryotic cell by
CC infection with the virions of (d); and (g) a retroviral vector system
CC containing (A) and a packaging cell line, that contains at least one
CC (recombinant) retrovirus construct that encodes for the packaging
CC proteins of (A). (A) are used for cell- or tissue-specific expression of
CC foreign genes for gene therapy and to produce virions for introducing
CC (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian
CC and specifically human. (A) retain the advantages of usual retroviral
CC promoters with all the signal structures required for transcription in a
CC small region within the U3-R segment, but without their disadvantages
CC (excessive strength and limited cell specificity). Since (A) are derived
CC from endogenous (harmless) viral sequences, they do not introduce any new
CC viral sequences into the genome and recombination will not create new
CC types of retrovirus. The promoters provide cell or tissue specific
CC expression, according to which HERV they are derived from
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
|||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1218
AAA50197
ID AAA50197 standard; DNA; 17 BP.
XX
AC AAA50197;
XX
DT 07-NOV-2000 (first entry)
XX
DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.
XX
KW Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .19
FT /*tag= a
FT /note= "2'-methoxyethoxy modified thymidine"
FT modified_base 1. .17
FT /*tag= b
FT /note= "phosphorothioate internucleoside linkages"
XX
PN WO200047593-A1.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US003543.
XX
PR 12-FEB-1999; 99US-00250075.
XX
PA (ISIS-) ISIS PHARM INC.
XX

PI Manoharan M, Maier MA;
XX
DR WPI; 2000-558188/51.
XX
PT Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT linkages to phosphodiester internucleoside linkages.
XX
PS Example 12; Page 34; 49pp; English.
XX
CC The present sequence is that of a phosphorothioate oligonucleotide
CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound
CC produced according to the methods of the invention. The invention
CC provides compounds and methods for the preparation of mixed backbone
CC oligomeric, or chimeric, compounds having phosphodiester internucleoside
CC linkages in addition to phosphorothioate and/or phosphoramidate
CC internucleoside linkages. The methods also include incorporation of
CC boranophosphate internucleoside linkages. The methods utilise H-
CC phosphonate intermediates that are coupled together forming contiguous
CC regions of 1 or more H-phosphonate internucleoside linkages. Each
CC contiguous region is subsequently oxidized to phosphodiester,
CC phosphorothioate, phosphoramidate or boranophosphate internucleoside
CC linkages prior to further elongation. Mixed backbone oligomeric compounds
CC are prepared in this manner by oxidizing adjacent regions with different
CC reagents. Oligomeric compounds of the invention are prepared using novel
CC oxidation steps that oxidize a region of 1 or more H-phosphonate
CC internucleoside linkages without degrading existing linkages that have
CC been previously oxidized. The oligonucleotides obtained are useful as
CC primers in PCR, probes, linkers, gene fragments and for other diagnostic
CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,
CC and as antiviral agents
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1219
ABK13941
ID ABK13941 standard; DNA; 17 BP.
XX
AC ABK13941;
XX
DT 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by FokI.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
PR 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G;
XX
DR WPI; 2002-217065/27.
XX
PT Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
PS Disclosure; Fig 2; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the production of a single pattern characteristic of a sample,
CC employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the
CC present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1220
ABK19050/c
ID ABK19050 standard; RNA; 17 BP.
XX
AC ABK19050;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG DNAzyme target sequence Seq ID No 1697.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,

PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 107; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 8 A; 4 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       4481 GAATGTATTTGATTT 4495
              |||||||||||||||
Db         16 GAATGTATTTGATTT 2
```

RESULT 1221
ABK98192
ID ABK98192 standard; DNA; 17 BP.
XX
AC ABK98192;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #52.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 25A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 13 T; 0 U; 2 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2126 TTCTTTTCTTTTTTTCT 2142
              || |||||| |||||||
Db          1 TTNTTTTCTNTTTTTCT 17
```

RESULT 1222
ABX79793
ID ABX79793 standard; cDNA; 17 BP.
XX
AC ABX79793;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #118.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX
DR WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 483; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1223
ADB04271
ID ADB04271 standard; DNA; 17 BP.
XX
AC ADB04271;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5257.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5257; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 1224
ADB04270
ID ADB04270 standard; DNA; 17 BP.
XX
AC ADB04270;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5256.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5256; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder

```
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          3 TTTTTTTTTTTTTTT 17


RESULT 1225
ABZ70578
ID   ABZ70578 standard; DNA; 17 BP.
XX
AC   ABZ70578;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Primer.
XX
KW   Aspergillus phoenices; oxalate decarboxylase; APOXD; transgenic plant;
KW   crop protection; primer; ss.
XX
OS   Synthetic.
XX
PN   CA2350328-A1.
XX
PD   26-DEC-2002.
XX
PF   26-JUN-2001; 2001CA-02350328.
XX
PR   26-JUN-2001; 2001CA-02350328.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Scelonge C,  Bidney D;
XX
DR   WPI; 2003-248733/25.
XX
PT   New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT   phoenices, for degrading oxalic acid, identifying transformed plant
PT   cells, and preventing pathogenic disease in plants.
XX
PS   Disclosure; Page 50; 60pp; English.
XX
CC   The present sequence is that of a primer used in the invention. The
CC   invention relates to a novel nucleic acid (see ABZ70560) encoding
CC   Aspergillus phoenices oxalate decarboxylase (APOXD) (see ABP72475). The
CC   gene and its encoded protein are useful in degrading oxalate, in
CC   diagnostic assays, for protecting plants against disease, and as a
CC   selectable marker
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 1226
AAD56441
ID   AAD56441 standard; DNA; 17 BP.
XX
AC   AAD56441;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    9. .10
FT                   /*tag=  a
FT                   /note= "Bases 9 and 10 are linked by a butanediol linker
FT                   which is represented as B in page 49 and X in page 59,
FT                   Fig 9 and 10 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Page 90; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1227
AAD56448
ID   AAD56448 standard; DNA; 17 BP.
XX
AC   AAD56448;
```

```
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature    9. .10
FT                   /*tag=  b
FT                   /note= "Bases 9 and 10 are linked by a butanediol linker
FT                   which is represented as B in page 49 and Fig 5 and as X
FT                   in page 52, 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1228
AAD56449
ID   AAD56449 standard; DNA; 17 BP.
XX
AC   AAD56449;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature    12. .13
FT                   /*tag=  b
FT                   /note= "Bases 12 and 13 are linked by a butanediol linker
FT                   which is represented as B in page 49 and Fig 5 and as X
FT                   in page 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1229
AAD56447
ID   AAD56447 standard; DNA; 17 BP.
XX
AC   AAD56447;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
```

```
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature    4. .5
FT                   /*tag=  b
FT                   /note= "Bases 4 and 5 are linked by a butanediol linker
FT                   which is represented as B in page 49 and Fig 5 and as X
FT                   in page 55 and Fig 6 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 5; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1230
AAD56450
ID   AAD56450 standard; DNA; 17 BP.
XX
AC   AAD56450;
XX
DT   07-AUG-2003  (first entry)
XX
DE   2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.
XX
KW   Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW   antisense; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT   misc_feature    9. .10
FT                   /*tag=  b
FT                   /note= "Bases 9 and 10 are linked by a secouridine linker
FT                   which is represented as S in page 49 and X in page 57 and
FT                   Fig 1, 2, 7 and 8 of the specification"
XX
PN   WO2003037909-A1.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-CA001628.
XX
PR   29-OCT-2001; 2001US-0330719P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Damha MJ,  Viazovkina E,  Mangos MM,  Parniak MA,  Min K;
XX
DR   WPI; 2003-421516/39.
XX
PT   Novel acyclic linker-containing oligonucleotide useful for preventing or
PT   decreasing translation, reverse transcription and/or replication of a
PT   target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS   Example 2; Fig 7; 104pp; English.
XX
CC   The invention relates to an acyclic linker-containing oligonucleotide
CC   comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC   the invention are useful for preventing or decreasing translation,
CC   reverse transcription and/or replication of a target RNA in a system.
CC   They are useful for selectively preventing gene expression in a sequence-
CC   specific manner, for hybridising to complementary RNA such as cellular
CC   mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC   RNA. They are also useful therapeutically in formulations or medicaments
CC   to prevent or treat a disease characterised by the expression of a
CC   particular target RNA. The invention is used in gene therapy. The present
CC   sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC   H degradation of target RNA. This sequence is used in the exemplification
CC   of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1231
ADB98902
ID   ADB98902 standard; DNA; 17 BP.
XX
AC   ADB98902;
XX
DT   04-DEC-2003  (first entry)
XX
DE   LRP5 mutagenic PCR primer #21.
XX
KW   Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW   bone mass modulation; osteoporosis; PCR; primer; ss.
XX
```

OS Synthetic.
XX
PN WO200292000-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX
DR WPI; 2003-129214/12.
XX
PT New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
PS Disclosure; Page 53; 629pp; English.
XX
CC The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4062 AGGCTGAGGGCCCCA 4076
||||||||||||||||
Db 1 AGGCTGAGGGCCCCA 15

RESULT 1232
ACF36345
ID ACF36345 standard; DNA; 17 BP.
XX
AC ACF36345;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA fragment.
XX
KW Gene variant identification; restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX
PN WO2003064689-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000255.
XX
PR 29-JAN-2002; 2002US-0352245P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Lonnerberg P, Oldin M, Linnarsson S, Ernfors P;
XX
DR WPI; 2003-627619/59.
XX
PT Determining polyadenylation sites within transcribed gene sequences
PT present in a sample comprises assigning to gene fragments gene candidates
PT within a database by comparing signals in the dataset with the database.
XX
PS Example; Fig 3; 81pp; English.
XX
CC The invention relates to determining the presence of and/or identifying a
CC polyadenylation site within a sequence of a transcribed gene or variants
CC present in a sample. The method involves assigning to gene fragments gene
CC candidates within a database by comparing signals in the dataset with the
CC database, the database comprising data representing mRNAs with known
CC polyA sites and/or 'virtual genes' representing a possible
CC polyadenylation site within an actual gene. The method is useful for
CC determining the presence of and/or identifying a polyadenylation site or
CC alternative polyadenylation sites within a sequence of a transcribed gene
CC or sequences of transcribed gene variants present or potentially present
CC in a sample, in identifying gene features, particularly in identifying
CC differences between sequence variants that occur in a population of
CC nucleic acid molecules, especially in identifying or discovering polyA
CC site usage or determining polyA site usage in a nucleic acid sample, and
CC gene variants arising from alternative polyA sites. The present sequence
CC represents a double stranded product DNA fragment
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
|||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1233
ACF36370
ID ACF36370 standard; DNA; 17 BP.
XX
AC ACF36370;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW electrophoresis; type II restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX
PN WO2003064691-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000843.
XX
PR 29-JAN-2002; 2002US-0352215P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
PI Montelius A;
XX
DR WPI; 2003-618365/58.
XX
PT Producing a population of double-stranded product DNA molecules, useful
PT for mRNA profiling, comprises amplification by nested polymerase chain
PT reaction.
XX
PS Example; Fig 2; 105pp; English.
XX
CC The invention relates to producing a population of double-stranded
CC product DNA molecules comprising amplification by a nested PCR method.

```
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   double stranded product DNA, which aids in outlining an approach to
CC   production of a single pattern characteristic of a sample, employing a
CC   type II restriction enzyme (FokI)
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1234
ADI34488
ID   ADI34488 standard; DNA; 17 BP.
XX
AC   ADI34488;
XX
DT   22-APR-2004  (first entry)
XX
DE   Nucleotide sequence of an oligo dT17.
XX
KW   Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO2003102243-A1.
XX
PD   11-DEC-2003.
XX
PF   30-MAY-2003; 2003WO-US017103.
XX
PR   31-MAY-2002; 2002US-0384454P.
XX
PA   (JANC ) JANSSEN PHARM NV.
XX
PI   Kamme FC,  Zhu JY;
XX
DR   WPI; 2004-035466/03.
XX
PT   Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT   RNA transcription from a polynucleotide template, comprises eliminating
PT   single-stranded oligonucleotide from the transcription sample.
XX
PS   Example 1; SEQ ID NO 7; 26pp; English.
XX
CC   The invention relates to amplifying for RNA in a sample comprises
CC   eliminating single-stranded oligonucleotide from the transcription
CC   sample. The method involves synthesizing single-stranded cDNA by
CC   incubating the sample RNA with reverse transcriptase and an
CC   oligonucleotide primer that primes synthesis in a direction toward 5' end
CC   of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC   to form a transcription sample containing a cDNA template; eliminating
CC   single-stranded oligonucleotide from the transcription sample; and
CC   transcribing the cDNA template into RNA using an RNA polymerase. The
CC   method is useful for improving RNA polymerase based RNA transcription
CC   from a polynucleotide template. The method inhibits the undesired non-
CC   template derived production of RNA in the transcription reaction.
CC   Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
CC   transcription reaction.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1235
ADO04016/c
ID   ADO04016 standard; DNA; 17 BP.
XX
AC   ADO04016;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Annealing primer used to generate single-stranded labelled UNA.
XX
KW   Intramolecular base pair; intermolecular base pair;
KW   unstructured nucleic acid; UNA; molecular biology;
KW   nucleic acid chemistry; polymerse extension reaction; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   US2004086880-A1.
XX
PD   06-MAY-2004.
XX
PF   18-DEC-2002; 2002US-00324409.
XX
PR   20-JUL-1999;   99US-00358141.
PR   31-JUL-2000; 2000US-00632639.
XX
PA   (SAMP/) SAMPSON J R.
PA   (ACHR/) ACH R A.
PA   (WOLB/) WOLBER P.
XX
PI   Sampson JR,  Ach RA,  Wolber P;
XX
DR   WPI; 2004-364526/34.
XX
PT   Generating nucleic acid having reduced ability to hybridize for use in
PT   molecular biology, comprises providing nucleotide triphosphates to
PT   synthesize nucleic acid complementary to a template nucleic acid.
XX
PS   Disclosure; SEQ ID NO 16; 74pp; English.
XX
CC   The present invention provides a system for the production of nucleic
CC   acids with reduced levels of intramolecular base pairing (secondary
CC   structure) and intermolecular base pairing by generating unstructured
CC   nucleic acids (UNAs). The invention is useful for generating nucleic acid
CC   having a reduced ability to hybridise. The invention is also useful in
CC   molecular biology and nucleic acid chemistry. The present sequence is an
CC   annealing primer used to generate single-stranded labelled unstructured
CC   nucleic acid (UNA) by polymerase extension reaction (PCR). This sequence
CC   is used in the invention.
XX
SQ   Sequence 17 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         17 TTTTTTTTTTTTTTT 3


RESULT 1236
ADP71261/c
ID   ADP71261 standard; DNA; 17 BP.
XX
AC   ADP71261;
XX
DT   26-AUG-2004  (first entry)
```

```
XX
DE   Oligo #13 for gaseous sample sensor array detection method.
XX
KW   ss; sensor array system; gaseous sample; vapor sample; chemical hazard;
KW   air quality; medical condition; explosive detection; mining;
KW   hazardous chemical; odor; smell.
XX
OS   Synthetic.
XX
PN   WO2004048937-A2.
XX
PD   10-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US038186.
XX
PR   25-NOV-2002; 2002US-00303548.
PR   25-NOV-2002; 2002US-0428869P.
XX
PA   (TUFT ) UNIV TUFTS.
XX
PI   White JE,  Kauer JS;
XX
DR   WPI; 2004-487426/46.
XX
PT   Sensor array system for remote characterizing gaseous or vapor sample,
PT   has sensors having nucleic acid/fluorophore combination, measuring
PT   apparatus, transmitting device and computer having algorithm for
PT   characterizing analyte.
XX
PS   Disclosure; SEQ ID NO 11; 91pp; English.
XX
CC   The invention relates to a sensor array system for remote characterizing
CC   gaseous or vapor sample, has several sensors providing detectable signal
CC   on contacting analyte and each sensor has nucleic acid/fluorophore
CC   combination, measuring apparatus measures detectable signal, transmitting
CC   device transmits information with respect to detectable signal to remote
CC   location through internet, and computer having residential algorithm for
CC   characterizing analyte. (I) is useful in monitoring chemical hazards, air
CC   quality, and medical conditions, and detecting explosives, mines, and
CC   hazardous chemicals. (I) or (II) is useful in transmitting identified
CC   information on various odors or smells, e.g., vapor or gaseous analytes
CC   through internet. This sequence represents an oligonucleotide used in the
CC   method of the invention.
XX
SQ   Sequence 17 BP; 15 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 1237
ADP71260
ID   ADP71260 standard; DNA; 17 BP.
XX
AC   ADP71260;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Oligo #12 for gaseous sample sensor array detection method.
XX
KW   ss; sensor array system; gaseous sample; vapor sample; chemical hazard;
KW   air quality; medical condition; explosive detection; mining;
KW   hazardous chemical; odor; smell.
XX
OS   Synthetic.
XX
PN   WO2004048937-A2.
XX
PD   10-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US038186.
XX
PR   25-NOV-2002; 2002US-00303548.
PR   25-NOV-2002; 2002US-0428869P.
XX
PA   (TUFT ) UNIV TUFTS.
XX
PI   White JE,  Kauer JS;
XX
DR   WPI; 2004-487426/46.
XX
PT   Sensor array system for remote characterizing gaseous or vapor sample,
PT   has sensors having nucleic acid/fluorophore combination, measuring
PT   apparatus, transmitting device and computer having algorithm for
PT   characterizing analyte.
XX
PS   Disclosure; SEQ ID NO 10; 91pp; English.
XX
CC   The invention relates to a sensor array system for remote characterizing
CC   gaseous or vapor sample, has several sensors providing detectable signal
CC   on contacting analyte and each sensor has nucleic acid/fluorophore
CC   combination, measuring apparatus measures detectable signal, transmitting
CC   device transmits information with respect to detectable signal to remote
CC   location through internet, and computer having residential algorithm for
CC   characterizing analyte. (I) is useful in monitoring chemical hazards, air
CC   quality, and medical conditions, and detecting explosives, mines, and
CC   hazardous chemicals. (I) or (II) is useful in transmitting identified
CC   information on various odors or smells, e.g., vapor or gaseous analytes
CC   through internet. This sequence represents an oligonucleotide used in the
CC   method of the invention.
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1238
ADP86177
ID   ADP86177 standard; DNA; 17 BP.
XX
AC   ADP86177;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #48 (DNA-RNA hybrid).
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   misc_RNA         4. .17
FT                    /*tag=  b
FT                    /label= RNA
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
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XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 48; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide (DNA-RNA hrbrid).
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 1 T; 14 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   6.7%;  Pred. No. 8.4e+02;
  Matches    1;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTT 4514
              |:::::::::::::
Db          3 GUUUUUUUUUUUUU 17


RESULT 1239
ADP86146
ID   ADP86146 standard; DNA; 17 BP.
XX
AC   ADP86146;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #17.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 17; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTT 4514
              ||||||||||||||
Db          3 GTTTTTTTTTTTTT 17


RESULT 1240
ADP86154
ID   ADP86154 standard; DNA; 17 BP.
XX
AC   ADP86154;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #25.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
```

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XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 25; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 1241
ADP86178
ID   ADP86178 standard; RNA; 17 BP.
XX
AC   ADP86178;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #49.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 49; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 0 T; 17 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 8.4e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1242
ADP86185
ID   ADP86185 standard; DNA; 17 BP.
XX
AC   ADP86185;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #56 (DNA-RNA hybrid).
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   misc_RNA        2
FT                   /*tag=  b
FT                   /label= RNA
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
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```
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 56; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide (DNA-RNA hrbrid).
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 15 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 1243
ADP86145
ID   ADP86145 standard; DNA; 17 BP.
XX
AC   ADP86145;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #16.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 16; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 1244
ADP86137
ID   ADP86137 standard; DNA; 17 BP.
XX
AC   ADP86137;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #8.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
```

```
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 8; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1245
ADP86183
ID   ADP86183 standard; DNA; 17 BP.
XX
AC   ADP86183;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #54 (DNA-RNA hybrid).
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   misc_RNA         1
FT                    /*tag=  a
FT                    /label= RNA
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 54; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide (DNA-RNA hrbrid).
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 14 T; 1 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 1246
ADP86144
ID   ADP86144 standard; DNA; 17 BP.
XX
AC   ADP86144;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #15.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .17
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
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XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Example; SEQ ID NO 15; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 1247
ADP86131
ID   ADP86131 standard; DNA; 17 BP.
XX
AC   ADP86131;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #2.
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
PF   11-DEC-2003; 2003WO-US039775.
XX
PR   11-DEC-2002; 2002US-0432409P.
PR   25-SEP-2003; 2003US-0506108P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Jurk M,  Vollmer J,  Uhlmann E;
XX
DR   WPI; 2004-487902/46.
XX
PT   New oligonucleotides, useful for treating allergy or asthma, viral and
PT   bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT   cancer, cervical cancer.
XX
PS   Claim 12; SEQ ID NO 2; 104pp; English.
XX
CC   The invention relates to a class of CpG immunostimulatory
CC   oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC   are useful for stimulating an immune response. Oligonucleotides and
CC   compositions of the invention are useful for treating allergy or asthma,
CC   viral and bacterial infections and cancer e.g. biliary tract cancer,
CC   breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC   endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC   liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC   neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC   rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC   and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC   Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC   testicular cancer, as well as other carcinomas and sarcomas. The
CC   invention is also useful in gene therapy. The present sequence is a CpG
CC   immunostimulatory oligonucleotide.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4500 GTTTTTTTTTTTTTT 4514
              |||||||||||||||
Db          3 GTTTTTTTTTTTTTT 17


RESULT 1248
ADP86184
ID   ADP86184 standard; DNA; 17 BP.
XX
AC   ADP86184;
XX
DT   09-SEP-2004  (first entry)
XX
DE   CpG immunostimulatory oligonucleotide #55 (DNA-RNA hybrid).
XX
KW   CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW   viral infection; bacterial infection; cancer; lymphoma;
KW   intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW   carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   misc_RNA        3
FT                   /*tag=  b
FT                   /label= RNA
XX
PN   WO2004053104-A2.
XX
PD   24-JUN-2004.
XX
```

PF 11-DEC-2003; 2003WO-US039775.
XX
PR 11-DEC-2002; 2002US-0432409P.
PR 25-SEP-2003; 2003US-0506108P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX
DR WPI; 2004-487902/46.
XX
PT New oligonucleotides, useful for treating allergy or asthma, viral and
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.
XX
PS Example; SEQ ID NO 55; 104pp; English.
XX
CC The invention relates to a class of CpG immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and
CC compositions of the invention are useful for treating allergy or asthma,
CC viral and bacterial infections and cancer e.g. biliary tract cancer,
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC testicular cancer, as well as other carcinomas and sarcomas. The
CC invention is also useful in gene therapy. The present sequence is a CpG
CC immunostimulatory oligonucleotide (DNA-RNA hrbrid).
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 15 T; 1 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.4e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
:|||||||||||||
Db 3 UTTTTTTTTTTTTTT 17

RESULT 1249
AAQ34110/c
ID AAQ34110 standard; DNA; 18 BP.
XX
AC AAQ34110;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA60B.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 375; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
|||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1250
AAQ75025
ID AAQ75025 standard; RNA; 18 BP.
XX
AC AAQ75025;
XX
DT 25-MAR-2003 (revised)
DT 03-AUG-1995 (first entry)
XX
DE PCR primer.
XX
KW Synthetic oligo; solid phase immunoassay; ss.
XX
OS Synthetic.
XX
PN WO9426932-A1.
XX
PD 24-NOV-1994.
XX
PF 13-MAY-1994; 94WO-US005407.
XX
PR 13-MAY-1993; 93US-00061694.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Fields HA, Khudyakov YE;
XX
DR WPI; 1995-006819/01.
XX
PT Solid phase immunoassay using oligo:nucleotide as label - also new
PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT diagnosing hepatitis C or E virus infection.
XX
PS Example; Page 12; 34pp; English.
XX
CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC They are used in a method for detecting an antigen in a subject. The
CC method involves binding the antigen to a solid support and then reacting

```
CC   it with an immunoreactive ligand (L) bound to an oligo; removing any
CC   unreacted L, and then detecting the presence of the oligo. A similar
CC   method can be used to detect Abs, in which case the ligand is an oligo-
CC   labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC   to be detected at very low levels. An exemplary olgi is AAQ75024 which
CC   can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC   a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC   oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC   contain HEV Abs were immobilised on plastic tubes or wells, then
CC   incubated for 30-60 mins with the peptide-oligo proruct. The vessels were
CC   washed; bound oligo was released with 0.2M glycine and amplified in a
CC   separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC   The amplification product - AAQ75031 - was treated with uracil DNA
CC   glycoslase to remove the U18 fragment, and the product captured by
CC   immoblised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   0.0%;  Pred. No. 8.8e+02;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 1251
AAT94667
ID   AAT94667 standard; DNA; 18 BP.
XX
AC   AAT94667;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchA.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1252
AAT94668
ID   AAT94668 standard; DNA; 18 BP.
XX
AC   AAT94668;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Anchored poly(T) oligonucleotide polyT-AnchC.
XX
KW   Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW   snapdragon; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9732023-A1.
XX
PD   04-SEP-1997.
XX
PF   28-FEB-1997;   97WO-AU000124.
XX
PR   01-MAR-1996;   96AU-00008386.
XX
PA   (FLOR-) FLORIGENE LTD.
XX
PI   Brugliera F,  Holton TA,  Michael MZ;
XX
DR   WPI; 1997-448691/41.
XX
PT   Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT   corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS   Example 15; Page 59; 234pp; English.
XX
CC   Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC   (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC   region of a polyadenylation sequence. They were used to prime cDNA
CC   synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC   were also utilised in the PCR amplification of plant cytochrome P450
CC   sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC   flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC   display approach. This can be used to manipulate the pigmentation of
CC   transgenic plants
XX
SQ   Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.3%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTT 4515
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 1253
AAV37712/c
ID   AAV37712 standard; cDNA; 18 BP.
XX
AC   AAV37712;
XX
DT   25-MAR-2003  (revised)
DT   07-SEP-1998  (first entry)
XX
```

DE Human protein AQ2_1i 3'-portion and polyA tail.
XX
KW Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
KW bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i;
KW AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
XX
OS Homo sapiens.
XX
PN WO9820130-A2.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US019857.
XX
PR 01-NOV-1996; 96US-00742973.
PR 29-OCT-1997; 97US-00960024.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-286946/25.
XX
PT New secreted proteins and associated polynucleotides - obtained from
PT murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT and murine adult thymus.
XX
PS Disclosure; Page 58; 75pp; English.
XX
CC The present invention describes novel proteins isolated from cDNA clones:
CC AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; or
CC L256_1i, deposited as ATCC 98237. The present sequence represents the 3'-
CC portion of AQ2_1i isolated from a human ovary cDNA library. The proteins
CC from the present invention may be administered in a composition to
CC prevent, treat or ameliorate a medical condition. The proteins may
CC exhibit biological activities such as nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating or
CC suppressing activity, haematopoiesis regulating activity, tissue growth
CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC inflammatory activity, cadherin/tumour invasion suppressor activity,
CC tumour inhibition activity and other activities. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 18 TTTTTTTTTTTTTTT 4

RESULT 1254
AAV21970
ID AAV21970 standard; DNA; 18 BP.
XX
AC AAV21970;
XX
DT 14-JUL-1998 (first entry)
XX
DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX
KW Nuclease resistant; bacterial infection; antibiotic; target;
KW veterinary medicine; treatment; human; industrial process;
KW bacterial control; ss.
XX
OS Synthetic.
XX
PN WO9803533-A1.
XX
PD 29-JAN-1998.
XX
PF 23-JUL-1997; 97WO-US012961.
XX
PR 24-JUL-1996; 96US-00685575.
XX
PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
PI Arrow A, Dale RMK, Thompson TL;
XX
DR WPI; 1998-120687/11.
XX
PT Treating bacterial infections in humans or animals with
PT oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT with antibiotics.
XX
PS Claim 49; Page 87; 163pp; English.
XX
CC This antisense oligonucleotide is nuclease resistant and can be used in
CC the treatment of animals, including humans, having a bacterial infection.
CC The treatment comprises administration of such nuclease resistant
CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC and formulated with a carrier. A compound comprising this nuclease
CC resistant oligonucleotide can be covalently linked to an antibiotic. The
CC method is used to treat infections by a wide variety of Gram-positive and
CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC The methods are particularly used in immuno-compromised individuals (e.g.
CC patients with acquired immunodeficiency syndrome or those receiving
CC chemotherapy or radiation therapy), optionally in combination with, or
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC therapeutic use, the oligonucleotides can be used to control bacteria in
CC laboratory cultures, foods, beverages and industrial processes. The
CC oligonucleotides are specific for bacteria, without affecting metabolism
CC in mammalian cells. They may also activate RNase H and have a general,
CC non-specific immune-stimulating effect. The oligonucleotides can be
CC administered orally, intranasally, rectally, topically or by injection,
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC enhances cellular uptake
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4501 TTTTTTTTTTTTTTT 4515
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 1255
AAX19943
ID AAX19943 standard; DNA; 18 BP.
XX
AC AAX19943;
XX
DT 14-JUN-1999 (first entry)
XX
DE Primer SEQ ID NO:3 from JP11075880.
XX
KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS Synthetic.
XX
PN JP11075880-A.
XX
PD 23-MAR-1999.
XX
PF 10-JUL-1998; 98JP-00195719.
XX
PR 14-JUL-1997; 97JP-00205378.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2005, 03:27:55 ; Search time 87 Seconds
(without alignments)
376.156 Million cell updates/sec

Title: US-10-619-253-30
Perfect score: 20
Sequence: 1 tcagtgaccctgagcattct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	277	4	US-09-513-999C-734	Sequence 734, App
c	2	20	100.0	5648	4	US-09-919-172-70	Sequence 70, Appl
c	3	18.4	92.0	55927	4	US-09-949-016-15017	Sequence 15017, A
	4	16.8	84.0	4308	4	US-09-578-063-79	Sequence 79, Appl
c	5	16.8	84.0	27223	4	US-09-949-016-13036	Sequence 13036, A
	6	16.4	82.0	128	3	US-09-199-637A-109	Sequence 109, App
	7	16.4	82.0	454	4	US-09-963-137-62	Sequence 62, Appl
	8	16	80.0	101349	4	US-09-949-016-17433	Sequence 17433, A
	9	15.8	79.0	386	3	US-08-905-223-171	Sequence 171, App
	10	15.8	79.0	601	4	US-09-949-016-57688	Sequence 57688, A
	11	15.8	79.0	601	4	US-09-949-016-57689	Sequence 57689, A
	12	15.8	79.0	601	4	US-09-949-016-182711	Sequence 182711,
	13	15.8	79.0	601	4	US-09-949-016-206786	Sequence 206786,
c	14	15.8	79.0	691	4	US-09-573-080A-282	Sequence 282, App
	15	15.8	79.0	1006	4	US-09-603-208A-183	Sequence 183, App
	16	15.8	79.0	1341	4	US-09-603-208A-181	Sequence 181, App
c	17	15.8	79.0	11662	4	US-09-949-016-16978	Sequence 16978, A
	18	15.8	79.0	13187	3	US-09-422-936-61	Sequence 61, Appl
	19	15.8	79.0	17050	4	US-09-949-016-12784	Sequence 12784, A
	20	15.8	79.0	17050	4	US-09-949-016-13680	Sequence 13680, A
	21	15.8	79.0	29326	4	US-09-949-016-15356	Sequence 15356, A
c	22	15.8	79.0	47419	4	US-09-949-016-11841	Sequence 11841, A
c	23	15.8	79.0	47420	4	US-09-949-016-15484	Sequence 15484, A
c	24	15.8	79.0	63385	4	US-09-949-016-14856	Sequence 14856, A
c	25	15.8	79.0	75674	4	US-09-949-016-17597	Sequence 17597, A
c	26	15.8	79.0	98962	4	US-09-949-016-14133	Sequence 14133, A
c	27	15.8	79.0	102884	4	US-09-949-016-17100	Sequence 17100, A
	28	15.8	79.0	236474	4	US-09-949-016-13418	Sequence 13418, A
c	29	15.8	79.0	317366	4	US-09-949-016-16001	Sequence 16001, A
	30	15.8	79.0	678533	4	US-09-949-016-14577	Sequence 14577, A
	31	15.8	79.0	678533	4	US-09-949-016-14578	Sequence 14578, A
c	32	15.4	77.0	41	3	US-08-463-682-6	Sequence 6, Appli
	33	15.4	77.0	448	4	US-09-621-976-17435	Sequence 17435, A
	34	15.4	77.0	454	3	US-08-991-789A-211	Sequence 211, App
	35	15.4	77.0	454	3	US-09-062-451-211	Sequence 211, App
	36	15.4	77.0	454	3	US-09-598-326-211	Sequence 211, App
	37	15.4	77.0	454	4	US-09-289-198-211	Sequence 211, App
	38	15.4	77.0	454	4	US-09-429-755-211	Sequence 211, App
	39	15.4	77.0	454	4	US-09-699-295-211	Sequence 211, App
	40	15.4	77.0	601	4	US-09-949-016-70559	Sequence 70559, A
	41	15.4	77.0	601	4	US-09-949-016-70560	Sequence 70560, A
c	42	15.4	77.0	645	4	US-09-252-991A-16221	Sequence 16221, A
	43	15.4	77.0	960	2	US-07-841-591A-1	Sequence 1, Appli
	44	15.4	77.0	960	5	PCT-US93-02034-1	Sequence 1, Appli
c	45	15.4	77.0	1059	3	US-09-439-313-372	Sequence 372, App

ALIGNMENTS

RESULT 1
US-09-513-999C-734/c
; Sequence 734, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 734
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..275
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 213
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 249
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 250
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 49
; OTHER INFORMATION: Xaa=Ala or Ser
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 61
; OTHER INFORMATION: Xaa= * or Ala or Glu or Gly or Leu or Ser or Val
US-09-513-999C-734

Query Match 100.0%; Score 20; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        123 TCAGTGACCCTGAGCATTCT 104
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RESULT 2
US-09-919-172-70/c
; Sequence 70, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 70
; LENGTH: 5648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 464689.64
US-09-919-172-70

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  Query Match             100.0%;  Score 20;  DB 4;  Length 5648;
  Best Local Similarity   100.0%;  Pred. No. 0.99;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db       3175 TCAGTGACCCTGAGCATTCT 3156
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RESULT 3
US-09-949-016-15017/c
; Sequence 15017, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15017
; LENGTH: 55927
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(55927)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15017

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  Query Match             92.0%;  Score 18.4;  DB 4;  Length 55927;
  Best Local Similarity   95.0%;  Pred. No. 10;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              |||||||||||||||||| |||
Db      20538 TCAGTGACCCTGAGCAATCT 20519
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RESULT 4
US-09-578-063-79
; Sequence 79, Application US/09578063
; Patent No. 6764677
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A
; APPLICANT: Barnes, Thomas M
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 210147.0023/6U1
; CURRENT APPLICATION NUMBER: US/09/578,063
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Bos sp.
US-09-578-063-79

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  Query Match             84.0%;  Score 16.8;  DB 4;  Length 4308;
  Best Local Similarity   90.0%;  Pred. No. 46;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||  ||||||||||
Db        311 TCAGTGACTGTGAGCATTCT 330
```

RESULT 5
US-09-949-016-13036/c
; Sequence 13036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13036
; LENGTH: 27223
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13036

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  Query Match             84.0%;  Score 16.8;  DB 4;  Length 27223;
  Best Local Similarity   90.0%;  Pred. No. 64;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              |||||  ||||||||||||
Db        878 TCAGTCTCCCTGAGCATTCT 859
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RESULT 6
US-09-199-637A-109
; Sequence 109, Application US/09199637A

```
; Patent No. 6355411
; GENERAL INFORMATION:
;  APPLICANT:  Ausubel, Frederick
;  APPLICANT:  Goodman, Howard M.
;  APPLICANT:  Rahme, Laurence G.
;  APPLICANT:  Mahajan-Miklos, Shalina
;  APPLICANT:  Tan, Man-Wah
;  APPLICANT:  Cao, Hui
;  APPLICANT:  Drenkard, Eliana
;  APPLICANT:  Tsongalis, John
;  TITLE OF INVENTION:  VIRULENCE-ASSOCIATED NUCLEIC ACID
;  TITLE OF INVENTION:  SEQUENCES AND USES THEREOF
;  FILE REFERENCE:  00786/361002
;  CURRENT APPLICATION NUMBER: US/09/199,637A
;  CURRENT FILING DATE:  1998-11-25
;  PRIOR APPLICATION NUMBER:  60/066,517
;  PRIOR FILING DATE:  1997-11-25
;  NUMBER OF SEQ ID NOS:  437
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 109
;   LENGTH: 128
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-109

  Query Match             82.0%;  Score 16.4;  DB 3;  Length 128;
  Best Local Similarity   94.4%;  Pred. No. 40;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 AGTGACCCTGAGCATTCT 20
              |||||||||||||||| ||
Db         24 AGTGACCCTGAGCATGCT 41


RESULT 7
US-09-963-137-62
; Sequence 62, Application US/09963137
; Patent No. 6596036
; GENERAL INFORMATION:
;  APPLICANT: Pedersen, Finn S
;  APPLICANT:  Sorensen, Annette B
;  APPLICANT:  Hernandez, Javier Martin
;  APPLICANT:  Nielsen, Anne A
;  APPLICANT:  Moving, Helle
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR LYMPHOMA AND LEUKEMIA
;  FILE REFERENCE: A-70981/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/09/963,137
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/668,644
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US 09/905,390
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 09/905,491
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 09/962,929
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/962,854
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/962,916
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/962,855
;  PRIOR FILING DATE: 2001-09-24
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 454
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(434)
;   OTHER INFORMATION: "n" at 9, 124 and 434 can be any base.
US-09-963-137-62

  Query Match             82.0%;  Score 16.4;  DB 4;  Length 454;
  Best Local Similarity   94.4%;  Pred. No. 51;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CAGTGACCCTGAGCATTC 19
              |||||||||| ||||||
Db         98 CAGTGACCCTGTGCATTC 115


RESULT 8
US-09-949-016-17433
; Sequence 17433, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17433
;   LENGTH: 101349
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17433

  Query Match             80.0%;  Score 16;  DB 4;  Length 101349;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCA 16
              ||||||||||||||||
Db      87317 TCAGTGACCCTGAGCA 87332


RESULT 9
US-08-905-223-171
; Sequence 171, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
```

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;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  171:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  386 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  CDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      TISSUE TYPE:  Brain
;    FEATURE:
;      NAME/KEY:  other
;      LOCATION:  52..228
;      IDENTIFICATION METHOD:  blastn
;      OTHER INFORMATION:  identity 94
;      OTHER INFORMATION:  region 1..177
;      OTHER INFORMATION:  id AA074050
;      OTHER INFORMATION:  est
;    FEATURE:
;      NAME/KEY:  other
;      LOCATION:  266..387
;      IDENTIFICATION METHOD:  blastn
;      OTHER INFORMATION:  identity 99
;      OTHER INFORMATION:  region 218..339
;      OTHER INFORMATION:  id AA074050
;      OTHER INFORMATION:  est
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  135..284
;      IDENTIFICATION METHOD:  Von Heijne matrix
;      OTHER INFORMATION:  score 9.8
;      OTHER INFORMATION:  seq LLRLLQLVSTCVA/FS
US-08-905-223-171

  Query Match             79.0%;  Score 15.8;  DB 3;  Length 386;
  Best Local Similarity   85.0%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              || |||||||||| ||| ||
Db        363 TCNGTGACCCTGATCATCCT 382


RESULT 10
US-09-949-016-57688
; Sequence 57688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57688
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-57688

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 601;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTC 19
              ||||||||||||| || |
Db        545 TCAGTGACCCTGAGAATCC 563


RESULT 11
US-09-949-016-57689
; Sequence 57689, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57689
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-57689

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 601;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTC 19
              ||||||||||||| || |
Db         87 TCAGTGACCCTGAGAATCC 105


RESULT 12
US-09-949-016-182711
; Sequence 182711, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182711
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-182711

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 601;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTC 19
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Db        221 TCAGTGGCCCTGAGTATTC 239


RESULT 13
US-09-949-016-206786
; Sequence 206786, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206786
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-206786

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 601;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTC 19
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Db        514 TCAATGACCCTGAGCAGTC 532


RESULT 14
US-09-573-080A-282/c
; Sequence 282, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
;  APPLICANT:  JOAN, KNOLL
;  APPLICANT:  ROGAN, PETER
;  TITLE OF INVENTION:   SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
;  FILE REFERENCE:   30307
;  CURRENT APPLICATION NUMBER: US/09/573,080A
;  CURRENT FILING DATE:  2000-05-16
;  NUMBER OF SEQ ID NOS:   479
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 282
;   LENGTH: 691
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(691)
;   OTHER INFORMATION: ltr8
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n is a, c, g or t
;  PUBLICATION INFORMATION:
;  PUBLICATION INFORMATION:
;   AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
;   TITLE: Prototypic sequences for human repetitive DNA
;   JOURNAL: Journal of Molecular Evolution
;   VOLUME: 35
;   ISSUE: 4
;   PAGES: 286-291
;   DATE: 1992-10-__
;   DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
;   DATABASE ENTRY DATE: ____-__-__
;   DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-282

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 691;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTC 19
              ||||| |||||||||||
Db        555 TCAGTCTCCCTGAGCATTC 537


RESULT 15
US-09-603-208A-183
; Sequence 183, Application US/09603208A
; Patent No. 6822084
; GENERAL INFORMATION:
;  APPLICANT:  Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  APPLICANT:  Lee, Heung-Shick
;  APPLICANT:  Kim, Hyung-Joon
;  TITLE OF INVENTION:  CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
;  TITLE OF INVENTION:  RESISTANCE AND TOLERANCE PROTEINS
;  FILE REFERENCE:  BGI-124CP
;  CURRENT APPLICATION NUMBER: US/09/603,208A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER:  60/141031
;  PRIOR FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER:  60/142692
;  PRIOR FILING DATE:  1999-07-01
;  PRIOR APPLICATION NUMBER:  60/151214
;  PRIOR FILING DATE:  1999-08-27
;  PRIOR APPLICATION NUMBER:  DE 19930429.7
;  PRIOR FILING DATE:  1999-07-01
;  PRIOR APPLICATION NUMBER:  DE 19931413.6
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931457.8
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931541.8
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19932209.0
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  DE 19932230.9
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  DE 19932914.1
;  PRIOR FILING DATE:  1999-07-14
;  PRIOR APPLICATION NUMBER:  DE 19940764.9
;  PRIOR FILING DATE:  1999-08-27
;  PRIOR APPLICATION NUMBER:  DE 19941382.7
;  PRIOR FILING DATE:  1999-08-31
;  NUMBER OF SEQ ID NOS:  306
; SEQ ID NO 183
;   LENGTH: 1006
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1006)
;   OTHER INFORMATION: FRXA02116
US-09-603-208A-183

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 1006;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CAGTGACCCTGAGCATTCT 20
              ||| |||||||||| ||||
Db        673 CAGCGACCCTGAGCCTTCT 691


Search completed: October 22, 2005, 21:05:30
Job time : 91 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2005, 05:48:05 ; Search time 456 Seconds
(without alignments)
361.804 Million cell updates/sec

Title: US-10-619-253-30
Perfect score: 20
Sequence: 1 tcagtgaccctgagcattct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9772231 seqs, 4124568258 residues

Total number of hits satisfying chosen parameters: 19544462

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	10	US-09-918-187-30	Sequence 30, Appl
2	20	100.0	20	20	US-10-484-442-30	Sequence 30, Appl
3	20	100.0	20	21	US-10-619-253-30	Sequence 30, Appl
4	20	100.0	430	9	US-09-920-300A-1542	Sequence 1542, Ap
5	20	100.0	430	13	US-10-033-528-1542	Sequence 1542, Ap
6	20	100.0	430	16	US-10-099-926-1542	Sequence 1542, Ap
7	20	100.0	430	22	US-10-961-527-1542	Sequence 1542, Ap
c 8	20	100.0	462	10	US-09-918-995-11367	Sequence 11367, A
c 9	20	100.0	474	10	US-09-918-995-20094	Sequence 20094, A
c 10	20	100.0	497	10	US-09-918-995-2132	Sequence 2132, Ap
c 11	20	100.0	499	14	US-10-060-036-124	Sequence 124, App
c 12	20	100.0	2251	9	US-09-925-302-180	Sequence 180, App
c 13	20	100.0	2251	10	US-09-925-302-180	Sequence 180, App
c 14	20	100.0	2797	16	US-10-252-157-432	Sequence 432, App
c 15	20	100.0	5206	14	US-10-060-036-175	Sequence 175, App
c 16	20	100.0	5221	10	US-09-918-187-3	Sequence 3, Appli
c 17	20	100.0	5221	15	US-10-177-293-410	Sequence 410, App
c 18	20	100.0	5221	17	US-10-377-133-1	Sequence 1, Appli
c 19	20	100.0	5221	17	US-10-377-133-6	Sequence 6, Appli
c 20	20	100.0	5221	18	US-10-236-417-17	Sequence 17, Appl
c 21	20	100.0	5221	18	US-10-236-417-23	Sequence 23, Appl
c 22	20	100.0	5221	18	US-10-236-417-29	Sequence 29, Appl
c 23	20	100.0	5221	18	US-10-236-417-33	Sequence 33, Appl
c 24	20	100.0	5221	20	US-10-484-442-3	Sequence 3, Appli
c 25	20	100.0	5221	21	US-10-619-253-3	Sequence 3, Appli
c 26	20	100.0	5329	17	US-10-377-133-2	Sequence 2, Appli
c 27	20	100.0	5329	21	US-10-887-553A-495	Sequence 495, App
c 28	20	100.0	5329	22	US-10-974-148-31	Sequence 31, Appl
c 29	20	100.0	5354	13	US-10-087-192-11	Sequence 11, Appl
30	20	100.0	5618	20	US-10-723-860-4811	Sequence 4811, Ap
31	20	100.0	5618	20	US-10-723-860-4843	Sequence 4843, Ap
c 32	20	100.0	5648	9	US-09-919-172-70	Sequence 70, Appl
c 33	20	100.0	5648	9	US-09-981-353-183	Sequence 183, App
c 34	20	100.0	5648	20	US-10-752-986-70	Sequence 70, Appl
c 35	20	100.0	5652	16	US-10-252-157-431	Sequence 431, App
c 36	20	100.0	6160	16	US-10-133-013-226	Sequence 226, App
37	20	100.0	17704	9	US-09-764-847-1865	Sequence 1865, Ap
38	20	100.0	17704	14	US-10-092-154-1865	Sequence 1865, Ap
39	20	100.0	17707	9	US-09-764-847-1864	Sequence 1864, Ap
40	20	100.0	17707	14	US-10-092-154-1864	Sequence 1864, Ap
c 41	20	100.0	18508	21	US-10-619-253-81	Sequence 81, Appl
c 42	20	100.0	37698	13	US-10-087-192-10	Sequence 10, Appl
43	18.4	92.0	363	9	US-09-983-965-1695	Sequence 1695, Ap
c 44	18.4	92.0	416	13	US-10-079-623-177	Sequence 177, App
c 45	18.4	92.0	455	13	US-10-079-623-207	Sequence 207, App

ALIGNMENTS

RESULT 1
US-09-918-187-30
; Sequence 30, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-30

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
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Db 1 TCAGTGACCCTGAGCATTCT 20

RESULT 2

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US-10-484-442-30
; Sequence 30, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH?0695
;  CURRENT APPLICATION NUMBER: US/10/484,442
;  CURRENT FILING DATE:  2004-01-29
;  PRIOR APPLICATION NUMBER: 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 30
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-484-442-30

  Query Match             100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db          1 TCAGTGACCCTGAGCATTCT 20


RESULT 3
US-10-619-253-30
; Sequence 30, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590US.P1
;  CURRENT APPLICATION NUMBER: US/10/619,253
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US 09/918,187
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 30
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-253-30

  Query Match             100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db          1 TCAGTGACCCTGAGCATTCT 20


RESULT 4
US-09-920-300A-1542
; Sequence 1542, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,300A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1542
;   LENGTH: 430
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-300A-1542

  Query Match             100.0%;  Score 20;  DB 9;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db        335 TCAGTGACCCTGAGCATTCT 354


RESULT 5
US-10-033-528-1542
; Sequence 1542, Application US/10033528
; Publication No. US20020131971A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C1
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE:  2001-12-26
;  NUMBER OF SEQ ID NOS: 1896
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1542
;   LENGTH: 430
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-528-1542

  Query Match             100.0%;  Score 20;  DB 13;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db        335 TCAGTGACCCTGAGCATTCT 354


RESULT 6
US-10-099-926-1542
; Sequence 1542, Application US/10099926
; Publication No. US20030166064A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C2
;  CURRENT APPLICATION NUMBER: US/10/099,926
;  CURRENT FILING DATE:  2002-03-17
;  NUMBER OF SEQ ID NOS: 1982
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1542
;   LENGTH: 430
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-099-926-1542
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  Query Match             100.0%;  Score 20;  DB 16;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        335 TCAGTGACCCTGAGCATTCT 354


RESULT 7
US-10-961-527-1542
; Sequence 1542, Application US/10961527
; Publication No. US20050147615A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C4
;  CURRENT APPLICATION NUMBER: US/10/961,527
;  CURRENT FILING DATE:  2004-10-07
;  PRIOR APPLICATION NUMBER: US 09/920,300
;  PRIOR FILING DATE: 2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/302,051
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/279,763
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/223,283
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1542
;   LENGTH: 430
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-961-527-1542

  Query Match             100.0%;  Score 20;  DB 22;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        335 TCAGTGACCCTGAGCATTCT 354


RESULT 8
US-09-918-995-11367/c
; Sequence 11367, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11367
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(462)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-11367

  Query Match             100.0%;  Score 20;  DB 10;  Length 462;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        162 TCAGTGACCCTGAGCATTCT 143


RESULT 9
US-09-918-995-20094/c
; Sequence 20094, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20094
;   LENGTH: 474
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(474)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20094

  Query Match             100.0%;  Score 20;  DB 10;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        134 TCAGTGACCCTGAGCATTCT 115


RESULT 10
US-09-918-995-2132/c
; Sequence 2132, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2132
;   LENGTH: 497
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(497)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2132

  Query Match             100.0%;  Score 20;  DB 10;  Length 497;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        489 TCAGTGACCCTGAGCATTCT 470


RESULT 11
US-10-060-036-124/c
; Sequence 124, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
;   LENGTH: 499
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 119, 253, 318, 442, 482, 483
;   OTHER INFORMATION: n = A,T,C or G
US-10-060-036-124

  Query Match             100.0%;  Score 20;  DB 14;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        190 TCAGTGACCCTGAGCATTCT 171


RESULT 12
US-09-925-302-180/c
; Sequence 180, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
;   LENGTH: 2251
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-302-180

  Query Match             100.0%;  Score 20;  DB 9;  Length 2251;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         24 TCAGTGACCCTGAGCATTCT 5


RESULT 13
US-09-925-302-180/c
; Sequence 180, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA104
;  CURRENT APPLICATION NUMBER: US/09/925,302
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05918
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 896
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
;   LENGTH: 2251
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-302-180

  Query Match             100.0%;  Score 20;  DB 10;  Length 2251;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         24 TCAGTGACCCTGAGCATTCT 5


RESULT 14
US-10-252-157-432/c
; Sequence 432, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT:  Pearson, Cecelia I.
;  TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
;  FILE REFERENCE: PA-0027-1 US
;  CURRENT APPLICATION NUMBER: US/10/252,157
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/295,048
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 501
;  SOFTWARE: PERL Program
; SEQ ID NO 432
;   LENGTH: 2797
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030190640A1 464689.15
US-10-252-157-432

  Query Match             100.0%;  Score 20;  DB 16;  Length 2797;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db       1315 TCAGTGACCCTGAGCATTCT 1296


RESULT 15
US-10-060-036-175/c
; Sequence 175, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
```

; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 5206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-175

Query Match 100.0%; Score 20; DB 14; Length 5206;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db       3030 TCAGTGACCCTGAGCATTCT 3011
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Search completed: October 22, 2005, 21:13:12
Job time : 459 secs

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2005, 02:30:25 ; Search time 1501 Seconds
(without alignments)
645.639 Million cell updates/sec

Title: US-10-619-253-30
Perfect score: 20
Sequence: 1 tcagtgaccctgagcattct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	277	6	AX884871	AX884871 Sequence
c	2	20	100.0	277	6	BD024481	BD024481 Sequence
	3	20	100.0	430	6	AX397327	AX397327 Sequence
c	4	20	100.0	2129	11	BV176633	BV176633 sqnm90040
c	5	20	100.0	5134	4	AY487829	AY487829 Sus scrof
c	6	20	100.0	5221	9	AF097514	AF097514 Homo sapi
c	7	20	100.0	5329	6	AX779833	AX779833 Sequence
c	8	20	100.0	5329	9	AB032261	AB032261 Homo sapi
c	9	20	100.0	5648	6	AR447360	AR447360 Sequence
c	10	20	100.0	20985	4	AY487830	AY487830 Sus scrof
c	11	20	100.0	67598	2	AC124282	AC124282 Homo sapi
c	12	20	100.0	115278	9	AL139819	AL139819 Human DNA
c	13	20	100.0	146455	9	AC127512	AC127512 Homo sapi
	14	20	100.0	159351	2	AC018783	AC018783 Homo sapi
c	15	20	100.0	171936	2	AC120031	AC120031 Homo sapi
	16	20	100.0	179249	2	AC129489	AC129489 Homo sapi
c	17	20	100.0	190784	2	AC139669	AC139669 Lemur cat
c	18	20	100.0	191673	2	AL356743	AL356743 Homo sapi
	19	20	100.0	194138	2	AC131270	AC131270 Homo sapi
c	20	20	100.0	194265	9	AC126365	AC126365 Homo sapi
c	21	20	100.0	198017	2	AC151025	AC151025 Callithri
	22	20	100.0	207418	9	AC090774	AC090774 Homo sapi
c	23	18.4	92.0	5108	4	AY241933	AY241933 Bos tauru
c	24	18.4	92.0	5123	4	AF325499	AF325499 Capra hir
c	25	18.4	92.0	5351	4	AB075020	AB075020 Bos tauru
c	26	18.4	92.0	17088	4	AY241932	AY241932 Bos tauru
	27	18.4	92.0	40006	9	AC005579	AC005579 Homo sapi
c	28	18.4	92.0	41766	9	AL359555	AL359555 Human DNA
c	29	18.4	92.0	128961	2	AC122114	AC122114 Atelerix
	30	18.4	92.0	156592	9	AL135786	AL135786 Human DNA
c	31	18.4	92.0	161827	2	AC139668	AC139668 Papio ham
c	32	18.4	92.0	170966	5	BX000991	BX000991 Zebrafish
c	33	18.4	92.0	179879	2	AC026883	AC026883 Homo sapi
c	34	18.4	92.0	205265	2	AC146621	AC146621 Otolemur
c	35	18	90.0	240425	10	AC110256	AC110256 Mus muscu
	36	17.4	87.0	6309	9	HSM808303	BX648156 Homo sapi
c	37	17.4	87.0	89012	9	AC011406	AC011406 Homo sapi
c	38	17.4	87.0	110000	2	AC143955_0	AC143955 Macaca mu
c	39	17.4	87.0	132562	9	AC106899	AC106899 Homo sapi
	40	17.4	87.0	148945	2	CR388411	CR388411 Danio rer
c	41	17.4	87.0	149480	6	AX329775	AX329775 Sequence
c	42	17.4	87.0	149480	6	AX329776	AX329776 Sequence
c	43	17.4	87.0	149480	6	AX336193	AX336193 Sequence
c	44	17.4	87.0	149480	9	HUU95740	U95740 Human Chrom
	45	17.4	87.0	149490	9	AC130455	AC130455 Homo sapi

ALIGNMENTS

RESULT 1
AX884871/c
LOCUS AX884871 277 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 734 from Patent EP1033401.
ACCESSION AX884871
VERSION AX884871.1 GI:40040465
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 734 06-SEP-2000;
Genset (FR)
FEATURES Location/Qualifiers
source 1. .277
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS 69. .>275
/note="unnamed protein product"
/codon_start=1
/protein_id="CAE98985.1"
/db_xref="GI:40040466"
/translation="MTCCPGSSLLHTECSGSLNHCFSFESRASCHFHVASAVSPPTPV
LPCHXDGSRQGWQTLPXTSLAQKAS"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 277;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 123 TCAGTGACCCTGAGCATTCT 104

RESULT 2
BD024481/c
LOCUS BD024481 277 bp DNA linear PAT 27-AUG-2002

```
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD024481
VERSION     BD024481.1  GI:22565704
KEYWORDS    JP 2001269182-A/727.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 277)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 727 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/727
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
              G06F15/40
            CC
            FH   Key             Location/Qualifiers
            FT   CDS             69. .275.
FEATURES             Location/Qualifiers
     source          1. .277
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 277;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        123 TCAGTGACCCTGAGCATTCT 104


RESULT 3
AX397327
LOCUS       AX397327                 430 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 1542 from Patent WO0212328.
ACCESSION   AX397327
VERSION     AX397327.1  GI:21068074
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   King,G.E., Meagher,M.J., Xu,J. and Secrist,H.
  TITLE     Compositions and methods for the therapy and diagnosis of colon
            cancer
  JOURNAL   Patent: WO 0212328-A 1542 14-FEB-2002;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .430
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        335 TCAGTGACCCTGAGCATTCT 354


RESULT 4
BV176633/c
LOCUS       BV176633                 2129 bp    DNA     linear   STS 10-JUN-2004
DEFINITION  sqnm90040 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
            tagged site.
ACCESSION   BV176633
VERSION     BV176633.1  GI:48012510
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2129)
  AUTHORS   Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
            Cantor,C.R. and Braun,A.
  TITLE     Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
            Regions
  JOURNAL   Genome Res. (2004) In press
COMMENT
            Contact: Andreas Braun
            Pharmaceuticals division
            Sequenom, Inc.
            3595 John Hopkins Court, San Diego, CA 92121, USA
            Tel: 18582029018
            Fax: 18582029020
            Email: abraun@sequenom.com
            Primer A: No primer sequence submitted
            Primer B: No primer sequence submitted
            STS size: 2129.
FEATURES             Location/Qualifiers
     source          1. .2129
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Human DNA (Sequenom)"
     STS             <1. .>2129
ORIGIN

  Query Match             100.0%;  Score 20;  DB 11;  Length 2129;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        676 TCAGTGACCCTGAGCATTCT 657


RESULT 5
AY487829/c
LOCUS       AY487829                 5134 bp    mRNA    linear   MAM 15-SEP-2004
DEFINITION  Sus scrofa stearoyl-CoA desaturase (SCD) mRNA, complete cds.
ACCESSION   AY487829
VERSION     AY487829.1  GI:40549307
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 5134)
  AUTHORS   Ren,J., Knorr,C., Huang,L. and Brenig,B.
  TITLE     Isolation and molecular characterization of the porcine
            stearoyl-CoA desaturase gene
  JOURNAL   Gene 340 (1), 19-30 (2004)
REFERENCE   2  (bases 1 to 5134)
  AUTHORS   Ren,J., Knorr,C. and Brenig,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-NOV-2003) Institute of Veterinary Medicine,
            Georg-August-University of Goettingen, Groner Landstr.2, Goettingen
            37073, Germany
FEATURES             Location/Qualifiers
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                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
     gene            1. .5134
                     /gene="SCD"
     5'UTR           1. .176
                     /gene="SCD"
     CDS             177. .1256
                     /gene="SCD"
                     /codon_start=1
                     /product="stearoyl-CoA desaturase"
                     /protein_id="AAR87713.1"
                     /db_xref="GI:40549308"
                     /translation="MPAHLLQEEISSSYTTTTTITAPSSRVLQNGGGKLEKTPQYVEE
                     DIRPEMKDDIYDPTYQDKEGPRPKLEYVWRNIILMSLLHLGALYGIILIPTCKIYTLL
                     WAFAYYLLSAVGVTAGAHRLWSHRTYKARLPLRVFLIIANTMAFQNDVYEWARDHRAH
                     HKFSETDADPHNSRRGFFFSHVGWLLVRKHPAVKEKGGLLNMSDLKAEKLVMFQRRYY
                     KPGILLMCFILPTIVPWYCWGEAFPQSLFVATFLRYAIVLNATWLVNSAAHLYGYRPY
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                     DRKKVSKAAILARIKRTGDESYKSG"
     variation       299
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     3'UTR           1257. .5134
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     variation       3251
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                     /replace="g"
     variation       3297
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db       2942 TCAGTGACCCTGAGCATTCT 2923


RESULT 6
AF097514/c
LOCUS       AF097514                5221 bp    mRNA    linear   PRI 19-MAY-1999
DEFINITION  Homo sapiens stearoyl-CoA desaturase (SCD) mRNA, complete cds.
ACCESSION   AF097514
VERSION     AF097514.1  GI:4808600
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5221)
  AUTHORS   Zhang,L., Ge,L., Parimoo,S., Stenn,K. and Prouty,S.M.
  TITLE     Human stearoyl-CoA desaturase: alternative transcripts generated
            from a single gene by usage of tandem polyadenylation sites
  JOURNAL   Biochem. J. 340 (Pt 1), 255-264 (1999)
  MEDLINE   99247918
   PUBMED   10229681
REFERENCE   2  (bases 1 to 5221)
  AUTHORS   Zhang,L., Ge,L., Parimoo,S., Stenn,K. and Prouty,S.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-OCT-1998) Skin Biology TRC, Johnson and Johnson CPWW,
            199 Grandview Road, Skillman, NJ 08558, USA
FEATURES             Location/Qualifiers
     source          1. .5221
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /tissue_type="liver; brain; adipose; scalp skin; foreskin
                     keratinocytes"
                     /dev_stage="adult"
     gene            1. .5221
                     /gene="SCD"
     CDS             236. .1315
                     /gene="SCD"
                     /EC_number="1.14.99.5"
                     /function="catalysis of delta 9 cis-desaturation of
                     palmitoyl-CoA and stearoyl-CoA"
                     /codon_start=1
                     /product="stearoyl-CoA desaturase"
                     /protein_id="AAD29870.1"
                     /db_xref="GI:4808601"
                     /translation="MPAHLLQDDISSSYTTTTTITAPPSRVLQNGGDKLETMPLYLED
                     DIRPDIKDDIYDPTYKDKEGPSPKVEYVWRNIILMSLLHLGALYGITLIPTCKFYTWL
                     WGVFYYFVSALGITAGAHRLWSHRSYKARLPLRLFLIIANTMAFQNDVYEWARDHRAH
                     HKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGSTLDLSDLEAEKLVMFQRRYY
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                     DKNISPRENILVSLGAVGEGFHNYHHSFPYDYSASEYRWHINFTTFFIDCMAALGLAY
                     DRKKVSKAAILARIKRTGDGNYKSG"
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                     /gene="SCD"
     polyA_signal    5187. .5192
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ORIGIN

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Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db       3030 TCAGTGACCCTGAGCATTCT 3011


RESULT 7
AX779833/c
LOCUS       AX779833                5329 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 1990 from Patent WO03039443.
ACCESSION   AX779833
VERSION     AX779833.1  GI:32696827
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
            Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
  TITLE     Novel genetic markers for leukemias
  JOURNAL   Patent: WO 03039443-A 1990 15-MAY-2003;
            Deutsches Krebsforschungszentrum (DE) ;
            Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
            PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES             Location/Qualifiers
     source          1. .5329
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 5329;
  Best Local Similarity   100.0%;  Pred. No. 25;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db       3157 TCAGTGACCCTGAGCATTCT 3138


RESULT 8
AB032261/c
LOCUS       AB032261               5329 bp    mRNA    linear   PRI 04-APR-2000
DEFINITION  Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds.
ACCESSION   AB032261
VERSION     AB032261.1  GI:7415720
KEYWORDS    stearoyl-CoA desaturase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hoshino,T. and Ohtsu,K.
  TITLE     Cloning, Sequencing and Expression of Human Stearoyl-CoA Desaturase
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 5329)
  AUTHORS   Hoshino,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1999) Toshimitsu Hoshino, Mitsubishi Kasei
            Institute of Life Sciences, Division of Pioneering Research; 11,
            Minamiooya, Machida, Tokyo 194-8511, Japan
            (E-mail:toshi@libra.ls.m-kagaku.co.jp, Tel:81-42-724-6252,
            Fax:81-42-724-6316)
FEATURES             Location/Qualifiers
     source          1. .5329
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .5329
                     /gene="Scd"
     CDS             381. .1460
                     /gene="Scd"
                     /codon_start=1
                     /product="stearoyl-CoA desaturase"
                     /protein_id="BAA93510.1"
                     /db_xref="GI:7415721"
                     /translation="MPAHLLQDDISSSYTTTTTITAPPSRVLQNGGDKLETMPLYLED
                     DIRPDIKDDIYDPTYKDKEGPSPKVEYVWRNIILMSLLHLGALYGITLIPTCKFYTWL
                     WGVFYYFVSALGITAGAHRLWSHRSYKARLPLRLFLIIANTMAFQNDVYEWARDHRAH
                     HKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGSTLDLSDLEAEKLVMFQRRYY
                     KPGLLLMCFILPTLVPWYFWGETFQNSVFVATFLRYAVVLNATWLVNSAAHLFGYRPY
                     DKNISPRENILVSLGAVGEGFHNYHHSFPYDYSASEYRWHINFTTFFIDCMAALGLAY
                     DRKKVSKAAILARIKRTGDGNYKSG"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 5329;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db       3157 TCAGTGACCCTGAGCATTCT 3138


RESULT 9
AR447360/c
LOCUS       AR447360               5648 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 70 from patent US 6673545.
ACCESSION   AR447360
VERSION     AR447360.1  GI:42675660
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5648)
  AUTHORS   Faris,M. and Turner,C.M.
  TITLE     Prostate cancer markers
  JOURNAL   Patent: US 6673545-A 70 06-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .5648
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 5648;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db       3175 TCAGTGACCCTGAGCATTCT 3156


RESULT 10
AY487830/c
LOCUS       AY487830               20985 bp    DNA     linear   MAM 15-SEP-2004
DEFINITION  Sus scrofa stearoyl-CoA desaturase (SCD) gene, exons 1 through 6
            and complete cds.
ACCESSION   AY487830
VERSION     AY487830.1  GI:40549309
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 20985)
  AUTHORS   Ren,J., Knorr,C., Huang,L. and Brenig,B.
  TITLE     Isolation and molecular characterization of the porcine
            stearoyl-CoA desaturase gene
  JOURNAL   Gene 340 (1), 19-30 (2004)
REFERENCE   2  (bases 1 to 20985)
  AUTHORS   Ren,J., Knorr,C., Guo,Y.M., Ding,N.S., Ai,H.S., Brenig,B. and
            Huang,L.S.
  TITLE     Characterization of five single nucleotide polymorphisms in the
            porcine stearoyl-CoA desaturase (SCD) gene
  JOURNAL   Anim. Genet. 35 (3), 255-257 (2004)
  PUBMED    15147407
REFERENCE   3  (bases 1 to 20985)
  AUTHORS   Ren,J., Knorr,C. and Brenig,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-NOV-2003) Institute of Veterinary Medicine,
            Georg-August-University of Goettingen, Groner Landstr.2, Goettingen
            37073, Germany
FEATURES             Location/Qualifiers
     source          1. .20985
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /chromosome="14"
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                     /clone="TAIGP714K14117Q"
     repeat_region   1. .209
                     /note="L1M4"
                     /rpt_family="LINE/L1"
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     repeat_region   241. .507
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                     /rpt_family="SINE/Pig"
                     /rpt_type=dispersed
     repeat_region   508. .853
                     /note="L1M4"
                     /rpt_family="LINE/L1"
                     /rpt_type=dispersed
     repeat_region   826. .1070
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     variation       1423
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promoter        2020. .2270
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variation       2108
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                /replace="t"
variation       2228
                /gene="SCD"
                /replace="c"
TATA_signal     2255. .2262
                /gene="SCD"
mRNA            join(2285. .2487,3006. .3288,8073. .8203,9562. .9767,
                11236. .11468,14423. .18470)
                /gene="SCD"
                /product="stearoyl-CoA desaturase"
exon            2285. .2487
                /gene="SCD"
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5'UTR           2285. .2460
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CDS             join(2461. .2487,3006. .3288,8073. .8203,9562. .9767,
                11236. .11468,14423. .14622)
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                WAFAYYLLSAVGVTAGAHRLWSHRTYKARLPLRVFLIIANTMAFQNDVYEWARDHRAH
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variation       2650
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variation       2894
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exon            3006. .3288
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repeat_region   5739. .5953
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                /rpt_family="SINE/Pig"
                /rpt_type=dispersed
repeat_region   6808. .7068
                /note="PRE1_SS"
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repeat_region   7071. .7145
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                /rpt_type=dispersed
repeat_region   7188. .7440
                /note="PRE1_SS"
                /rpt_family="SINE/Pig"
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repeat_region   7571. .7598
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exon            8073. .8203
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                /rpt_family="SINE/MIR"
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variation       9261
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exon            9562. .9767
                /gene="SCD"
                /number=4
variation       10188
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variation       10216. .10221
                /gene="SCD"
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variation       10246
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variation       10447
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exon            11236. .11468
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variation       13756. .13758
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variation       14416
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exon            14423. .18470
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variation       16418
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Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db      16308 TCAGTGACCCTGAGCATTCT 16289


RESULT 11
AC124282/c
LOCUS       AC124282               67598 bp    DNA     linear   HTG 05-JUL-2002
DEFINITION  Homo sapiens chromosome 17 clone RP13-601O21 map 17, LOW-PASS
            SEQUENCE SAMPLING.
ACCESSION   AC124282
VERSION     AC124282.2  GI:21699375
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 67598)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP13-601O21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 67598)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
            Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
            Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
            Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
            Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 67598)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jul 5, 2002 this sequence version replaced gi:21426305.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L27358
                Center clone name: 601_O_21
            --------------.
            * NOTE: This record contains 82 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      708: contig of 708 bp in length
            *      709      808: gap of 100 bp
            *      809     1545: contig of 737 bp in length
            *     1546     1645: gap of 100 bp
            *     1646     2370: contig of 725 bp in length
            *     2371     2470: gap of 100 bp
            *     2471     3194: contig of 724 bp in length
            *     3195     3294: gap of 100 bp
            *     3295     4034: contig of 740 bp in length
            *     4035     4134: gap of 100 bp
            *     4135     4849: contig of 715 bp in length
            *     4850     4949: gap of 100 bp
            *     4950     5638: contig of 689 bp in length
            *     5639     5738: gap of 100 bp
            *     5739     6473: contig of 735 bp in length
            *     6474     6573: gap of 100 bp
            *     6574     7322: contig of 749 bp in length
            *     7323     7422: gap of 100 bp
            *     7423     8153: contig of 731 bp in length
            *     8154     8253: gap of 100 bp
            *     8254     8964: contig of 711 bp in length
            *     8965     9064: gap of 100 bp
            *     9065     9791: contig of 727 bp in length
            *     9792     9891: gap of 100 bp
            *     9892    10618: contig of 727 bp in length
            *    10619    10718: gap of 100 bp
            *    10719    11460: contig of 742 bp in length
            *    11461    11560: gap of 100 bp
            *    11561    12288: contig of 728 bp in length
            *    12289    12388: gap of 100 bp
            *    12389    13120: contig of 732 bp in length
            *    13121    13220: gap of 100 bp
            *    13221    13942: contig of 722 bp in length
            *    13943    14042: gap of 100 bp
            *    14043    14759: contig of 717 bp in length
            *    14760    14859: gap of 100 bp
            *    14860    15575: contig of 716 bp in length
            *    15576    15675: gap of 100 bp
            *    15676    16414: contig of 739 bp in length
            *    16415    16514: gap of 100 bp
            *    16515    17230: contig of 716 bp in length
            *    17231    17330: gap of 100 bp
            *    17331    18044: contig of 714 bp in length
            *    18045    18144: gap of 100 bp
            *    18145    18863: contig of 719 bp in length
            *    18864    18963: gap of 100 bp
            *    18964    19693: contig of 730 bp in length
            *    19694    19793: gap of 100 bp
```

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          *    19794    20523: contig of 730 bp in length
          *    20524    20623: gap of 100 bp
          *    20624    21337: contig of 714 bp in length
          *    21338    21437: gap of 100 bp
          *    21438    22162: contig of 725 bp in length
          *    22163    22262: gap of 100 bp
          *    22263    23000: contig of 738 bp in length
          *    23001    23100: gap of 100 bp
          *    23101    23831: contig of 731 bp in length
          *    23832    23931: gap of 100 bp
          *    23932    24626: contig of 695 bp in length
          *    24627    24726: gap of 100 bp
          *    24727    25459: contig of 733 bp in length
          *    25460    25559: gap of 100 bp
          *    25560    26284: contig of 725 bp in length
          *    26285    26384: gap of 100 bp
          *    26385    27091: contig of 707 bp in length
          *    27092    27191: gap of 100 bp
          *    27192    27911: contig of 720 bp in length
          *    27912    28011: gap of 100 bp
          *    28012    28744: contig of 733 bp in length
          *    28745    28844: gap of 100 bp
          *    28845    29576: contig of 732 bp in length
          *    29577    29676: gap of 100 bp
          *    29677    30403: contig of 727 bp in length
          *    30404    30503: gap of 100 bp
          *    30504    31233: contig of 730 bp in length
          *    31234    31333: gap of 100 bp
          *    31334    32067: contig of 734 bp in length
          *    32068    32167: gap of 100 bp
          *    32168    32886: contig of 719 bp in length
          *    32887    32986: gap of 100 bp
          *    32987    33702: contig of 716 bp in length
          *    33703    33802: gap of 100 bp
          *    33803    34533: contig of 731 bp in length
          *    34534    34633: gap of 100 bp
          *    34634    35344: contig of 711 bp in length
          *    35345    35444: gap of 100 bp
          *    35445    36170: contig of 726 bp in length
          *    36171    36270: gap of 100 bp
          *    36271    36980: contig of 710 bp in length
          *    36981    37080: gap of 100 bp
          *    37081    37822: contig of 742 bp in length
          *    37823    37922: gap of 100 bp
          *    37923    38664: contig of 742 bp in length
          *    38665    38764: gap of 100 bp
          *    38765    39497: contig of 733 bp in length
          *    39498    39597: gap of 100 bp
          *    39598    40322: contig of 725 bp in length
          *    40323    40422: gap of 100 bp
          *    40423    41156: contig of 734 bp in length
          *    41157    41256: gap of 100 bp
          *    41257    41998: contig of 742 bp in length
          *    41999    42098: gap of 100 bp
          *    42099    42826: contig of 728 bp in length
          *    42827    42926: gap of 100 bp
          *    42927    43655: contig of 729 bp in length
          *    43656    43755: gap of 100 bp
          *    43756    44491: contig of 736 bp in length
          *    44492    44591: gap of 100 bp
          *    44592    45328: contig of 737 bp in length
          *    45329    45428: gap of 100 bp
          *    45429    46158: contig of 730 bp in length
          *    46159    46258: gap of 100 bp
          *    46259    46989: contig of 731 bp in length
          *    46990    47089: gap of 100 bp

  Query Match             100.0%;  Score 20;  DB 2;  Length 67598;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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```
Db      40820 TCAGTGACCCTGAGCATTCT 40801


RESULT 12
AL139819/c
LOCUS       AL139819              115278 bp    DNA     linear   PRI 18-SEP-2001
DEFINITION  Human DNA sequence from clone RP11-34D15 on chromosome 10, complete
            sequence.
ACCESSION   AL139819
VERSION     AL139819.8  GI:15705162
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 115278)
  AUTHORS   Tracey,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 19, 2001 this sequence version replaced gi:14586033.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 10, constructed by the Sanger Centre Chromosome 10
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr10
            RP11-34D15 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            IMPORTANT: This sequence is not the entire insert of clone
            RP11-34D15 It may be shorter because we sequence overlapping
            sections only once, except for a short overlap.
            The true right end of clone RP11-34D15 is at 115278 in this
            sequence. The true left end of clone RP11-285F16 is at 56886 in
            this sequence. The true right end of clone RP11-316M21 is at 2000
            in this sequence.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /clone="RP11-34D15"
                     /clone_lib="RPCI-11.1"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 115278;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db      83833 TCAGTGACCCTGAGCATTCT 83814
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RESULT 13
AC127512/c
LOCUS       AC127512               146455 bp    DNA     linear   PRI 17-DEC-2002
DEFINITION  Homo sapiens chromosome 17, clone RP13-72M22, complete sequence.
ACCESSION   AC127512
VERSION     AC127512.11  GI:27151438
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 146455)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP13-72M22
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 146455)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
            Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUL-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 146455)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
            Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
            Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
            Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 146455)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
            Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
            Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
            Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Dec 17, 2002 this sequence version replaced gi:26291688.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L27733
                Center clone name: 72_M_22
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /map="17"
                     /clone="RP13-72M22"
                     /clone_lib="RPCI-13 Human Female BAC"
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     repeat_region   complement(23. .295)
                     /rpt_family="AluSp"
     repeat_region   complement(296. .684)
                     /rpt_family="MER82"
     repeat_region   1757. .1857
                     /rpt_family="MER5B"
     repeat_region   complement(2030. .2178)
                     /rpt_family="MER5B"
     repeat_region   3196. .3220
                     /rpt_family="(GGA)n"
     repeat_region   5265. .5343
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     repeat_region   7287. .7791
                     /rpt_family="MER9"
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                     /rpt_family="AluY"
     repeat_region   complement(9366. .9727)
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     repeat_region   complement(10034. .10297)
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     repeat_region   10830. .10875
                     /rpt_family="(CA)n"
     repeat_region   11296. .11583
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     repeat_region   12842. .12974
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                     /rpt_family="AluSx"
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                     /rpt_family="(CA)n"
     repeat_region   18560. .18862
                     /rpt_family="AluY"
     repeat_region   19477. .19505
                     /rpt_family="(TG)n"
     repeat_region   19578. .19711
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     repeat_region   complement(19907. .20082)
                     /rpt_family="LTR67"
     repeat_region   complement(20725. .20857)
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     repeat_region   21081. .22114
                     /rpt_family="L1ME"
     repeat_region   22117. .22681
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  Query Match             100.0%;  Score 20;  DB 9;  Length 146455;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db     138537 TCAGTGACCCTGAGCATTCT 138518


RESULT 14
AC018783
LOCUS       AC018783               159351 bp    DNA     linear   HTG 14-MAR-2000
DEFINITION  Homo sapiens clone RP11-2M13, WORKING DRAFT SEQUENCE, 12 unordered
            pieces.
ACCESSION   AC018783
VERSION     AC018783.3  GI:7229991
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 159351)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-2M13
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 159351)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
            Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
            Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
            Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
            Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H.,
            O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A.,
            Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
            Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A.
            and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 12, 2000 this sequence version replaced gi:6692332.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L2667
                Center clone name: 2_M_13
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 151339 bases at least Q40
                Consensus quality: 155177 bases at least Q30
                Consensus quality: 157011 bases at least Q20
                Insert size: 167000; agarose-fp
                Insert size: 158251; sum-of-contigs
                Quality coverage: 4.9 in Q20 bases; agarose-fp
                Quality coverage: 5.2 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 12 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2297: contig of 2297 bp in length
            *     2298     2397: gap of 100 bp
            *     2398     5719: contig of 3322 bp in length
            *     5720     5819: gap of 100 bp
            *     5820    10149: contig of 4330 bp in length
            *    10150    10249: gap of 100 bp
            *    10250    16496: contig of 6247 bp in length
            *    16497    16596: gap of 100 bp
            *    16597    21823: contig of 5227 bp in length
            *    21824    21923: gap of 100 bp
```

```
            *    21924    25747: contig of 3824 bp in length
            *    25748    25847: gap of 100 bp
            *    25848    31971: contig of 6124 bp in length
            *    31972    32071: gap of 100 bp
            *    32072    44449: contig of 12378 bp in length
            *    44450    44549: gap of 100 bp
            *    44550    64978: contig of 20429 bp in length
            *    64979    65078: gap of 100 bp
            *    65079    91491: contig of 26413 bp in length
            *    91492    91591: gap of 100 bp
            *    91592   121937: contig of 30346 bp in length
            *   121938   122037: gap of 100 bp
            *   122038   159351: contig of 37314 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="RP11-2M13"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .2297
                     /note="assembly_fragment"
     misc_feature    2398. .5719
                     /note="assembly_fragment"
     misc_feature    5820. .10149
                     /note="assembly_fragment"
     misc_feature    10250. .16496
                     /note="assembly_fragment"
     misc_feature    16597. .21823
                     /note="assembly_fragment"
     misc_feature    21924. .25747
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
     misc_feature    25848. .31971
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:left"
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                     /note="assembly_fragment"
     misc_feature    44550. .64978
                     /note="assembly_fragment"
     misc_feature    65079. .91491
                     /note="assembly_fragment"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db      17573 TCAGTGACCCTGAGCATTCT 17592


RESULT 15
AC120031/c
LOCUS       AC120031              171936 bp    DNA     linear   HTG 17-JUN-2002
DEFINITION  Homo sapiens chromosome 17 clone RP11-77B12 map 17, WORKING DRAFT
            SEQUENCE, 8 ordered pieces.
ACCESSION   AC120031
VERSION     AC120031.2  GI:21431233
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171936)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-77B12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171936)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
            Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 171936)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
            Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
            Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
            Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
            Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jun 17, 2002 this sequence version replaced gi:20389700.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L26268
                Center clone name: 77_B_12
            -------------- Summary Statistics
                Sequencing vector: Plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 169539 bases at least Q40
                Consensus quality: 170437 bases at least Q30
                Consensus quality: 170824 bases at least Q20
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                Insert size: 168000; agarose-fp
                Insert size: 171236; sum-of-contigs
                Quality coverage: 15.0 in Q20 bases; agarose-fp
                Quality coverage: 14.7 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    26459: contig of 26459 bp in length
            *    26460    26559: gap of 100 bp
            *    26560    27658: contig of 1099 bp in length
            *    27659    27758: gap of 100 bp
            *    27759    28845: contig of 1087 bp in length
            *    28846    28945: gap of 100 bp
            *    28946    42768: contig of 13823 bp in length
            *    42769    42868: gap of 100 bp
            *    42869    64973: contig of 22105 bp in length
            *    64974    65073: gap of 100 bp
            *    65074   102439: contig of 37366 bp in length
            *   102440   102539: gap of 100 bp
            *   102540   138494: contig of 35955 bp in length
            *   138495   138594: gap of 100 bp
            *   138595   171936: contig of 33342 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /map="17"
                     /clone="RP11-77B12"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .26459
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    26560. .27658
                     /note="assembly_fragment"
     misc_feature    27759. .28845
                     /note="assembly_fragment"
     misc_feature    28946. .42768
                     /note="assembly_fragment"
     misc_feature    42869. .64973
                     /note="assembly_fragment"
     misc_feature    65074. .102439
                     /note="assembly_fragment"
     misc_feature    102540. .138494
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     misc_feature    138595. .171936
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                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 171936;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db     134757 TCAGTGACCCTGAGCATTCT 134738


Search completed: October 22, 2005, 03:23:43
Job time : 1509 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2005, 02:30:25 ; Search time 238 Seconds
(without alignments)
497.457 Million cell updates/sec

Title: US-10-619-253-30
Perfect score: 20
Sequence: 1 tcagtgaccctgagcattct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	10	ABZ77075	Abz77075 Human ste
c	2	20	100.0	277	3	AAC00736	Aac00736 Human sec
	3	20	100.0	430	6	ABK45991	Abk45991 cDNA enco
c	4	20	100.0	462	9	ACH24155	Ach24155 Human adu
c	5	20	100.0	474	9	ACH32882	Ach32882 Human end
c	6	20	100.0	497	9	ACH14920	Ach14920 Human adu
c	7	20	100.0	499	6	ABV94743	Abv94743 Human pan
c	8	20	100.0	2251	3	AAF18161	Aaf18161 Lung canc
c	9	20	100.0	2797	10	ADE54085	Ade54085 Human pro
c	10	20	100.0	5206	6	ABV94773	Abv94773 Human pan
c	11	20	100.0	5221	8	ACC50285	Acc50285 Breast ca
c	12	20	100.0	5221	8	ACC62247	Acc62247 Human NOV
c	13	20	100.0	5221	8	ACC62244	Acc62244 Human NOV
c	14	20	100.0	5221	8	ACC62252	Acc62252 Human NOV
c	15	20	100.0	5221	8	ACC62250	Acc62250 Human NOV
c	16	20	100.0	5221	10	ADC72210	Adc72210 Human ste
c	17	20	100.0	5221	10	ADC72205	Adc72205 Human ste
c	18	20	100.0	5221	10	ABZ77048	Abz77048 Human ste
c	19	20	100.0	5221	13	ADP24434	Adp24434 PRO polyp
c	20	20	100.0	5329	10	ADC72206	Adc72206 Human ste
c	21	20	100.0	5329	10	ADF81434	Adf81434 Leukaemia
c	22	20	100.0	5329	13	ADP23034	Adp23034 PRO polyp
c	23	20	100.0	5350	13	ACN40125	Acn40125 Tumour-as
c	24	20	100.0	5354	11	ACN43855	Acn43855 Human mRN
	25	20	100.0	5618	12	ADQ22023	Adq22023 Human sof
	26	20	100.0	5618	12	ADQ21991	Adq21991 Human sof
c	27	20	100.0	5648	6	ABS62777	Abs62777 Prostate
c	28	20	100.0	5648	9	ADA11065	Ada11065 Human cDN
c	29	20	100.0	5652	10	ADE54084	Ade54084 Human pro
c	30	20	100.0	6160	10	ADI02685	Adi02685 Human cDN
	31	20	100.0	17704	4	ABK42978	Abk42978 Genomic s
	32	20	100.0	17704	9	ADB61134	Adb61134 Connectiv
	33	20	100.0	17707	4	ABK42977	Abk42977 Genomic s
	34	20	100.0	17707	9	ADB61133	Adb61133 Connectiv
c	35	20	100.0	37698	11	ACN43854	Acn43854 Human gen
	36	18.4	92.0	363	8	ABX51766	Abx51766 Bovine ES
	37	18.4	92.0	484	8	ABX51598	Abx51598 Bovine ES
	38	18.4	92.0	2256	4	ABK42975	Abk42975 Genomic s
	39	18.4	92.0	2256	9	ADB61131	Adb61131 Connectiv
c	40	18.4	92.0	4964	13	ADR47283	Adr47283 Bos tauru
c	41	17.4	87.0	552	13	ADQ50307	Adq50307 Novel can
c	42	17.4	87.0	149480	6	ABL61947	Abl61947 Colon ade
c	43	17.4	87.0	149480	6	ABL68365	Abl68365 Kidney ca
c	44	17.4	87.0	149480	6	ABL61948	Abl61948 Colon ade
	45	17	85.0	19	10	ADE27514	Ade27514 Stearoyl-

ALIGNMENTS

RESULT 1
ABZ77075
ID ABZ77075 standard; DNA; 20 BP.
XX
AC ABZ77075;
XX
DT 07-MAY-2003 (first entry)
XX
DE Human stearoyl-CoA desaturase phosphorothioate oligonucleotide SEQ:30.
XX
KW Human; stearoyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW 2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN WO2003012031-A2.
XX
PD 13-FEB-2003.
XX
PF 16-JUL-2002; 2002WO-US022676.
XX
PR 30-JUL-2001; 2001US-00918187.
XX
PA (ISIS-) ISIS PHARM INC.
XX

PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-248160/24.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding human
PT stearoyl-CoA desaturase, useful for treating diseases associated with the
PT desaturase, e.g. atherosclerosis, and in diagnostic and research
PT applications.
XX
PS Claim 3; Page 94; 117pp; English.
XX
CC The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding human stearoyl-CoA
CC desaturase, and which specifically hybridises with and inhibits the
CC expression of human stearoyl-CoA desaturase, or which specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding human stearoyl-CoA desaturase. Human
CC stearoyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC activities, and can be used in antisense therapy. The antisense compounds
CC (I) can be used for modulating the expression of human stearoyl-CoA
CC desaturase and for treating diseases or conditions associated with
CC expression of human stearoyl-CoA desaturase, e.g. abnormal lipid or
CC cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC antisense compounds (I) can also be used for diagnostics, therapeutics
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC tumour formation, as research reagents and kits, and in distinguishing
CC between functions of various members of a biological pathway. The present
CC sequence represents a human stearoyl-CoA desaturase inhibiting chimeric
CC phosphorothioate antisense oligonucleotide, which is given in an example
CC from the present invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 1 TCAGTGACCCTGAGCATTCT 20

RESULT 2
AAC00736/c
ID AAC00736 standard; cDNA; 277 BP.
XX
AC AAC00736;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 734.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
DR P-PSDB; AAG00730.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 734; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 277 BP; 52 A; 95 C; 56 G; 71 T; 0 U; 3 Other;

Query Match 100.0%; Score 20; DB 3; Length 277;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 123 TCAGTGACCCTGAGCATTCT 104

RESULT 3
ABK45991
ID ABK45991 standard; cDNA; 430 BP.
XX
AC ABK45991;
XX
DT 05-JUN-2002 (first entry)
XX
DE cDNA encoding colon tumour protein, SEQ ID No 1542.
XX
KW Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200212328-A2.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US024218.
XX
PR 03-AUG-2000; 2000US-0223283P.
PR 28-MAR-2001; 2001US-0279763P.
PR 29-JUN-2001; 2001US-0302051P.
XX
PA (CORI-) CORIXA CORP.
XX
PI King GE, Meagher MJ, Xu J, Secrist H;
XX
DR WPI; 2002-241739/29.
XX
PT New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT for diagnosing, preventing, and treating colon cancer, and as markers for
PT the progression of cancer.
XX
PS Claim 1; SEQ ID NO 1542; 147pp; English.
XX
CC The invention relates to polynucleotides encoding colon tumour proteins.
CC The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC compositions, such as vaccines, for the diagnosis, prevention, and
CC treatment of colon cancer. Polynucleotide sequences may be used as

CC hybridisation probes or primers, and in the design and preparation of
CC ribozyme molecules for inhibiting expression of tumour polypeptides and
CC proteins in tumour cells. The compositions are useful for stimulating an
CC immune response against cancer, particularly for the immunotherapy of
CC colon cancer, and as markers for the progression of cancer. ABK44450-
CC ABK46237 represent coding sequences of human colon tumour proteins of the
CC invention. Note: With the exception of SEQ ID No 1 and 2, the sequence
CC data for this patent did not form part of the printed specification but
CC was supplied by the European Patent Office
XX
SQ Sequence 430 BP; 97 A; 102 C; 143 G; 88 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 335 TCAGTGACCCTGAGCATTCT 354

RESULT 4
ACH24155/c
ID ACH24155 standard; cDNA; 462 BP.
XX
AC ACH24155;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult ovary cDNA #2535.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 11367; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 462 BP; 92 A; 148 C; 105 G; 112 T; 0 U; 5 Other;

Query Match 100.0%; Score 20; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 162 TCAGTGACCCTGAGCATTCT 143

RESULT 5
ACH32882/c
ID ACH32882 standard; cDNA; 474 BP.
XX
AC ACH32882;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human endothelial cell cDNA #1015.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 20094; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at

```
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 474 BP; 93 A; 156 C; 116 G; 108 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        134 TCAGTGACCCTGAGCATTCT 115


RESULT 6
ACH14920/c
ID   ACH14920 standard; cDNA; 497 BP.
XX
AC   ACH14920;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human adult brain cDNA #2132.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Claim 1; SEQ ID NO 2132; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 497 BP; 111 A; 118 C; 108 G; 150 T; 0 U; 10 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 497;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        489 TCAGTGACCCTGAGCATTCT 470


RESULT 7
ABV94743/c
ID   ABV94743 standard; cDNA; 499 BP.
XX
AC   ABV94743;
XX
DT   14-JAN-2003  (first entry)
XX
DE   Human pancreatic cancer expressed cDNA SEQ ID NO 124.
XX
KW   Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW   cytostatic; tumour; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200260317-A2.
XX
PD   08-AUG-2002.
XX
PF   30-JAN-2002; 2002WO-US002781.
XX
PR   30-JAN-2001; 2001US-0265305P.
PR   31-JAN-2001; 2001US-0265682P.
PR   09-FEB-2001; 2001US-0267568P.
PR   21-MAR-2001; 2001US-0278651P.
PR   28-APR-2001; 2001US-0287112P.
PR   16-MAY-2001; 2001US-0291631P.
PR   12-JUL-2001; 2001US-0305484P.
PR   20-AUG-2001; 2001US-0313999P.
PR   27-NOV-2001; 2001US-0333626P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Benson DR,  Kalos MD,  Lodes MJ,  Persing DH,  Hepler WT,  Jiang Y;
XX
DR   WPI; 2002-627435/67.
XX
PT   New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT   diagnosing, preventing and/or treating cancer, particularly pancreatic
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 124; 300pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising: (a)
CC   any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC   complements of (a); (c) sequences consisting of at least 20 contiguous
CC   residues of (a); (d) sequences that hybridize to (a), under moderately
CC   stringent conditions; (e) sequences having at least 75% or 90% identity
CC   to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC   ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC   in a patient and compositions comprising polypeptides, polynucleotides,
CC   antibodies, fusion proteins, T cell populations and antigen presenting
CC   cells expressing the polypeptide are useful in treating pancreatic cancer
CC   and stimulating an immune response. The polynucleotides can be used as
CC   probes or primers for nucleic acid hybridisation, in the design and
CC   preparation of ribozyme molecules for inhibiting expression of the tumour
CC   polypeptides and proteins in the tumour cells, in vaccines and for gene
CC   therapy. Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 499 BP; 96 A; 164 C; 103 G; 130 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 499;
```

```
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        190 TCAGTGACCCTGAGCATTCT 171


RESULT 8
AAF18161/c
ID   AAF18161 standard; DNA; 2251 BP.
XX
AC   AAF18161;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Lung cancer associated polynucleotide sequence SEQ ID 180.
XX
KW   Human; lung cancer associated protein; neuroprotective; cytostatic;
KW   cardioactive; immunomodulatory; muscular active; vulnerary;
KW   gastrointestinal; nephrotropic; antiinfective; gynecological;
KW   antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW   proliferative disorder; wound healing; infectious disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055180-A2.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005918.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Ruben SM;
XX
DR   WPI; 2000-587514/55.
DR   P-PSDB; AAB58285.
XX
PT   Lung cancer associated gene sequences, referred to as lung cancer
PT   antigens, useful for treatment, prevention, and diagnosis of disorders
PT   such as lung cancer.
XX
PS   Claim 1; Page 643-644; 1425pp; English.
XX
CC   Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC   associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC   associated proteins and polynucleotide sequences, their agonists, and
CC   antagonists may have neuroprotective; cytostatic; cardioactive;
CC   immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC   general; nephrotropic; antiinfective; gynecological; or antibacterial
CC   activity. The invention also includes antibodies specific for the protein
CC   or polynucleotide sequences. The lung cancer associated polynucleotide
CC   sequences may be used for detection of lung cancer, chromosome
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The proteins may be used to treat disorders such as
CC   neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC   cardiovascular, renal, and proliferative disorders. The proteins may also
CC   be used in the treatment of wounds and infectious diseases.
CC   Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC   used in the course of the invention for the identification and
CC   characterisation of the polynucleotide and protein sequences
XX
SQ   Sequence 2251 BP; 617 A; 484 C; 514 G; 635 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 20;  DB 3;  Length 2251;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         24 TCAGTGACCCTGAGCATTCT 5


RESULT 9
ADE54085/c
ID   ADE54085 standard; cDNA; 2797 BP.
XX
AC   ADE54085;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human prostate cancer cDNA #432.
XX
KW   Human; prostate cancer; ss; cDNA combination; differential expression;
KW   gene.
XX
OS   Homo sapiens.
XX
PN   US2003190640-A1.
XX
PD   09-OCT-2003.
XX
PF   29-MAY-2002; 2002US-00252157.
XX
PR   31-MAY-2001; 2001US-0295048P.
XX
PA   (FARI/) FARIS M.
PA   (PEAR/) PEARSON C I.
XX
PI   Faris M,  Pearson CI;
XX
DR   WPI; 2003-831619/77.
XX
PT   New combination comprising cDNAs that are differentially expressed in
PT   prostate cancer, useful for diagnosing, treating or monitoring the
PT   progression of treatment of prostate cancer.
XX
PS   Claim 1; SEQ ID NO 432; 42pp; English.
XX
CC   The invention relates to a combination comprising a number of cDNAs
CC   expressed in prostate cancer. The invention also relates to a method for
CC   detecting differential expression of one or more cDNAs in a sample
CC   containing nucleic acids by hybridising a substrate with the nucleic
CC   acids, thus forming one or more hybridisation complexes, detecting
CC   hybridisation complex formation and comparing the complexes formed with
CC   standard complexes, where differences between the standard and the sample
CC   complex formation indicate differential expression of cDNAs in the
CC   sample. The differential expression is diagnostic of prostate cancer. The
CC   invention also relates to proteins and antibodies related to the cDNAs.
CC   The combination is useful for diagnosing, treating or monitoring the
CC   progression of treatment of prostate cancer. The antibodies are useful
CC   for detecting prostate cancer. This sequence represents a human prostate
CC   cancer cDNA of the invention.
XX
SQ   Sequence 2797 BP; 714 A; 640 C; 645 G; 798 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 10;  Length 2797;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db       1315 TCAGTGACCCTGAGCATTCT 1296


RESULT 10
ABV94773/c
ID   ABV94773 standard; cDNA; 5206 BP.
XX
AC   ABV94773;
XX
DT   14-JAN-2003  (first entry)
```

XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 175.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
DR P-PSDB; ABP68626.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 175; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5206 BP; 1329 A; 1217 C; 1200 G; 1460 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 5206;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 3030 TCAGTGACCCTGAGCATTCT 3011

RESULT 11
ACC50285/c
ID ACC50285 standard; cDNA; 5221 BP.
XX
AC ACC50285;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated cDNA sequence SEQ ID NO:410.
XX
KW Human; breast cancer; cytostatic; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR P-PSDB; ABR47586.
XX
PT Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
PS Claim 1; SEQ ID NO 410; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5221 BP; 1344 A; 1217 C; 1200 G; 1460 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 5221;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 3030 TCAGTGACCCTGAGCATTCT 3011

RESULT 12
ACC62247/c
ID ACC62247 standard; cDNA; 5221 BP.
XX
AC ACC62247;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human NOV3d encoding cDNA SEQ ID NO:23.
XX
KW Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;

KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003023001-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028538.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318184P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 14-DEC-2001; 2001US-0341144P.
PR 26-FEB-2002; 2002US-0359599P.
PR 05-MAR-2002; 2002US-0361663P.
PR 03-MAY-2002; 2002US-0377908P.
PR 17-MAY-2002; 2002US-0381483P.
PR 29-MAY-2002; 2002US-0383863P.
PR 02-JUL-2002; 2002US-0393332P.
PR 17-JUL-2002; 2002US-0396412P.
PR 13-AUG-2002; 2002US-0403517P.
PR 06-SEP-2002; 2002US-00236417.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
PI Malyankar UM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M;
PI Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
PI Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong M;
XX
DR WPI; 2003-313241/30.
DR P-PSDB; ABR54178.
XX
PT Novel human proteins and nucleic acid encoding the proteins, useful for
PT diagnosis, treatment and prevention of disorders involving the human
PT protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS Claim 20; Page 108-109; 460pp; English.
XX
CC The present invention describes isolated human NOVX proteins, where X is
CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
CC antiparkinsonian and antilipaemic activities, and can be used in gene
CC therapy. NOVX proteins are useful for treating or preventing a pathology
CC associated with a NOVX protein in humans and for treating a syndrome
CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human trypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
SQ Sequence 5221 BP; 1344 A; 1217 C; 1200 G; 1460 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 5221;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3030 TCAGTGACCCTGAGCATTCT 3011

RESULT 13
ACC62244/c
ID ACC62244 standard; cDNA; 5221 BP.
XX
AC ACC62244;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human NOV3a encoding cDNA SEQ ID NO:17.
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KW Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003023001-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028538.
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PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318184P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.

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PR   26-SEP-2001; 2001US-0324990P.
PR   14-DEC-2001; 2001US-0341144P.
PR   26-FEB-2002; 2002US-0359599P.
PR   05-MAR-2002; 2002US-0361663P.
PR   03-MAY-2002; 2002US-0377908P.
PR   17-MAY-2002; 2002US-0381483P.
PR   29-MAY-2002; 2002US-0383863P.
PR   02-JUL-2002; 2002US-0393332P.
PR   17-JUL-2002; 2002US-0396412P.
PR   13-AUG-2002; 2002US-0403517P.
PR   06-SEP-2002; 2002US-00236417.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Agee ML,  Alsobrook JP,  Anderson DW,  Berghs C,  Boldog FL;
PI   Burgess CE,  Casman SJ,  Catterton E,  Chant JS,  Chaudhuri A;
PI   Crabtree J,  Dipippo VA,  Edinger SR,  Eisen AJ,  Ellerman K;
PI   Gangolli EA,  Gerlach VL,  Giot L,  Gorman L,  Guo X,  Gusev VY,  Ji W;
PI   Kekuda R,  Khramtsov NV,  Leach MD,  Lepley DM,  Li L,  Liu X;
PI   Malyankar UM,  Miller CE,  Ooi CE,  Ort T,  Padigaru M,  Patturajan M;
PI   Pena CEA,  Rieger DK,  Rothenberg ME,  Shenoy SG,  Shimkets RA;
PI   Spaderna SK,  Spytek KA,  Taupier RJ,  Twomlow N,  Vernet CAM,  Voss EZ;
PI   Zerhusen BD,  Zhong M;
XX
DR   WPI; 2003-313241/30.
DR   P-PSDB; ABR54175.
XX
PT   Novel human proteins and nucleic acid encoding the proteins, useful for
PT   diagnosis, treatment and prevention of disorders involving the human
PT   protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS   Claim 20; Page 106-107; 460pp; English.
XX
CC   The present invention describes isolated human NOVX proteins, where X is
CC   1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC   ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC   hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC   antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC   antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
CC   antiparkinsonian and antilipaemic activities, and can be used in gene
CC   therapy. NOVX proteins are useful for treating or preventing a pathology
CC   associated with a NOVX protein in humans and for treating a syndrome
CC   associated with the human disease. NOVX nucleic acids, proteins and
CC   antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC   atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC   valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC   congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC   disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC   hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC   disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC   infectious disease, anorexia, cancer-associated cachexia, cancer,
CC   Alzheimer's disease, Parkinson's disease, immune disorders,
CC   haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC   ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC   sequences, which are used in examples from the present invention.
CC   ABR54277 represents a human trypsinogen protein given in comparison with
CC   the human NOV35b protein in the exemplification of the present invention
XX
SQ   Sequence 5221 BP; 1344 A; 1217 C; 1200 G; 1460 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 8;  Length 5221;
  Best Local Similarity  100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       3030 TCAGTGACCCTGAGCATTCT 3011


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AC   ACC62252;
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DT   23-JUN-2003  (first entry)
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DE   Human NOV3i encoding cDNA SEQ ID NO:33.
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KW   Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW   anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW   haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW   neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW   gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW   congenital heart defect; aortic stenosis; valve disease; transplantation;
KW   tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW   prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW   fertility; haemophilia; hypercoagulation; graft versus host disease;
KW   idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW   Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW   cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia;
KW   metabolic syndrome X; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003023001-A2.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028538.
XX
PR   07-SEP-2001; 2001US-0318120P.
PR   07-SEP-2001; 2001US-0318184P.
PR   10-SEP-2001; 2001US-0318430P.
PR   17-SEP-2001; 2001US-0322636P.
PR   17-SEP-2001; 2001US-0322781P.
PR   17-SEP-2001; 2001US-0322816P.
PR   17-SEP-2001; 2001US-0322817P.
PR   19-SEP-2001; 2001US-0323519P.
PR   20-SEP-2001; 2001US-0323631P.
PR   20-SEP-2001; 2001US-0323636P.
PR   25-SEP-2001; 2001US-0324969P.
PR   25-SEP-2001; 2001US-0325091P.
PR   26-SEP-2001; 2001US-0324990P.
PR   14-DEC-2001; 2001US-0341144P.
PR   26-FEB-2002; 2002US-0359599P.
PR   05-MAR-2002; 2002US-0361663P.
PR   03-MAY-2002; 2002US-0377908P.
PR   17-MAY-2002; 2002US-0381483P.
PR   29-MAY-2002; 2002US-0383863P.
PR   02-JUL-2002; 2002US-0393332P.
PR   17-JUL-2002; 2002US-0396412P.
PR   13-AUG-2002; 2002US-0403517P.
PR   06-SEP-2002; 2002US-00236417.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Agee ML,  Alsobrook JP,  Anderson DW,  Berghs C,  Boldog FL;
PI   Burgess CE,  Casman SJ,  Catterton E,  Chant JS,  Chaudhuri A;
PI   Crabtree J,  Dipippo VA,  Edinger SR,  Eisen AJ,  Ellerman K;
PI   Gangolli EA,  Gerlach VL,  Giot L,  Gorman L,  Guo X,  Gusev VY,  Ji W;
PI   Kekuda R,  Khramtsov NV,  Leach MD,  Lepley DM,  Li L,  Liu X;
PI   Malyankar UM,  Miller CE,  Ooi CE,  Ort T,  Padigaru M,  Patturajan M;
PI   Pena CEA,  Rieger DK,  Rothenberg ME,  Shenoy SG,  Shimkets RA;
PI   Spaderna SK,  Spytek KA,  Taupier RJ,  Twomlow N,  Vernet CAM,  Voss EZ;
PI   Zerhusen BD,  Zhong M;
XX
DR   WPI; 2003-313241/30.
DR   P-PSDB; ABR54183.
XX
PT   Novel human proteins and nucleic acid encoding the proteins, useful for
PT   diagnosis, treatment and prevention of disorders involving the human
PT   protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS   Claim 20; Page 112-113; 460pp; English.
```

```
XX
CC   The present invention describes isolated human NOVX proteins, where X is
CC   1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC   ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC   hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC   antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC   antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
CC   antiparkinsonian and antilipaemic activities, and can be used in gene
CC   therapy. NOVX proteins are useful for treating or preventing a pathology
CC   associated with a NOVX protein in humans and for treating a syndrome
CC   associated with the human disease. NOVX nucleic acids, proteins and
CC   antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC   atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC   valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC   congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC   disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC   hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC   disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC   infectious disease, anorexia, cancer-associated cachexia, cancer,
CC   Alzheimer's disease, Parkinson's disease, immune disorders,
CC   haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC   ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC   sequences, which are used in examples from the present invention.
CC   ABR54277 represents a human trypsinogen protein given in comparison with
CC   the human NOV35b protein in the exemplification of the present invention
XX
SQ   Sequence 5221 BP; 1344 A; 1217 C; 1200 G; 1460 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 8;  Length 5221;
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Db       3030 TCAGTGACCCTGAGCATTCT 3011


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AC   ACC62250;
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DT   23-JUN-2003  (first entry)
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DE   Human NOV3g encoding cDNA SEQ ID NO:29.
XX
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KW   anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW   haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW   neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic;
KW   gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW   congenital heart defect; aortic stenosis; valve disease; transplantation;
KW   tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW   prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW   fertility; haemophilia; hypercoagulation; graft versus host disease;
KW   idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW   Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW   cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia;
KW   metabolic syndrome X; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003023001-A2.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028538.
XX
PR   07-SEP-2001; 2001US-0318120P.
PR   07-SEP-2001; 2001US-0318184P.
PR   10-SEP-2001; 2001US-0318430P.
PR   17-SEP-2001; 2001US-0322636P.
PR   17-SEP-2001; 2001US-0322781P.
PR   17-SEP-2001; 2001US-0322816P.
PR   17-SEP-2001; 2001US-0322817P.
PR   19-SEP-2001; 2001US-0323519P.
PR   20-SEP-2001; 2001US-0323631P.
PR   20-SEP-2001; 2001US-0323636P.
PR   25-SEP-2001; 2001US-0324969P.
PR   25-SEP-2001; 2001US-0325091P.
PR   26-SEP-2001; 2001US-0324990P.
PR   14-DEC-2001; 2001US-0341144P.
PR   26-FEB-2002; 2002US-0359599P.
PR   05-MAR-2002; 2002US-0361663P.
PR   03-MAY-2002; 2002US-0377908P.
PR   17-MAY-2002; 2002US-0381483P.
PR   29-MAY-2002; 2002US-0383863P.
PR   02-JUL-2002; 2002US-0393332P.
PR   17-JUL-2002; 2002US-0396412P.
PR   13-AUG-2002; 2002US-0403517P.
PR   06-SEP-2002; 2002US-00236417.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Agee ML,  Alsobrook JP,  Anderson DW,  Berghs C,  Boldog FL;
PI   Burgess CE,  Casman SJ,  Catterton E,  Chant JS,  Chaudhuri A;
PI   Crabtree J,  Dipippo VA,  Edinger SR,  Eisen AJ,  Ellerman K;
PI   Gangolli EA,  Gerlach VL,  Giot L,  Gorman L,  Guo X,  Gusev VY,  Ji W;
PI   Kekuda R,  Khramtsov NV,  Leach MD,  Lepley DM,  Li L,  Liu X;
PI   Malyankar UM,  Miller CE,  Ooi CE,  Ort T,  Padigaru M,  Patturajan M;
PI   Pena CEA,  Rieger DK,  Rothenberg ME,  Shenoy SG,  Shimkets RA;
PI   Spaderna SK,  Spytek KA,  Taupier RJ,  Twomlow N,  Vernet CAM,  Voss EZ;
PI   Zerhusen BD,  Zhong M;
XX
DR   WPI; 2003-313241/30.
DR   P-PSDB; ABR54181.
XX
PT   Novel human proteins and nucleic acid encoding the proteins, useful for
PT   diagnosis, treatment and prevention of disorders involving the human
PT   protein or nucleic acid e.g. cardiac and neurological disorders.
XX
PS   Claim 20; Page 110-111; 460pp; English.
XX
CC   The present invention describes isolated human NOVX proteins, where X is
CC   1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC   ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC   hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC   antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
CC   antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,
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CC   therapy. NOVX proteins are useful for treating or preventing a pathology
CC   associated with a NOVX protein in humans and for treating a syndrome
CC   associated with the human disease. NOVX nucleic acids, proteins and
CC   antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC   atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC   valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
CC   congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC   disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC   hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC   disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC   infectious disease, anorexia, cancer-associated cachexia, cancer,
CC   Alzheimer's disease, Parkinson's disease, immune disorders,
CC   haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC   ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC   sequences, which are used in examples from the present invention.
CC   ABR54277 represents a human trypsinogen protein given in comparison with
CC   the human NOV35b protein in the exemplification of the present invention
XX
SQ   Sequence 5221 BP; 1344 A; 1217 C; 1200 G; 1460 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 8;  Length 5221;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TCAGTGACCCTGAGCATTCT 20
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Db       3030 TCAGTGACCCTGAGCATTCT 3011
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Search completed: October 22, 2005, 03:27:45
Job time : 244 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2005, 03:23:50 ; Search time 1730 Seconds
(without alignments)
440.049 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 23	20	100.0	413	1	AV654525	AV654525 AV654525
c 24	20	100.0	425	1	AA488522	AA488522 ab37e04.r
c 25	20	100.0	428	7	N76244	N76244 yv37f07.r1
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ALIGNMENTS

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VERSION N42677.1 GI:1167107
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 204)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 160
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 160.
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/clone="IMAGE:271847"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 204;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
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Db 89 TCAGTGACCCTGAGCATTCT 70

RESULT 2
T30737/c
LOCUS T30737 252 bp mRNA linear EST 06-SEP-1995
DEFINITION EST21632 Human Adrenal gland Homo sapiens cDNA 5' end similar to None, mRNA sequence.
ACCESSION T30737
VERSION T30737.1 GI:612835
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 252)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Other_ESTs: THC9846
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .252
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):100640"
/db_xref="taxon:9606"
/clone_lib="Human Adrenal gland"
/note="Organ: adrenal gland"
ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 252;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 139 TCAGTGACCCTGAGCATTCT 120

RESULT 3
T31651/c
LOCUS T31651 267 bp mRNA linear EST 06-SEP-1995
DEFINITION EST36481 Human Embryo Homo sapiens cDNA 5' end similar to None, mRNA sequence.
ACCESSION T31651
VERSION T31651.1 GI:613749
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 267)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Other_ESTs: THC9846
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .267
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):101890"
/db_xref="taxon:9606"
/tissue_type="embryo"
/clone_lib="Human Embryo"
ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 267;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 222 TCAGTGACCCTGAGCATTCT 203

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RESULT 4
R11600/c
LOCUS       R11600                  272 bp    mRNA    linear   EST 11-APR-1995
DEFINITION  yf47b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:129979 5', mRNA sequence.
ACCESSION   R11600
VERSION     R11600.1  GI:764335
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 272)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 588
            High quality sequence stops: 229 Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 588   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 229.
FEATURES             Location/Qualifiers
     source          1. .272
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:482140"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:129979"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 272;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        102 TCAGTGACCCTGAGCATTCT 83


RESULT 5
T98412/c
LOCUS       T98412                  274 bp    mRNA    linear   EST 31-MAR-1995
DEFINITION  ye60a08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:122102 5', mRNA sequence.
ACCESSION   T98412
VERSION     T98412.1  GI:748149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 274)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 781
            High qality sequence stops: 231 Source: IMAGE Consortium, LLNL This
            clone is available royalty-free through LLNL ; contact the IMAGE
            Consortium (info@image.llnl.gov) for further information.
            Insert Length: 781   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 231.
FEATURES             Location/Qualifiers
     source          1. .274
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                     /mol_type="mRNA"
                     /db_xref="GDB:474647"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:122102"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        104 TCAGTGACCCTGAGCATTCT 85


RESULT 6
BF954609
LOCUS       BF954609                278 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  RC5-NN1165-141100-012-C04 NN1165 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF954609
VERSION     BF954609.1  GI:12371884
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 278)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
```

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            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC5&t2=RC5-NN1165-
            141100-012-C04&t3=2000-11-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 278.
FEATURES             Location/Qualifiers
     source          1. .278
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NN1165"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 278;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         63 TCAGTGACCCTGAGCATTCT 82


RESULT 7
BQ340410
LOCUS       BQ340410                280 bp    mRNA    linear   EST 20-MAY-2002
DEFINITION  QV2-NN2006-110501-654-h05 NN2006 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ340410
VERSION     BQ340410.1  GI:21001235
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-NN2006-
            110501-654-h05&t3=2001-05-11&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 280.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NN2006"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 5;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         83 TCAGTGACCCTGAGCATTCT 102


RESULT 8
H47264/c
LOCUS       H47264                  281 bp    mRNA    linear   EST 16-AUG-1995
DEFINITION  yp73h11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:193125 5', mRNA sequence.
ACCESSION   H47264
VERSION     H47264.1  GI:923316
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 281)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2606
            High quality sequence stops: 266
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 2606   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 266.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3762146"
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/db_xref="taxon:9606"
/clone="IMAGE:193125"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
||||||||||||||||||||
Db 275 TCAGTGACCCTGAGCATTCT 256

RESULT 9
T96436/c
LOCUS T96436 295 bp mRNA linear EST 27-MAR-1995
DEFINITION ye49b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121035 5', mRNA sequence.
ACCESSION T96436
VERSION T96436.1 GI:735060
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 295)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1307
High quality sequence stops: 250 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1307 . Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 250.
FEATURES Location/Qualifiers
source 1. .295
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:473580"
/db_xref="taxon:9606"
/clone="IMAGE:121035"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 295;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
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Db 218 TCAGTGACCCTGAGCATTCT 199

RESULT 10
AA248240/c
LOCUS AA248240 316 bp mRNA linear EST 11-MAR-1997
DEFINITION csg1715.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence.
ACCESSION AA248240
VERSION AA248240.1 GI:1878893
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 316)
AUTHORS Liew,C.C.
TITLE cDNAs from human fetal heart (1997)
JOURNAL Unpublished (1997)
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
PCR PRimers
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
FEATURES Location/Qualifiers
source 1. .316
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="E. coli XL1-Blue"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAGTGACCCTGAGCATTCT 20
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Db 55 TCAGTGACCCTGAGCATTCT 36

RESULT 11
CB139587/c
LOCUS CB139587 330 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0192610 L15CKK1 Homo sapiens cDNA clone L15CKK1-15-C12 5', mRNA sequence.

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ACCESSION   CB139587
VERSION     CB139587.1  GI:28112612
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 15  row: C  column: 12
            High quality sequence stop: 330.
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L15CKK1-15-C12"
                     /sex="M"
                     /cell_line="CK-K1"
                     /lab_host="Top10F'"
                     /clone_lib="L15CKK1"
                     /note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including
                     EcoRI site by treatment of T4 RNA ligase and the first
                     strand cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        239 TCAGTGACCCTGAGCATTCT 220


RESULT 12
AA350449/c
LOCUS       AA350449                340 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST57717 Infant brain Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION   AA350449
VERSION     AA350449.1  GI:2002766
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: EST57716 THC172395
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):104040"
                     /db_xref="taxon:9606"
                     /sex="female"
                     /dev_stage="infant"
                     /clone_lib="Infant brain"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 41;
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Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         90 TCAGTGACCCTGAGCATTCT 71


RESULT 13
F11726/c
LOCUS       F11726                  341 bp    mRNA    linear   EST 12-MAR-1995
DEFINITION  HSC30G091 normalized infant brain cDNA Homo sapiens cDNA clone
            c-30g09, mRNA sequence.
ACCESSION   F11726
VERSION     F11726.1  GI:706032
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 341)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
```

```
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
   PUBMED   7757816
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-30g09
            Seq primer: (-21)M13_universal.
FEATURES             Location/Qualifiers
     source          1. .341
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="c-30g09"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /clone_lib="normalized infant brain cDNA"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient; tissue_type=total
                     brain; total mRNA was oligo-(dT) primed and directionally
                     cloned 5' -> 3' into the HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares, Psychiatry
                     Dept. Columbia University, USA. Normalization_method:
                     Bento Soares, P.N.A.S in press"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        325 TCAGTGACCCTGAGCATTCT 306


RESULT 14
BF850358
LOCUS       BF850358                365 bp    mRNA    linear   EST 16-JAN-2001
DEFINITION  CM3-EN0111-181100-510-f10 EN0111 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF850358
VERSION     BF850358.1  GI:12237520
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 365)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-EN0111-
            181100-510-f10&t3=2000-11-18&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 365.
FEATURES             Location/Qualifiers
     source          1. .365
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="EN0111"
                     /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 365;
  Best Local Similarity   100.0%;  Pred. No. 41;
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Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db        157 TCAGTGACCCTGAGCATTCT 176


RESULT 15
BE617225/c
LOCUS       BE617225                366 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601441908F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846361 5',
            mRNA sequence.
ACCESSION   BE617225
VERSION     BE617225.1  GI:9888163
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9558  row: o  column: 02
            High quality sequence stop: 366.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3846361"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_65"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "
ORIGIN
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Query Match 100.0%; Score 20; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCAGTGACCCTGAGCATTCT 20
              ||||||||||||||||||||
Db         81 TCAGTGACCCTGAGCATTCT 62
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Search completed: October 22, 2005, 21:03:59
Job time : 1737 secs

10/619,253
SDO 3, res. 883-5206

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 15:42:35 ; Search time 17 Seconds
(without alignments)
3.814 Million cell updates/sec

Title: US-10-619-253-3
Perfect score: 4324
Sequence: 1 gtactacaaacctggcttgc.....aataaaagtgaagtgaatct 4324

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 457 seqs, 7497 residues

Total number of hits satisfying chosen parameters: 914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 739 summaries

Database : rni.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	39	0.9	39	1	US-08-332-420-62	Sequence 62, Appl
c	2	20.8	0.5	26	1	US-09-380-262B-2	Sequence 2, Appli
c	3	20	0.5	20	1	US-09-780-045-110	Sequence 110, App
c	4	19.4	0.4	21	1	US-09-422-978-11421	Sequence 11421, A
c	5	18.4	0.4	23	1	PCT-US94-05407-7	Sequence 7, Appli
	6	18.4	0.4	23	1	PCT-US94-05407-8	Sequence 8, Appli
	7	17.4	0.4	20	1	US-08-203-198-3	Sequence 3, Appli
	8	17.4	0.4	21	1	US-08-128-011-4	Sequence 4, Appli
	9	17.4	0.4	21	1	US-08-403-888A-142	Sequence 142, App
	10	17	0.4	17	1	US-09-788-338-3	Sequence 3, Appli
	11	17	0.4	17	1	US-09-300-958A-64	Sequence 64, Appl
	12	17	0.4	17	1	US-09-090-672B-106	Sequence 106, App
c	13	17	0.4	20	1	US-09-120-853-4	Sequence 4, Appli
c	14	17	0.4	20	1	US-09-228-942-7	Sequence 7, Appli
	15	17	0.4	20	1	US-08-482-918-32	Sequence 32, Appl
	16	17	0.4	20	1	US-09-224-681-32	Sequence 32, Appl
	17	17	0.4	20	1	US-08-336-728A-32	Sequence 32, Appl
	18	17	0.4	20	1	US-09-635-251-32	Sequence 32, Appl
	19	16.8	0.4	20	1	US-08-004-552-1	Sequence 1, Appli
c	20	16.8	0.4	20	1	US-08-863-639A-72	Sequence 72, Appl
	21	16.8	0.4	20	1	US-08-863-639A-93	Sequence 93, Appl
c	22	16.8	0.4	20	1	US-09-725-265-31	Sequence 31, Appl
c	23	16.8	0.4	20	1	US-09-909-595-56	Sequence 56, Appl
	24	16.8	0.4	20	1	US-09-081-385-40	Sequence 40, Appl
	25	16.8	0.4	20	1	US-09-860-473-56	Sequence 56, Appl
c	26	16.8	0.4	20	1	US-09-556-127-31	Sequence 31, Appl
	27	16.8	0.4	21	1	US-09-581-822-2	Sequence 2, Appli
c	28	16.4	0.4	18	1	US-09-475-947A-104	Sequence 104, App
	29	16.4	0.4	18	1	US-09-725-265-16	Sequence 16, Appl
	30	16.4	0.4	18	1	US-09-556-127-16	Sequence 16, Appl
	31	16.4	0.4	19	1	US-09-696-791-924	Sequence 924, App
	32	16.4	0.4	20	1	US-09-965-599-4	Sequence 4, Appli
	33	16	0.4	17	1	US-09-129-603-4	Sequence 4, Appli
	34	16	0.4	17	1	US-09-090-672B-105	Sequence 105, App
	35	16	0.4	17	1	US-09-090-672B-107	Sequence 107, App
	36	16	0.4	18	1	US-09-437-076-2	Sequence 2, Appli
	37	16	0.4	18	1	US-09-637-751A-5	Sequence 5, Appli
	38	16	0.4	18	1	US-09-637-751A-6	Sequence 6, Appli
	39	16	0.4	18	1	US-09-994-311-5	Sequence 5, Appli
	40	16	0.4	18	1	US-09-994-311-6	Sequence 6, Appli
	41	16	0.4	18	1	US-09-142-108C-29	Sequence 29, Appl
	42	16	0.4	18	1	US-09-904-744-2	Sequence 2, Appli
	43	16	0.4	20	1	US-09-487-445-55	Sequence 55, Appl
c	44	16	0.4	20	1	US-09-112-580-161	Sequence 161, App
c	45	15.8	0.4	19	1	US-08-850-880-10	Sequence 10, Appl
c	46	15.8	0.4	19	1	US-08-944-916-10	Sequence 10, Appl
c	47	15.8	0.4	19	1	US-09-159-363-2	Sequence 2, Appli
c	48	15.8	0.4	19	1	US-09-635-969-6	Sequence 6, Appli
c	49	15.8	0.4	19	1	US-09-632-021-4	Sequence 4, Appli
c	50	15.8	0.4	19	1	US-09-272-432A-10	Sequence 10, Appl
	51	15.8	0.4	19	1	US-09-350-852A-3	Sequence 3, Appli
	52	15.8	0.4	19	1	US-09-696-791-3907	Sequence 3907, Ap
c	53	15.8	0.4	19	1	5212080-3	Patent No. 5212080
c	54	15.8	0.4	19	1	5212080-3	Patent No. 5212080
	55	15.6	0.4	17	1	US-08-937-067-17	Sequence 17, Appl
c	56	15.4	0.4	17	1	US-08-373-124A-2151	Sequence 2151, Ap
c	57	15.4	0.4	17	1	US-08-373-124A-2153	Sequence 2153, Ap
c	58	15.4	0.4	17	1	US-08-435-628-2151	Sequence 2151, Ap
c	59	15.4	0.4	17	1	US-08-435-628-2153	Sequence 2153, Ap
	60	15.4	0.4	17	1	US-08-584-040-2549	Sequence 2549, Ap
	61	15.4	0.4	17	1	US-09-371-772B-1073	Sequence 1073, Ap
	62	15.4	0.4	17	1	US-09-685-664B-1073	Sequence 1073, Ap
c	63	15.4	0.4	18	1	US-08-974-565C-10	Sequence 10, Appl
	64	15.4	0.4	18	1	US-09-725-265-17	Sequence 17, Appl
	65	15.4	0.4	18	1	US-09-725-265-20	Sequence 20, Appl
	66	15.4	0.4	18	1	US-09-556-127-17	Sequence 17, Appl
	67	15.4	0.4	18	1	US-09-556-127-20	Sequence 20, Appl
	68	15.4	0.4	18	1	PCT-US91-03680-73	Sequence 73, Appl
	69	15.4	0.4	19	1	US-09-696-791-253	Sequence 253, App
	70	15.4	0.4	19	1	US-09-696-791-254	Sequence 254, App
	71	15.4	0.4	19	1	US-09-696-791-925	Sequence 925, App
	72	15.2	0.4	17	1	US-09-390-324B-2	Sequence 2, Appli
	73	15.2	0.4	17	1	US-10-015-593-2	Sequence 2, Appli
c	74	15.2	0.4	19	1	US-09-130-079-1	Sequence 1, Appli
c	75	15.2	0.4	19	1	US-10-103-614A-4	Sequence 4, Appli
	76	15.2	0.4	19	1	US-09-371-307-85	Sequence 85, Appl
c	77	15	0.3	15	1	US-08-452-196A-6	Sequence 6, Appli
	78	15	0.3	15	1	US-07-971-978-1	Sequence 1, Appli
c	79	15	0.3	15	1	US-08-756-728A-2	Sequence 2, Appli
	80	15	0.3	15	1	US-08-663-918-3	Sequence 3, Appli
c	81	15	0.3	15	1	US-08-663-918-4	Sequence 4, Appli
	82	15	0.3	15	1	US-08-292-620A-361	Sequence 361, App
	83	15	0.3	15	1	US-08-292-620A-362	Sequence 362, App
	84	15	0.3	15	1	US-08-771-789-3	Sequence 3, Appli
c	85	15	0.3	15	1	US-08-771-789-4	Sequence 4, Appli
	86	15	0.3	15	1	US-08-358-556A-10	Sequence 10, Appl
c	87	15	0.3	15	1	US-08-358-556A-16	Sequence 16, Appl
c	88	15	0.3	15	1	US-08-585-684B-638	Sequence 638, App
	89	15	0.3	15	1	US-08-922-170B-5	Sequence 5, Appli
c	90	15	0.3	15	1	US-08-863-639A-5	Sequence 5, Appli
	91	15	0.3	15	1	US-08-863-639A-9	Sequence 9, Appli
	92	15	0.3	15	1	US-08-693-831-1	Sequence 1, Appli
	93	15	0.3	15	1	US-08-832-021-51	Sequence 51, Appl
	94	15	0.3	15	1	US-09-183-619-4	Sequence 4, Appli
	95	15	0.3	15	1	US-09-071-845-361	Sequence 361, App
	96	15	0.3	15	1	US-09-071-845-362	Sequence 362, App
c	97	15	0.3	15	1	US-09-038-073-638	Sequence 638, App
c	98	15	0.3	15	1	US-09-167-375-1	Sequence 1, Appli
	99	15	0.3	15	1	US-08-150-156A-19	Sequence 19, Appl
c	100	15	0.3	15	1	US-08-150-156A-20	Sequence 20, Appl
	101	15	0.3	15	1	US-08-108-591B-17	Sequence 17, Appl
c	102	15	0.3	15	1	US-08-108-591B-18	Sequence 18, Appl
c	103	15	0.3	15	1	US-09-619-103-21	Sequence 21, Appl
	104	15	0.3	15	1	US-09-300-958A-68	Sequence 68, Appl
	105	15	0.3	15	1	US-08-988-024C-9	Sequence 9, Appli
	106	15	0.3	15	1	US-09-435-739-5	Sequence 5, Appli

107	15	0.3	15	1	US-10-091-231-2	Sequence 2, Appli
108	15	0.3	15	1	US-09-930-218-5	Sequence 5, Appli
109	15	0.3	15	1	US-08-468-719A-17	Sequence 17, Appl
c 110	15	0.3	15	1	US-08-468-719A-18	Sequence 18, Appl
111	15	0.3	15	1	US-08-462-977B-17	Sequence 17, Appl
c 112	15	0.3	15	1	US-08-462-977B-18	Sequence 18, Appl
113	15	0.3	15	1	US-09-988-113-5	Sequence 5, Appli
114	15	0.3	15	1	US-10-352-704-10	Sequence 10, Appl
c 115	15	0.3	15	1	US-10-352-704-16	Sequence 16, Appl
116	15	0.3	16	1	US-07-971-978-36	Sequence 36, Appl
117	15	0.3	16	1	US-07-971-978-42	Sequence 42, Appl
118	15	0.3	16	1	US-07-971-978-60	Sequence 60, Appl
119	15	0.3	16	1	US-08-415-370-2	Sequence 2, Appli
120	15	0.3	16	1	US-08-687-551-15	Sequence 15, Appl
121	15	0.3	16	1	US-09-141-764-2	Sequence 2, Appli
c 122	15	0.3	16	1	US-08-851-843A-131	Sequence 131, App
c 123	15	0.3	16	1	US-08-854-050-131	Sequence 131, App
c 124	15	0.3	16	1	US-09-430-323-131	Sequence 131, App
125	15	0.3	16	1	US-09-507-345A-2	Sequence 2, Appli
126	15	0.3	16	1	US-09-507-345A-3	Sequence 3, Appli
127	15	0.3	16	1	US-09-507-345A-4	Sequence 4, Appli
128	15	0.3	16	1	US-09-507-345A-5	Sequence 5, Appli
129	15	0.3	16	1	US-09-507-345A-6	Sequence 6, Appli
130	15	0.3	16	1	US-09-507-345A-7	Sequence 7, Appli
131	15	0.3	16	1	US-09-507-345A-8	Sequence 8, Appli
c 132	15	0.3	16	1	US-09-619-103-22	Sequence 22, Appl
133	15	0.3	16	1	US-09-739-928-2	Sequence 2, Appli
134	15	0.3	16	1	US-09-739-928-3	Sequence 3, Appli
135	15	0.3	16	1	US-09-739-928-4	Sequence 4, Appli
136	15	0.3	16	1	US-09-739-928-5	Sequence 5, Appli
137	15	0.3	16	1	US-09-739-928-6	Sequence 6, Appli
138	15	0.3	16	1	US-09-739-928-7	Sequence 7, Appli
139	15	0.3	16	1	US-09-739-928-8	Sequence 8, Appli
c 140	15	0.3	16	1	US-09-958-610A-1	Sequence 1, Appli
141	15	0.3	16	1	US-09-895-585-9	Sequence 9, Appli
142	15	0.3	16	1	US-09-152-059-70	Sequence 70, Appl
c 143	15	0.3	16	1	US-09-766-253-131	Sequence 131, App
144	15	0.3	17	1	US-08-851-843A-132	Sequence 132, App
145	15	0.3	17	1	US-09-250-075-5	Sequence 5, Appli
146	15	0.3	17	1	US-08-854-050-132	Sequence 132, App
147	15	0.3	17	1	US-08-821-827C-30	Sequence 30, Appl
148	15	0.3	17	1	US-09-290-202B-30	Sequence 30, Appl
149	15	0.3	17	1	US-09-430-323-132	Sequence 132, App
150	15	0.3	17	1	US-08-584-040-2550	Sequence 2550, Ap
151	15	0.3	17	1	US-08-584-040-2551	Sequence 2551, Ap
152	15	0.3	17	1	US-08-584-040-2552	Sequence 2552, Ap
c 153	15	0.3	17	1	US-08-584-040-5642	Sequence 5642, Ap
c 154	15	0.3	17	1	US-09-619-103-23	Sequence 23, Appl
155	15	0.3	17	1	US-09-726-096A-5	Sequence 5, Appli
156	15	0.3	17	1	US-09-475-947A-118	Sequence 118, App
157	15	0.3	17	1	US-09-300-958A-63	Sequence 63, Appl
158	15	0.3	17	1	US-09-371-772B-1074	Sequence 1074, Ap
159	15	0.3	17	1	US-09-371-772B-1075	Sequence 1075, Ap
160	15	0.3	17	1	US-09-371-772B-1076	Sequence 1076, Ap
c 161	15	0.3	17	1	US-09-371-772B-2532	Sequence 2532, Ap
162	15	0.3	17	1	US-09-766-253-132	Sequence 132, App
163	15	0.3	17	1	US-09-685-664B-1074	Sequence 1074, Ap
164	15	0.3	17	1	US-09-685-664B-1075	Sequence 1075, Ap
165	15	0.3	17	1	US-09-685-664B-1076	Sequence 1076, Ap
c 166	15	0.3	17	1	US-09-685-664B-2532	Sequence 2532, Ap
167	15	0.3	18	1	US-08-621-914A-16	Sequence 16, Appl
c 168	15	0.3	18	1	US-08-346-429-3	Sequence 3, Appli
169	15	0.3	18	1	US-08-358-556A-12	Sequence 12, Appl
c 170	15	0.3	18	1	US-08-358-556A-18	Sequence 18, Appl
171	15	0.3	18	1	US-08-469-852A-4	Sequence 4, Appli
172	15	0.3	18	1	US-08-295-509B-4	Sequence 4, Appli
173	15	0.3	18	1	US-08-884-029-9	Sequence 9, Appli
c 174	15	0.3	18	1	US-08-941-445A-30	Sequence 30, Appl
c 175	15	0.3	18	1	US-09-437-076-1	Sequence 1, Appli
176	15	0.3	18	1	US-09-637-751A-7	Sequence 7, Appli
177	15	0.3	18	1	US-09-545-225-9	Sequence 9, Appli
c 178	15	0.3	18	1	US-09-619-103-24	Sequence 24, Appl
179	15	0.3	18	1	US-09-370-541-14	Sequence 14, Appl
180	15	0.3	18	1	US-10-125-295-9	Sequence 9, Appli
c 181	15	0.3	18	1	US-09-803-263-6	Sequence 6, Appli
182	15	0.3	18	1	US-09-803-263-7	Sequence 7, Appli
183	15	0.3	18	1	US-09-994-311-7	Sequence 7, Appli
184	15	0.3	18	1	US-09-142-108C-27	Sequence 27, Appl
185	15	0.3	18	1	US-09-142-108C-28	Sequence 28, Appl
186	15	0.3	18	1	US-09-809-545A-84	Sequence 84, Appl
187	15	0.3	18	1	US-10-352-704-12	Sequence 12, Appl
c 188	15	0.3	18	1	US-10-352-704-18	Sequence 18, Appl
c 189	15	0.3	18	1	US-09-904-744-1	Sequence 1, Appli
190	15	0.3	18	1	PCT-US91-03680-74	Sequence 74, Appl
191	15	0.3	18	1	PCT-US94-05407-4	Sequence 4, Appli
192	14.8	0.3	18	1	US-08-384-324-4	Sequence 4, Appli
193	14.8	0.3	18	1	US-08-885-126-12	Sequence 12, Appl
194	14.8	0.3	18	1	US-08-944-483-13	Sequence 13, Appl
c 195	14.8	0.3	18	1	US-08-700-530-3	Sequence 3, Appli
196	14.8	0.3	18	1	US-08-700-530-4	Sequence 4, Appli
197	14.8	0.3	18	1	PCT-US96-01473-4	Sequence 4, Appli
198	14.4	0.3	16	1	US-08-087-387-6	Sequence 6, Appli
199	14.4	0.3	16	1	US-08-455-627-6	Sequence 6, Appli
200	14.4	0.3	16	1	US-07-971-978-2	Sequence 2, Appli
c 201	14.4	0.3	16	1	US-07-971-978-2	Sequence 2, Appli
202	14.4	0.3	16	1	US-08-461-271-6	Sequence 6, Appli
203	14.4	0.3	16	1	US-08-713-685A-6	Sequence 6, Appli
204	14.4	0.3	16	1	US-08-689-856-6	Sequence 6, Appli
205	14.4	0.3	16	1	US-09-070-477-6	Sequence 6, Appli
206	14.4	0.3	16	1	US-08-882-649A-8	Sequence 8, Appli
c 207	14.4	0.3	16	1	US-09-371-772B-5823	Sequence 5823, Ap
208	14.4	0.3	17	1	US-08-373-124A-1060	Sequence 1060, Ap
c 209	14.4	0.3	17	1	US-08-373-124A-2149	Sequence 2149, Ap
c 210	14.4	0.3	17	1	US-08-373-124A-2155	Sequence 2155, Ap
211	14.4	0.3	17	1	US-08-435-628-1060	Sequence 1060, Ap
c 212	14.4	0.3	17	1	US-08-435-628-2149	Sequence 2149, Ap
c 213	14.4	0.3	17	1	US-08-435-628-2155	Sequence 2155, Ap
214	14.4	0.3	17	1	US-08-584-040-2548	Sequence 2548, Ap
c 215	14.4	0.3	17	1	US-08-584-040-2553	Sequence 2553, Ap
c 216	14.4	0.3	17	1	US-08-584-040-2554	Sequence 2554, Ap
c 217	14.4	0.3	17	1	US-08-584-040-5915	Sequence 5915, Ap
218	14.4	0.3	17	1	US-09-371-772B-1072	Sequence 1072, Ap
c 219	14.4	0.3	17	1	US-09-371-772B-1077	Sequence 1077, Ap
c 220	14.4	0.3	17	1	US-09-371-772B-1078	Sequence 1078, Ap
c 221	14.4	0.3	17	1	US-09-371-772B-2754	Sequence 2754, Ap
c 222	14.4	0.3	17	1	US-09-371-772B-4739	Sequence 4739, Ap
223	14.4	0.3	17	1	US-09-827-998-744	Sequence 744, App
224	14.4	0.3	17	1	US-09-827-998-745	Sequence 745, App
225	14.4	0.3	17	1	US-09-685-664B-1072	Sequence 1072, Ap
c 226	14.4	0.3	17	1	US-09-685-664B-1077	Sequence 1077, Ap
c 227	14.4	0.3	17	1	US-09-685-664B-1078	Sequence 1078, Ap
c 228	14.4	0.3	17	1	US-09-685-664B-2754	Sequence 2754, Ap
229	14.4	0.3	18	1	US-09-475-947A-104	Sequence 104, App
230	14.4	0.3	18	1	US-08-330-000-1	Sequence 1, Appli
231	14.4	0.3	18	1	US-08-965-908-1	Sequence 1, Appli
232	14.4	0.3	18	1	US-09-256-492-14	Sequence 14, Appl
c 233	14.4	0.3	18	1	US-09-143-212-64	Sequence 64, Appl
c 234	14.4	0.3	18	1	US-09-012-097A-58	Sequence 58, Appl
c 235	14.4	0.3	18	1	US-08-584-040-3020	Sequence 3020, Ap
236	14.4	0.3	18	1	US-09-725-265-15	Sequence 15, Appl
237	14.4	0.3	18	1	US-09-725-265-19	Sequence 19, Appl
c 238	14.4	0.3	18	1	US-09-481-620A-91	Sequence 91, Appl
239	14.4	0.3	18	1	US-09-422-978-4138	Sequence 4138, Ap
c 240	14.4	0.3	18	1	US-09-853-533A-17	Sequence 17, Appl
241	14.4	0.3	18	1	US-09-853-533A-18	Sequence 18, Appl
c 242	14.4	0.3	18	1	US-09-371-772B-1448	Sequence 1448, Ap
c 243	14.4	0.3	18	1	US-09-781-804-58	Sequence 58, Appl
c 244	14.4	0.3	18	1	US-09-747-391-19	Sequence 19, Appl
245	14.4	0.3	18	1	US-09-556-127-15	Sequence 15, Appl
246	14.4	0.3	18	1	US-09-556-127-19	Sequence 19, Appl
c 247	14.4	0.3	18	1	US-09-685-664B-1448	Sequence 1448, Ap
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249	14.2	0.3	20	1	US-09-725-265-31	Sequence 31, Appl
250	14.2	0.3	20	1	US-09-556-127-31	Sequence 31, Appl
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252	14	0.3	14	1	US-08-173-489C-76	Sequence 76, Appl

253	14	0.3	14	1	US-08-832-021-15	Sequence 15, Appl
254	14	0.3	14	1	US-08-724-466B-12	Sequence 12, Appl
255	14	0.3	14	1	US-08-882-164D-12	Sequence 12, Appl
256	14	0.3	14	1	US-09-462-569B-1	Sequence 1, Appli
c 257	14	0.3	14	1	US-09-619-103-20	Sequence 20, Appl
258	14	0.3	14	1	US-10-103-614A-1	Sequence 1, Appli
259	14	0.3	14	1	US-09-152-059-65	Sequence 65, Appl
260	14	0.3	14	1	US-09-152-059-66	Sequence 66, Appl
261	14	0.3	14	1	US-09-152-059-67	Sequence 67, Appl
262	14	0.3	14	1	US-09-152-059-68	Sequence 68, Appl
263	14	0.3	14	1	US-09-152-059-80	Sequence 80, Appl
c 264	14	0.3	14	1	US-09-152-059-81	Sequence 81, Appl
c 265	14	0.3	14	1	US-09-152-059-82	Sequence 82, Appl
266	14	0.3	14	1	US-09-152-059-83	Sequence 83, Appl
c 267	14	0.3	14	1	US-09-152-059-84	Sequence 84, Appl
c 268	14	0.3	14	1	US-09-152-059-85	Sequence 85, Appl
269	14	0.3	14	1	US-09-152-059-86	Sequence 86, Appl
c 270	14	0.3	14	1	US-09-152-059-87	Sequence 87, Appl
c 271	14	0.3	14	1	US-09-152-059-88	Sequence 88, Appl
272	14	0.3	14	1	US-09-152-059-89	Sequence 89, Appl
c 273	14	0.3	14	1	US-09-152-059-90	Sequence 90, Appl
c 274	14	0.3	14	1	US-09-152-059-91	Sequence 91, Appl
275	14	0.3	14	1	US-09-152-059-92	Sequence 92, Appl
c 276	14	0.3	14	1	US-09-152-059-93	Sequence 93, Appl
c 277	14	0.3	14	1	US-09-152-059-94	Sequence 94, Appl
c 278	14	0.3	14	1	US-09-152-059-96	Sequence 96, Appl
c 279	14	0.3	14	1	US-09-152-059-97	Sequence 97, Appl
280	14	0.3	14	1	US-09-152-059-98	Sequence 98, Appl
c 281	14	0.3	14	1	US-09-152-059-99	Sequence 99, Appl
c 282	14	0.3	14	1	US-09-152-059-100	Sequence 100, App
283	14	0.3	14	1	US-09-152-059-101	Sequence 101, App
c 284	14	0.3	14	1	US-09-152-059-102	Sequence 102, App
c 285	14	0.3	14	1	US-09-152-059-103	Sequence 103, App
286	14	0.3	14	1	US-09-152-059-104	Sequence 104, App
c 287	14	0.3	14	1	US-09-152-059-105	Sequence 105, App
c 288	14	0.3	14	1	US-09-152-059-106	Sequence 106, App
289	14	0.3	14	1	US-09-152-059-107	Sequence 107, App
c 290	14	0.3	14	1	US-09-152-059-108	Sequence 108, App
c 291	14	0.3	14	1	US-09-152-059-109	Sequence 109, App
292	14	0.3	14	1	US-09-152-059-110	Sequence 110, App
c 293	14	0.3	14	1	US-09-152-059-111	Sequence 111, App
c 294	14	0.3	14	1	US-09-152-059-112	Sequence 112, App
295	14	0.3	14	1	US-09-152-059-113	Sequence 113, App
c 296	14	0.3	14	1	US-09-152-059-114	Sequence 114, App
c 297	14	0.3	14	1	US-09-152-059-115	Sequence 115, App
298	14	0.3	14	1	US-09-152-059-117	Sequence 117, App
c 299	14	0.3	14	1	US-09-152-059-118	Sequence 118, App
c 300	14	0.3	14	1	US-09-152-059-119	Sequence 119, App
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c 302	14	0.3	14	1	US-09-152-059-121	Sequence 121, App
c 303	14	0.3	14	1	US-09-152-059-122	Sequence 122, App
304	14	0.3	14	1	US-09-152-059-123	Sequence 123, App
c 305	14	0.3	14	1	US-09-152-059-124	Sequence 124, App
c 306	14	0.3	14	1	US-09-152-059-125	Sequence 125, App
307	14	0.3	14	1	US-09-152-059-126	Sequence 126, App
c 308	14	0.3	14	1	US-09-152-059-127	Sequence 127, App
c 309	14	0.3	14	1	US-09-152-059-128	Sequence 128, App
310	14	0.3	14	1	US-09-152-059-129	Sequence 129, App
c 311	14	0.3	14	1	US-09-152-059-130	Sequence 130, App
c 312	14	0.3	14	1	US-09-152-059-131	Sequence 131, App
313	14	0.3	14	1	US-09-152-059-132	Sequence 132, App
c 314	14	0.3	14	1	US-09-152-059-133	Sequence 133, App
c 315	14	0.3	14	1	US-09-152-059-134	Sequence 134, App
316	14	0.3	14	1	US-09-152-059-135	Sequence 135, App
c 317	14	0.3	14	1	US-09-152-059-136	Sequence 136, App
c 318	14	0.3	14	1	US-09-152-059-137	Sequence 137, App
319	14	0.3	14	1	US-09-152-059-138	Sequence 138, App
c 320	14	0.3	14	1	US-09-152-059-139	Sequence 139, App
c 321	14	0.3	14	1	US-09-152-059-140	Sequence 140, App
322	14	0.3	14	1	US-09-152-059-141	Sequence 141, App
c 323	14	0.3	14	1	US-09-152-059-142	Sequence 142, App
c 324	14	0.3	14	1	US-09-152-059-143	Sequence 143, App
325	14	0.3	14	1	US-09-152-059-144	Sequence 144, App
c 326	14	0.3	14	1	US-09-152-059-145	Sequence 145, App
c 327	14	0.3	14	1	US-09-152-059-146	Sequence 146, App
328	14	0.3	14	1	US-09-859-736-7	Sequence 7, Appli
329	14	0.3	14	1	5453496-4	Patent No. 5453496
330	14	0.3	14	1	5453496-4	Patent No. 5453496
c 331	14	0.3	14	1	5453496-5	Patent No. 5453496
c 332	14	0.3	14	1	5453496-5	Patent No. 5453496
c 333	14	0.3	15	1	US-08-452-196A-3	Sequence 3, Appli
c 334	14	0.3	15	1	US-08-452-196A-4	Sequence 4, Appli
335	14	0.3	15	1	US-08-292-620A-360	Sequence 360, App
336	14	0.3	15	1	US-08-292-620A-363	Sequence 363, App
c 337	14	0.3	15	1	US-08-585-684B-639	Sequence 639, App
c 338	14	0.3	15	1	US-08-585-684B-640	Sequence 640, App
c 339	14	0.3	15	1	US-08-863-639A-7	Sequence 7, Appli
340	14	0.3	15	1	US-08-832-021-49	Sequence 49, Appl
341	14	0.3	15	1	US-08-832-021-50	Sequence 50, Appl
342	14	0.3	15	1	US-08-832-021-52	Sequence 52, Appl
343	14	0.3	15	1	US-09-071-845-360	Sequence 360, App
344	14	0.3	15	1	US-09-071-845-363	Sequence 363, App
c 345	14	0.3	15	1	US-09-038-073-639	Sequence 639, App
c 346	14	0.3	15	1	US-09-038-073-640	Sequence 640, App
347	14	0.3	15	1	US-09-475-947A-158	Sequence 158, App
348	14	0.3	15	1	US-09-344-624-28	Sequence 28, Appl
c 349	14	0.3	16	1	US-08-284-484A-4	Sequence 4, Appli
350	14	0.3	17	1	US-08-584-040-2553	Sequence 2553, Ap
351	14	0.3	17	1	US-09-371-772B-1077	Sequence 1077, Ap
352	14	0.3	17	1	US-09-685-664B-1077	Sequence 1077, Ap
c 353	14	0.3	17	1	US-09-434-131A-12	Sequence 12, Appl
c 354	13.8	0.3	17	1	US-08-584-040-2552	Sequence 2552, Ap
c 355	13.8	0.3	17	1	US-09-475-947A-118	Sequence 118, App
c 356	13.8	0.3	17	1	US-09-371-772B-1076	Sequence 1076, Ap
c 357	13.8	0.3	17	1	US-09-685-664B-1076	Sequence 1076, Ap
c 358	13.8	0.3	17	1	US-08-242-664-34	Sequence 34, Appl
c 359	13.8	0.3	17	1	US-08-233-130A-10	Sequence 10, Appl
360	13.8	0.3	17	1	US-08-233-130A-11	Sequence 11, Appl
361	13.8	0.3	17	1	US-08-390-850-496	Sequence 496, App
c 362	13.8	0.3	17	1	US-08-373-124A-172	Sequence 172, App
c 363	13.8	0.3	17	1	US-08-373-124A-174	Sequence 174, App
c 364	13.8	0.3	17	1	US-08-373-124A-1062	Sequence 1062, Ap
c 365	13.8	0.3	17	1	US-08-484-138-34	Sequence 34, Appl
366	13.8	0.3	17	1	US-08-435-634-496	Sequence 496, App
367	13.8	0.3	17	1	US-08-758-306-271	Sequence 271, App
368	13.8	0.3	17	1	US-08-758-306-1015	Sequence 1015, Ap
c 369	13.8	0.3	17	1	US-08-435-628-172	Sequence 172, App
c 370	13.8	0.3	17	1	US-08-435-628-174	Sequence 174, App
c 371	13.8	0.3	17	1	US-08-435-628-1062	Sequence 1062, Ap
372	13.8	0.3	17	1	US-08-173-489C-2	Sequence 2, Appli
c 373	13.8	0.3	17	1	US-08-849-021-3	Sequence 3, Appli
c 374	13.8	0.3	17	1	US-08-849-021-4	Sequence 4, Appli
375	13.8	0.3	17	1	US-08-849-021-5	Sequence 5, Appli
376	13.8	0.3	17	1	US-08-849-021-6	Sequence 6, Appli
377	13.8	0.3	17	1	US-08-985-162-813	Sequence 813, App
378	13.8	0.3	17	1	US-08-998-099-68	Sequence 68, Appl
379	13.8	0.3	17	1	US-08-584-040-2022	Sequence 2022, Ap
c 380	13.8	0.3	17	1	US-08-584-040-2555	Sequence 2555, Ap
381	13.8	0.3	17	1	US-08-584-040-3981	Sequence 3981, Ap
382	13.8	0.3	17	1	US-08-584-040-6075	Sequence 6075, Ap
c 383	13.8	0.3	17	1	US-08-679-645-882	Sequence 882, App
384	13.8	0.3	17	1	US-09-474-432B-724	Sequence 724, App
385	13.8	0.3	17	1	US-09-371-772B-567	Sequence 567, App
c 386	13.8	0.3	17	1	US-09-371-772B-1079	Sequence 1079, Ap
387	13.8	0.3	17	1	US-09-371-772B-1748	Sequence 1748, Ap
388	13.8	0.3	17	1	US-09-371-772B-2912	Sequence 2912, Ap
389	13.8	0.3	17	1	US-09-476-387-723	Sequence 723, App
390	13.8	0.3	17	1	US-09-401-063-813	Sequence 813, App
c 391	13.8	0.3	17	1	US-09-827-998-193	Sequence 193, App
c 392	13.8	0.3	17	1	US-09-827-998-194	Sequence 194, App
c 393	13.8	0.3	17	1	US-09-827-998-196	Sequence 196, App
c 394	13.8	0.3	17	1	US-09-827-998-197	Sequence 197, App
395	13.8	0.3	17	1	US-09-827-998-746	Sequence 746, App
396	13.8	0.3	17	1	US-09-827-998-747	Sequence 747, App
397	13.8	0.3	17	1	US-09-827-998-748	Sequence 748, App
398	13.8	0.3	17	1	US-09-827-998-753	Sequence 753, App

c 399	13.8	0.3	17	1	US-09-866-108A-73	Sequence 73, Appl
400	13.8	0.3	17	1	US-09-866-108A-774	Sequence 774, App
c 401	13.8	0.3	17	1	US-09-866-108A-1009	Sequence 1009, Ap
c 402	13.8	0.3	17	1	US-09-866-108A-7934	Sequence 7934, Ap
403	13.8	0.3	17	1	US-09-404-912-169	Sequence 169, App
404	13.8	0.3	17	1	US-09-685-664B-567	Sequence 567, App
c 405	13.8	0.3	17	1	US-09-685-664B-1079	Sequence 1079, Ap
406	13.8	0.3	17	1	US-09-685-664B-1748	Sequence 1748, Ap
407	13.8	0.3	17	1	US-09-685-664B-2912	Sequence 2912, Ap
408	13.8	0.3	17	1	US-09-596-141C-34	Sequence 34, Appl
409	13.8	0.3	17	1	US-09-595-526C-34	Sequence 34, Appl
410	13.8	0.3	17	1	PCT-US92-01015-7	Sequence 7, Appli
c 411	13.8	0.3	17	1	PCT-US95-06379-34	Sequence 34, Appl
c 412	13.8	0.3	18	1	US-09-725-265-17	Sequence 17, Appl
c 413	13.8	0.3	18	1	US-09-556-127-17	Sequence 17, Appl
414	13.8	0.3	18	1	US-09-437-076-1	Sequence 1, Appli
415	13.8	0.3	18	1	US-09-904-744-1	Sequence 1, Appli
c 416	13.8	0.3	20	1	US-09-965-599-4	Sequence 4, Appli
417	13.6	0.3	20	1	US-09-780-045-110	Sequence 110, App
418	13.6	0.3	20	1	US-09-228-942-7	Sequence 7, Appli
c 419	13.4	0.3	15	1	US-08-479-248-6	Sequence 6, Appli
420	13.4	0.3	15	1	US-08-479-248-12	Sequence 12, Appl
421	13.4	0.3	15	1	US-08-334-847-57	Sequence 57, Appl
c 422	13.4	0.3	15	1	US-08-334-847-516	Sequence 516, App
c 423	13.4	0.3	15	1	US-08-311-486C-33	Sequence 33, Appl
c 424	13.4	0.3	15	1	US-08-311-486C-674	Sequence 674, App
425	13.4	0.3	15	1	US-08-292-620A-359	Sequence 359, App
426	13.4	0.3	15	1	US-08-585-684B-666	Sequence 666, App
427	13.4	0.3	15	1	US-08-893-204C-2	Sequence 2, Appli
428	13.4	0.3	15	1	US-08-832-021-27	Sequence 27, Appl
c 429	13.4	0.3	15	1	US-08-832-021-33	Sequence 33, Appl
430	13.4	0.3	15	1	US-08-832-021-39	Sequence 39, Appl
431	13.4	0.3	15	1	US-08-832-021-43	Sequence 43, Appl
432	13.4	0.3	15	1	US-08-832-021-47	Sequence 47, Appl
433	13.4	0.3	15	1	US-08-832-021-55	Sequence 55, Appl
434	13.4	0.3	15	1	US-08-832-021-56	Sequence 56, Appl
435	13.4	0.3	15	1	US-08-832-021-59	Sequence 59, Appl
436	13.4	0.3	15	1	US-08-832-021-60	Sequence 60, Appl
437	13.4	0.3	15	1	US-08-832-021-63	Sequence 63, Appl
438	13.4	0.3	15	1	US-08-832-021-64	Sequence 64, Appl
439	13.4	0.3	15	1	US-09-071-845-359	Sequence 359, App
440	13.4	0.3	15	1	US-09-038-073-666	Sequence 666, App
441	13.4	0.3	15	1	US-09-475-947A-164	Sequence 164, App
c 442	13.4	0.3	15	1	US-09-234-245-17	Sequence 17, Appl
443	13.4	0.3	16	1	US-09-124-238A-4	Sequence 4, Appli
444	13.4	0.3	16	1	US-09-411-628-1	Sequence 1, Appli
445	13.4	0.3	16	1	US-09-331-930A-4	Sequence 4, Appli
446	13.4	0.3	16	1	US-09-721-975-4	Sequence 4, Appli
447	13.4	0.3	16	1	US-08-894-251A-5	Sequence 5, Appli
448	13.4	0.3	16	1	US-08-894-251A-7	Sequence 7, Appli
449	13.4	0.3	16	1	US-09-300-958A-56	Sequence 56, Appl
450	13.4	0.3	16	1	US-09-300-958A-57	Sequence 57, Appl
451	13.4	0.3	16	1	US-09-300-958A-58	Sequence 58, Appl
452	13.4	0.3	16	1	US-09-300-958A-83	Sequence 83, Appl
453	13.4	0.3	16	1	US-09-300-958A-84	Sequence 84, Appl
454	13.4	0.3	16	1	US-09-300-958A-85	Sequence 85, Appl
455	13.4	0.3	16	1	US-09-986-621-4	Sequence 4, Appli
456	13.4	0.3	16	1	US-09-371-772B-6072	Sequence 6072, Ap
457	13.4	0.3	16	1	US-09-527-972-15	Sequence 15, Appl
458	13.4	0.3	16	1	US-09-527-972-16	Sequence 16, Appl
459	13.4	0.3	16	1	US-09-527-972-17	Sequence 17, Appl
c 460	13.4	0.3	16	1	US-09-479-005A-437	Sequence 437, App
461	13.4	0.3	16	1	US-09-479-005A-508	Sequence 508, App
462	13.4	0.3	16	1	US-10-174-794-1	Sequence 1, Appli
463	13.4	0.3	16	1	US-09-949-271A-5	Sequence 5, Appli
464	13.4	0.3	16	1	US-09-949-271A-7	Sequence 7, Appli
465	13.4	0.3	16	1	US-09-949-476A-5	Sequence 5, Appli
466	13.4	0.3	16	1	US-09-949-476A-7	Sequence 7, Appli
c 467	13.4	0.3	16	1	US-09-563-794B-137	Sequence 137, App
c 468	13.4	0.3	16	1	US-10-124-038-42	Sequence 42, Appl
469	13.4	0.3	16	1	US-10-261-821-11	Sequence 11, Appl
470	13.4	0.3	16	1	US-10-261-821-13	Sequence 13, Appl
471	13.4	0.3	17	1	US-08-373-124A-1062	Sequence 1062, Ap
472	13.4	0.3	17	1	US-08-435-628-1062	Sequence 1062, Ap
c 473	13.4	0.3	18	1	US-08-330-000-1	Sequence 1, Appli
c 474	13.4	0.3	18	1	US-08-965-908-1	Sequence 1, Appli
c 475	13.4	0.3	19	1	US-09-371-307-85	Sequence 85, Appl
476	13.2	0.3	14	1	US-08-494-577-10	Sequence 10, Appl
477	13.2	0.3	14	1	US-08-795-868-10	Sequence 10, Appl
478	13.2	0.3	14	1	US-09-303-069-10	Sequence 10, Appl
479	13.2	0.3	14	1	US-09-134-250-10	Sequence 10, Appl
480	13.2	0.3	14	1	US-09-300-958A-65	Sequence 65, Appl
c 481	13.2	0.3	18	1	US-08-621-914A-16	Sequence 16, Appl
482	13.2	0.3	18	1	US-08-346-429-3	Sequence 3, Appli
c 483	13.2	0.3	18	1	US-08-358-556A-12	Sequence 12, Appl
484	13.2	0.3	18	1	US-08-358-556A-18	Sequence 18, Appl
c 485	13.2	0.3	18	1	US-08-469-852A-4	Sequence 4, Appli
c 486	13.2	0.3	18	1	US-08-295-509B-4	Sequence 4, Appli
c 487	13.2	0.3	18	1	US-08-884-029-9	Sequence 9, Appli
488	13.2	0.3	18	1	US-08-941-445A-30	Sequence 30, Appl
c 489	13.2	0.3	18	1	US-09-637-751A-7	Sequence 7, Appli
c 490	13.2	0.3	18	1	US-09-545-225-9	Sequence 9, Appli
491	13.2	0.3	18	1	US-09-619-103-24	Sequence 24, Appl
c 492	13.2	0.3	18	1	US-09-370-541-14	Sequence 14, Appl
c 493	13.2	0.3	18	1	US-10-125-295-9	Sequence 9, Appli
494	13.2	0.3	18	1	US-09-803-263-6	Sequence 6, Appli
c 495	13.2	0.3	18	1	US-09-803-263-7	Sequence 7, Appli
c 496	13.2	0.3	18	1	US-09-994-311-7	Sequence 7, Appli
c 497	13.2	0.3	18	1	US-09-142-108C-28	Sequence 28, Appl
c 498	13.2	0.3	18	1	US-09-809-545A-84	Sequence 84, Appl
c 499	13.2	0.3	18	1	US-10-352-704-12	Sequence 12, Appl
500	13.2	0.3	18	1	US-10-352-704-18	Sequence 18, Appl
c 501	13.2	0.3	18	1	PCT-US94-05407-4	Sequence 4, Appli
c 502	13.2	0.3	20	1	US-08-482-918-32	Sequence 32, Appl
c 503	13.2	0.3	20	1	US-09-224-681-32	Sequence 32, Appl
c 504	13.2	0.3	20	1	US-08-336-728A-32	Sequence 32, Appl
c 505	13.2	0.3	20	1	US-09-635-251-32	Sequence 32, Appl
506	13.2	0.3	23	1	PCT-US94-05407-7	Sequence 7, Appli
c 507	13.2	0.3	23	1	PCT-US94-05407-8	Sequence 8, Appli
508	13	0.3	17	1	US-08-584-040-2554	Sequence 2554, Ap
509	13	0.3	17	1	US-09-371-772B-1078	Sequence 1078, Ap
510	13	0.3	17	1	US-09-685-664B-1078	Sequence 1078, Ap
c 511	12.8	0.3	17	1	US-09-129-603-4	Sequence 4, Appli
c 512	12.8	0.3	17	1	US-09-090-672B-107	Sequence 107, App
c 513	12.8	0.3	17	1	US-08-584-040-2549	Sequence 2549, Ap
c 514	12.8	0.3	17	1	US-09-371-772B-1073	Sequence 1073, Ap
c 515	12.8	0.3	17	1	US-09-685-664B-1073	Sequence 1073, Ap
c 516	12.8	0.3	17	1	US-08-584-040-2550	Sequence 2550, Ap
c 517	12.8	0.3	17	1	US-08-584-040-2551	Sequence 2551, Ap
c 518	12.8	0.3	17	1	US-09-371-772B-1074	Sequence 1074, Ap
c 519	12.8	0.3	17	1	US-09-371-772B-1075	Sequence 1075, Ap
c 520	12.8	0.3	17	1	US-09-685-664B-1074	Sequence 1074, Ap
c 521	12.8	0.3	17	1	US-09-685-664B-1075	Sequence 1075, Ap
c 522	12.8	0.3	17	1	US-08-373-124A-1060	Sequence 1060, Ap
c 523	12.8	0.3	17	1	US-08-435-628-1060	Sequence 1060, Ap
c 524	12.8	0.3	18	1	US-09-725-265-16	Sequence 16, Appl
c 525	12.8	0.3	18	1	US-09-556-127-16	Sequence 16, Appl
c 526	12.8	0.3	18	1	US-09-725-265-20	Sequence 20, Appl
c 527	12.8	0.3	18	1	US-09-556-127-20	Sequence 20, Appl
c 528	12.8	0.3	39	1	US-08-332-420-62	Sequence 62, Appl
529	12.4	0.3	15	1	US-08-452-196A-3	Sequence 3, Appli
c 530	12.4	0.3	15	1	US-08-292-620A-363	Sequence 363, App
c 531	12.4	0.3	15	1	US-09-071-845-363	Sequence 363, App
c 532	12.4	0.3	15	1	US-08-893-204C-2	Sequence 2, Appli
c 533	12.4	0.3	17	1	US-09-788-338-3	Sequence 3, Appli
c 534	12.4	0.3	17	1	US-09-300-958A-64	Sequence 64, Appl
c 535	12.4	0.3	17	1	US-09-090-672B-106	Sequence 106, App
c 536	12.4	0.3	17	1	US-09-090-672B-105	Sequence 105, App
c 537	12.4	0.3	17	1	US-08-937-067-17	Sequence 17, Appl
c 538	12.4	0.3	18	1	US-09-437-076-2	Sequence 2, Appli
c 539	12.4	0.3	18	1	US-09-904-744-2	Sequence 2, Appli
540	12.4	0.3	19	1	US-09-130-079-1	Sequence 1, Appli
c 541	12.2	0.3	17	1	US-08-851-843A-132	Sequence 132, App
c 542	12.2	0.3	17	1	US-09-250-075-5	Sequence 5, Appli
c 543	12.2	0.3	17	1	US-08-854-050-132	Sequence 132, App
c 544	12.2	0.3	17	1	US-09-430-323-132	Sequence 132, App

545	12.2	0.3	17	1	US-09-619-103-23	Sequence 23, Appl
c 546	12.2	0.3	17	1	US-09-726-096A-5	Sequence 5, Appli
c 547	12.2	0.3	17	1	US-09-766-253-132	Sequence 132, App
c 548	12.2	0.3	17	1	US-08-584-040-2548	Sequence 2548, Ap
c 549	12.2	0.3	17	1	US-09-371-772B-1072	Sequence 1072, Ap
c 550	12.2	0.3	17	1	US-09-685-664B-1072	Sequence 1072, Ap
551	12.2	0.3	17	1	US-08-233-130A-10	Sequence 10, Appl
c 552	12.2	0.3	17	1	US-08-233-130A-11	Sequence 11, Appl
c 553	12.2	0.3	18	1	US-09-637-751A-5	Sequence 5, Appli
c 554	12.2	0.3	18	1	US-09-994-311-5	Sequence 5, Appli
c 555	12.2	0.3	18	1	US-09-142-108C-29	Sequence 29, Appl
c 556	12.2	0.3	18	1	PCT-US91-03680-73	Sequence 73, Appl
c 557	12.2	0.3	18	1	US-09-142-108C-27	Sequence 27, Appl
c 558	12.2	0.3	18	1	PCT-US91-03680-74	Sequence 74, Appl
c 559	12.2	0.3	18	1	US-09-725-265-15	Sequence 15, Appl
c 560	12.2	0.3	18	1	US-09-725-265-19	Sequence 19, Appl
c 561	12.2	0.3	18	1	US-09-556-127-15	Sequence 15, Appl
c 562	12.2	0.3	18	1	US-09-556-127-19	Sequence 19, Appl
563	12	0.3	15	1	US-08-832-021-33	Sequence 33, Appl
c 564	12	0.3	17	1	US-09-390-324B-2	Sequence 2, Appli
c 565	12	0.3	17	1	US-10-015-593-2	Sequence 2, Appli
566	12	0.3	17	1	US-08-584-040-2555	Sequence 2555, Ap
567	12	0.3	17	1	US-09-371-772B-1079	Sequence 1079, Ap
568	12	0.3	17	1	US-09-685-664B-1079	Sequence 1079, Ap
569	12	0.3	19	1	US-10-103-614A-4	Sequence 4, Appli
570	12	0.3	20	1	US-09-120-853-4	Sequence 4, Appli
571	11.8	0.3	15	1	US-08-452-196A-6	Sequence 6, Appli
c 572	11.8	0.3	15	1	US-07-971-978-1	Sequence 1, Appli
573	11.8	0.3	15	1	US-08-756-728A-2	Sequence 2, Appli
c 574	11.8	0.3	15	1	US-08-663-918-3	Sequence 3, Appli
575	11.8	0.3	15	1	US-08-663-918-4	Sequence 4, Appli
c 576	11.8	0.3	15	1	US-08-292-620A-361	Sequence 361, App
c 577	11.8	0.3	15	1	US-08-292-620A-362	Sequence 362, App
c 578	11.8	0.3	15	1	US-08-771-789-3	Sequence 3, Appli
579	11.8	0.3	15	1	US-08-771-789-4	Sequence 4, Appli
c 580	11.8	0.3	15	1	US-08-358-556A-10	Sequence 10, Appl
581	11.8	0.3	15	1	US-08-358-556A-16	Sequence 16, Appl
c 582	11.8	0.3	15	1	US-08-922-170B-5	Sequence 5, Appli
583	11.8	0.3	15	1	US-08-863-639A-5	Sequence 5, Appli
c 584	11.8	0.3	15	1	US-08-863-639A-9	Sequence 9, Appli
c 585	11.8	0.3	15	1	US-08-693-831-1	Sequence 1, Appli
c 586	11.8	0.3	15	1	US-09-183-619-4	Sequence 4, Appli
c 587	11.8	0.3	15	1	US-09-071-845-361	Sequence 361, App
c 588	11.8	0.3	15	1	US-09-071-845-362	Sequence 362, App
589	11.8	0.3	15	1	US-09-167-375-1	Sequence 1, Appli
c 590	11.8	0.3	15	1	US-08-150-156A-19	Sequence 19, Appl
591	11.8	0.3	15	1	US-08-150-156A-20	Sequence 20, Appl
c 592	11.8	0.3	15	1	US-08-108-591B-17	Sequence 17, Appl
593	11.8	0.3	15	1	US-08-108-591B-18	Sequence 18, Appl
594	11.8	0.3	15	1	US-09-619-103-21	Sequence 21, Appl
c 595	11.8	0.3	15	1	US-09-300-958A-68	Sequence 68, Appl
c 596	11.8	0.3	15	1	US-08-988-024C-9	Sequence 9, Appli
c 597	11.8	0.3	15	1	US-09-435-739-5	Sequence 5, Appli
c 598	11.8	0.3	15	1	US-10-091-231-2	Sequence 2, Appli
c 599	11.8	0.3	15	1	US-09-930-218-5	Sequence 5, Appli
c 600	11.8	0.3	15	1	US-08-468-719A-17	Sequence 17, Appl
601	11.8	0.3	15	1	US-08-468-719A-18	Sequence 18, Appl
c 602	11.8	0.3	15	1	US-08-462-977B-17	Sequence 17, Appl
603	11.8	0.3	15	1	US-08-462-977B-18	Sequence 18, Appl
c 604	11.8	0.3	15	1	US-09-988-113-5	Sequence 5, Appli
c 605	11.8	0.3	15	1	US-10-352-704-10	Sequence 10, Appl
606	11.8	0.3	15	1	US-10-352-704-16	Sequence 16, Appl
c 607	11.8	0.3	15	1	US-09-475-947A-164	Sequence 164, App
c 608	11.8	0.3	16	1	US-07-971-978-36	Sequence 36, Appl
c 609	11.8	0.3	16	1	US-07-971-978-42	Sequence 42, Appl
c 610	11.8	0.3	16	1	US-07-971-978-60	Sequence 60, Appl
c 611	11.8	0.3	16	1	US-08-415-370-2	Sequence 2, Appli
c 612	11.8	0.3	16	1	US-08-687-551-15	Sequence 15, Appl
c 613	11.8	0.3	16	1	US-09-141-764-2	Sequence 2, Appli
614	11.8	0.3	16	1	US-08-851-843A-131	Sequence 131, App
615	11.8	0.3	16	1	US-08-854-050-131	Sequence 131, App
616	11.8	0.3	16	1	US-09-430-323-131	Sequence 131, App
c 617	11.8	0.3	16	1	US-09-507-345A-2	Sequence 2, Appli
c 618	11.8	0.3	16	1	US-09-507-345A-3	Sequence 3, Appli
c 619	11.8	0.3	16	1	US-09-507-345A-4	Sequence 4, Appli
c 620	11.8	0.3	16	1	US-09-507-345A-5	Sequence 5, Appli
c 621	11.8	0.3	16	1	US-09-507-345A-6	Sequence 6, Appli
c 622	11.8	0.3	16	1	US-09-507-345A-7	Sequence 7, Appli
c 623	11.8	0.3	16	1	US-09-507-345A-8	Sequence 8, Appli
624	11.8	0.3	16	1	US-09-619-103-22	Sequence 22, Appl
c 625	11.8	0.3	16	1	US-09-739-928-2	Sequence 2, Appli
c 626	11.8	0.3	16	1	US-09-739-928-3	Sequence 3, Appli
c 627	11.8	0.3	16	1	US-09-739-928-4	Sequence 4, Appli
c 628	11.8	0.3	16	1	US-09-739-928-5	Sequence 5, Appli
c 629	11.8	0.3	16	1	US-09-739-928-6	Sequence 6, Appli
c 630	11.8	0.3	16	1	US-09-739-928-7	Sequence 7, Appli
c 631	11.8	0.3	16	1	US-09-739-928-8	Sequence 8, Appli
632	11.8	0.3	16	1	US-09-958-610A-1	Sequence 1, Appli
c 633	11.8	0.3	16	1	US-09-895-585-9	Sequence 9, Appli
c 634	11.8	0.3	16	1	US-09-152-059-70	Sequence 70, Appl
635	11.8	0.3	16	1	US-09-766-253-131	Sequence 131, App
c 636	11.8	0.3	16	1	US-08-087-387-6	Sequence 6, Appli
c 637	11.8	0.3	16	1	US-08-455-627-6	Sequence 6, Appli
c 638	11.8	0.3	16	1	US-08-461-271-6	Sequence 6, Appli
c 639	11.8	0.3	16	1	US-08-713-685A-6	Sequence 6, Appli
c 640	11.8	0.3	16	1	US-08-689-856-6	Sequence 6, Appli
c 641	11.8	0.3	16	1	US-09-070-477-6	Sequence 6, Appli
c 642	11.8	0.3	17	1	US-08-821-827C-30	Sequence 30, Appl
c 643	11.8	0.3	17	1	US-09-290-202B-30	Sequence 30, Appl
c 644	11.8	0.3	17	1	US-09-300-958A-63	Sequence 63, Appl
645	11.8	0.3	17	1	US-08-373-124A-2149	Sequence 2149, Ap
646	11.8	0.3	17	1	US-08-435-628-2149	Sequence 2149, Ap
c 647	11.8	0.3	18	1	US-09-637-751A-6	Sequence 6, Appli
c 648	11.8	0.3	18	1	US-09-994-311-6	Sequence 6, Appli
c 649	11.6	0.3	14	1	US-09-300-958A-65	Sequence 65, Appl
650	11.6	0.3	15	1	US-08-882-649A-7	Sequence 7, Appli
c 651	11.6	0.3	16	1	US-08-882-649A-8	Sequence 8, Appli
652	11.6	0.3	18	1	US-09-143-212-64	Sequence 64, Appl
653	11.6	0.3	19	1	US-08-850-880-10	Sequence 10, Appl
654	11.6	0.3	19	1	US-08-944-916-10	Sequence 10, Appl
655	11.6	0.3	19	1	US-09-159-363-2	Sequence 2, Appli
656	11.6	0.3	19	1	US-09-635-969-6	Sequence 6, Appli
657	11.6	0.3	19	1	US-09-632-021-4	Sequence 4, Appli
658	11.6	0.3	19	1	US-09-272-432A-10	Sequence 10, Appl
c 659	11.6	0.3	19	1	US-09-350-852A-3	Sequence 3, Appli
660	11.6	0.3	19	1	5212080-3	Patent No. 5212080
661	11.6	0.3	19	1	5212080-3	Patent No. 5212080
662	11.4	0.3	14	1	US-08-173-489C-75	Sequence 75, Appl
c 663	11.4	0.3	14	1	US-08-173-489C-76	Sequence 76, Appl
c 664	11.4	0.3	14	1	US-09-462-569B-1	Sequence 1, Appli
665	11.4	0.3	14	1	US-09-619-103-20	Sequence 20, Appl
c 666	11.4	0.3	14	1	US-09-152-059-65	Sequence 65, Appl
c 667	11.4	0.3	14	1	US-09-152-059-66	Sequence 66, Appl
c 668	11.4	0.3	14	1	US-09-152-059-67	Sequence 67, Appl
c 669	11.4	0.3	14	1	US-09-152-059-68	Sequence 68, Appl
c 670	11.4	0.3	14	1	US-09-152-059-80	Sequence 80, Appl
671	11.4	0.3	14	1	US-09-152-059-81	Sequence 81, Appl
672	11.4	0.3	14	1	US-09-152-059-82	Sequence 82, Appl
c 673	11.4	0.3	14	1	US-09-152-059-83	Sequence 83, Appl
674	11.4	0.3	14	1	US-09-152-059-84	Sequence 84, Appl
675	11.4	0.3	14	1	US-09-152-059-85	Sequence 85, Appl
c 676	11.4	0.3	14	1	US-09-152-059-86	Sequence 86, Appl
677	11.4	0.3	14	1	US-09-152-059-87	Sequence 87, Appl
678	11.4	0.3	14	1	US-09-152-059-88	Sequence 88, Appl
c 679	11.4	0.3	14	1	US-09-152-059-89	Sequence 89, Appl
680	11.4	0.3	14	1	US-09-152-059-90	Sequence 90, Appl
681	11.4	0.3	14	1	US-09-152-059-91	Sequence 91, Appl
c 682	11.4	0.3	14	1	US-09-152-059-92	Sequence 92, Appl
683	11.4	0.3	14	1	US-09-152-059-93	Sequence 93, Appl
684	11.4	0.3	14	1	US-09-152-059-94	Sequence 94, Appl
685	11.4	0.3	14	1	US-09-152-059-96	Sequence 96, Appl
686	11.4	0.3	14	1	US-09-152-059-97	Sequence 97, Appl
c 687	11.4	0.3	14	1	US-09-152-059-98	Sequence 98, Appl
688	11.4	0.3	14	1	US-09-152-059-99	Sequence 99, Appl
689	11.4	0.3	14	1	US-09-152-059-100	Sequence 100, App
c 690	11.4	0.3	14	1	US-09-152-059-101	Sequence 101, App

691	11.4	0.3	14	1	US-09-152-059-102	Sequence 102, App
692	11.4	0.3	14	1	US-09-152-059-103	Sequence 103, App
c 693	11.4	0.3	14	1	US-09-152-059-104	Sequence 104, App
694	11.4	0.3	14	1	US-09-152-059-105	Sequence 105, App
695	11.4	0.3	14	1	US-09-152-059-106	Sequence 106, App
c 696	11.4	0.3	14	1	US-09-152-059-107	Sequence 107, App
697	11.4	0.3	14	1	US-09-152-059-108	Sequence 108, App
698	11.4	0.3	14	1	US-09-152-059-109	Sequence 109, App
c 699	11.4	0.3	14	1	US-09-152-059-110	Sequence 110, App
700	11.4	0.3	14	1	US-09-152-059-111	Sequence 111, App
701	11.4	0.3	14	1	US-09-152-059-112	Sequence 112, App
c 702	11.4	0.3	14	1	US-09-152-059-113	Sequence 113, App
703	11.4	0.3	14	1	US-09-152-059-114	Sequence 114, App
704	11.4	0.3	14	1	US-09-152-059-115	Sequence 115, App
c 705	11.4	0.3	14	1	US-09-152-059-117	Sequence 117, App
706	11.4	0.3	14	1	US-09-152-059-118	Sequence 118, App
707	11.4	0.3	14	1	US-09-152-059-119	Sequence 119, App
c 708	11.4	0.3	14	1	US-09-152-059-120	Sequence 120, App
709	11.4	0.3	14	1	US-09-152-059-121	Sequence 121, App
710	11.4	0.3	14	1	US-09-152-059-122	Sequence 122, App
c 711	11.4	0.3	14	1	US-09-152-059-123	Sequence 123, App
712	11.4	0.3	14	1	US-09-152-059-124	Sequence 124, App
713	11.4	0.3	14	1	US-09-152-059-125	Sequence 125, App
c 714	11.4	0.3	14	1	US-09-152-059-126	Sequence 126, App
715	11.4	0.3	14	1	US-09-152-059-127	Sequence 127, App
716	11.4	0.3	14	1	US-09-152-059-128	Sequence 128, App
c 717	11.4	0.3	14	1	US-09-152-059-129	Sequence 129, App
718	11.4	0.3	14	1	US-09-152-059-130	Sequence 130, App
719	11.4	0.3	14	1	US-09-152-059-131	Sequence 131, App
c 720	11.4	0.3	14	1	US-09-152-059-132	Sequence 132, App
721	11.4	0.3	14	1	US-09-152-059-133	Sequence 133, App
722	11.4	0.3	14	1	US-09-152-059-134	Sequence 134, App
c 723	11.4	0.3	14	1	US-09-152-059-135	Sequence 135, App
724	11.4	0.3	14	1	US-09-152-059-136	Sequence 136, App
725	11.4	0.3	14	1	US-09-152-059-137	Sequence 137, App
c 726	11.4	0.3	14	1	US-09-152-059-138	Sequence 138, App
727	11.4	0.3	14	1	US-09-152-059-139	Sequence 139, App
728	11.4	0.3	14	1	US-09-152-059-140	Sequence 140, App
c 729	11.4	0.3	14	1	US-09-152-059-141	Sequence 141, App
730	11.4	0.3	14	1	US-09-152-059-142	Sequence 142, App
731	11.4	0.3	14	1	US-09-152-059-143	Sequence 143, App
c 732	11.4	0.3	14	1	US-09-152-059-144	Sequence 144, App
733	11.4	0.3	14	1	US-09-152-059-145	Sequence 145, App
734	11.4	0.3	14	1	US-09-152-059-146	Sequence 146, App
c 735	11.4	0.3	14	1	US-09-859-736-7	Sequence 7, Appli
c 736	11.4	0.3	14	1	5453496-4	Patent No. 5453496
c 737	11.4	0.3	14	1	5453496-4	Patent No. 5453496
738	11.4	0.3	14	1	5453496-5	Patent No. 5453496
739	11.4	0.3	14	1	5453496-5	Patent No. 5453496

ALIGNMENTS

```
RESULT 1
US-08-332-420-62
; Sequence 62, Application US/08332420
; Patent No. 5744300
;  GENERAL INFORMATION:
;    APPLICANT:  Maarten H.K. Linskens, et al.
;    TITLE OF INVENTION:  METHODS AND REAGENTS FOR THE
;    TITLE OF INVENTION:  IDENTIFICATION AND REGULATION
;    TITLE OF INVENTION:  OF SENESCENCE-RELATED GENES
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,420
;      FILING DATE:  October 31, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/235,180
;      FILING DATE:  April 29, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/041
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-332-420-62

  Query Match             0.9%;  Score 39;  DB 1;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 AGATGATGATGTTAACCCATTCCAGTACAGTATTCTTTT 39


RESULT 2
US-09-380-262B-2/c
; Sequence 2, Application US/09380262B
; Patent No. 6448055
; GENERAL INFORMATION:
;  APPLICANT: SHIMIZU, Sakayu
;  APPLICANT:  KOBAYASHI, Michihiko
;  TITLE OF INVENTION: (9-DESATURASE GENE
;  FILE REFERENCE: 9437/259314
;  CURRENT APPLICATION NUMBER: US/09/380,262B
;  CURRENT FILING DATE:  1999-08-27
;  PRIOR APPLICATION NUMBER: JP 44303/1997
;  PRIOR FILING DATE: 1997-02-27
;  PRIOR APPLICATION NUMBER: PCT/JP98/00819
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Mortierella alpina
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: n is located at positions (18) and (24)
;   OTHER INFORMATION: primer DNA for PCR; y is c or t; n is a or g or c or t;
;   OTHER INFORMATION: r is a or g; w is a or t
US-09-380-262B-2

  Query Match             0.5%;  Score 20.8;  DB 1;  Length 26;
  Best Local Similarity   61.5%;  Pred. No. 5.2;
  Matches   16;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         26 GGNGARGGNTWYCAYAAYTWYCAYCA 1


RESULT 3
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Db          4 UUUUUUUUUUUUUUUGGGGT 23


RESULT 7
US-08-203-198-3
; Sequence 3, Application US/08203198
; Patent No. 5512462
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Suzanne
;    TITLE OF INVENTION:  Methods and Reagents for the Polymerase
;    TITLE OF INVENTION:  Chain Reaction Amplification of Long DNA Sequences
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/203,198
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry Ph.D., Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8894
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-203-198-3

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 34;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2269 CTCTTTCTGCTCTGCCATC 2287
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Db          2 CTCTTTCCGCTCTGCCATC 20


RESULT 8
US-08-128-011-4
; Sequence 4, Application US/08128011
; Patent No. 5523389
;  GENERAL INFORMATION:
;    APPLICANT:  Ecker, David J.
;    APPLICANT:  Wyatt, Jacqueline R.
;    APPLICANT:  Imbach, Jean Louis
;    TITLE OF INVENTION:  Inhibitors of Human Immunodeficiency
;    TITLE OF INVENTION:  Virus
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and No. 5523389ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/128,011
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaumond, Rebecca R.
;      REGISTRATION NUMBER:  35,152
;      REFERENCE/DOCKET NUMBER:  ISIS-1161
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-128-011-4

  Query Match             0.4%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 35;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 TTTTTTTTTTTTTGGGGTT 19


RESULT 9
US-08-403-888A-142
; Sequence 142, Application US/08403888A
; Patent No. 5952490
;  GENERAL INFORMATION:
;    APPLICANT:  Hanecak et al.
;    TITLE OF INVENTION:  Oligonucleotides Having A Conserved G4 Core
;    TITLE OF INVENTION:  Sequence
;    NUMBER OF SEQUENCES:  146
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,888A
;      FILING DATE:  12-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/954,185
;      FILING DATE:  29-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul K. Legaard
;      REGISTRATION NUMBER:  38,534
;      REFERENCE/DOCKET NUMBER:  ISIS-1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  142:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21
;      TYPE:  nucleic acid
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US-09-780-045-110/c
; Sequence 110, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT E
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0130
;  CURRENT APPLICATION NUMBER: US/09/780,045
;  CURRENT FILING DATE:  2001-02-09
;  NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-045-110

  Query Match             0.5%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2391 AAAATATATATACATATATA 2410
             ||||||||||||||||||||
Db         20 AAAATATATATACATATATA 1


RESULT 4
US-09-422-978-11421/c
; Sequence 11421, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11421
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..21
;   OTHER INFORMATION: downstream amplification primer 99-5747 for SEQ 3556, in compleme
US-09-422-978-11421

  Query Match             0.4%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 10;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4688 CACTGACTTGCTGTGTGACCC 4708
             || ||||||||||||||||||
Db         21 CATTGACTTGCTGTGTGACCC 1


RESULT 5
PCT-US94-05407-7/c
; Sequence 7, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-7

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 23;
  Best Local Similarity   95.0%;  Pred. No. 21;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4501 TTTTTTTTTTTTTTTGGGTT 4520
             ||||||||||||||||||| |
Db         20 TTTTTTTTTTTTTTTGGGGT 1


RESULT 6
PCT-US94-05407-8
; Sequence 8, Application PC/TUS9405407
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "NUCLEIC ACID TAGGED IMMUNOASSAY"
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  Suite 1200, 127 Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05407
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/061,694
;      FILING DATE:  13-MAY-1993
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
PCT-US94-05407-8

  Query Match             0.4%;  Score 18.4;  DB 1;  Length 23;
  Best Local Similarity   20.0%;  Pred. No. 21;
  Matches    4;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;
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